

	423387	AJ012074		vasoactive intestinal peptide receptor 1	2.57
	442681	AI809182	Hs.130907	ESTs	2.57
	408652	R43409	Hs.6829	Homo sapiens mRNA for KIAA1644 protein,	2.56
5	402217			C19001662:gij6753872[ref]NP_034345.1[i]	2.56
	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.56
	455674	BE065941		gb:RC3-BT0319-100100-012-d12 BT0319 Homo	2.56
	457831	AA706937	Hs.120802	ESTs, Moderately similar to A26641 Na?ex	2.56
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.55
10	458648	AW444551	Hs.35380	x 001 protein	2.55
	456663	BE251104	Hs.113052	RNA cyclase homolog	2.54
	440178	AW502463	Hs.196521	ESTs	2.53
	457139	AI557280	Hs.184270	capping protein (actin filament) muscle	2.52
	405857			Target Exon	2.51
15	410204	AJ243425	Hs.326035	early growth response 1	2.50
	412851	AI826502	Hs.97269	ESTs	2.49
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	2.49
	409209	AA460160	Hs.73217	ESTs	2.49
	447173	AW449385	Hs.157294	ESTs	2.48
20	440034	AI908639	Hs.246781	ESTs	2.44
	418168	R85350	Hs.101368	ESTs	2.43
	417295	AW993524	Hs.43148	epithelial membrane protein 1	2.43
	406305			transcriptional adaptor 3 (ADA3, yeast h	2.42
	427886	AA417083	Hs.104789	ESTs	2.42
25	436409	AJ238982	Hs.183658	VNN3 protein	2.42
	413861	BE175424		gb:RC4-HT0578-170300-012-d01 HT0578 Homo	2.40
	403605			C3000142*:gij4503015[ref]NP_003900.1[co	2.37
	402594			C1002603*:gij9887091[gb]AAG01738.1JAF248	2.37
	402803			NM_001397:Homo sapiens endothelin conver	2.37
30	428336	AA503115	Hs.183752	microseminoprotein, beta-	2.36
	458568	AJ769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	2.36
	442630	AW572938	Hs.130580	ESTs	2.35
	409368	AA071059		gb:zm66a10.r1 Stratagene neuroepithelium	2.33
	405156			NM_003213*:Homo sapiens TEA domain famil	2.31
35	448162	AL039531	Hs.323363	hypothetical protein FLJ22169	2.31
	403591			Target Exon	2.31
	405193			Target Exon	2.30
	420813	X51501	Hs.99949	prolactin-induced protein	2.30
40	442941	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61	2.28
	400703			C11001794*:gij10946612[ref]NP_067286.1[2.27
	415026	AA159356	Hs.72308	ESTs	2.25
	400334	Y13187		Homo sapiens dmd gene, intron 11	2.18
	445878	AI262974	Hs.145587	ESTs	2.18
	404975			uncharacterized hypothalamus protein HT0	2.18
45	436370	R01220	Hs.185679	ESTs	2.17
	400513			Target Exon	2.16
	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	2.15
	415405	R59141		gb:yg96d11.r1 Soares infant brain 1N1B H	2.15
	407612	U26403	Hs.37142	ephrin-A5	2.12
50	409837	AW501504		gb:UI-HF-BP0p-ajd-h-04-0-UI.r1 NIH_MGC_5	2.08
	458637	AV657446		gb:AV657446 GLC Homo sapiens cDNA clone	2.07
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	2.00
	418922	AW956580	Hs.42699	ESTs	1.98
	402404			NM_024967*:Homo sapiens hypothetical pro	1.98
55	421993	R22497	Hs.110571	growth arrest and DNA-damage-inducible,	1.98
	413731	BE243845	Hs.75511	connective tissue growth factor	1.96
	456855	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Dr	1.96
	428193	NM_004235		Kruppel-like factor 4 (gulf)	1.93
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	1.92
60	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	1.92
	433883	AI925688	Hs.222312	ESTs	1.91
	406564			msh (Drosophila) homeo box homolog 2	1.91
	403581			Target Exon	1.90
	403716			Target Exon	1.90
	404758			Target Exon	1.90
65	439500	W73158	Hs.170434	Homo sapiens cDNA FLJ14242 fis, clone OV	1.89
	448793	AI864581		ESTs	1.84
	435857	AF253468	Hs.3736	delta-like 4 homolog (Drosophila)	1.83
	426653	AA530892	Hs.171695	dual specificity phosphatase 1	1.82
70	402051			Target Exon	1.81
	409859	AW501926		gb:UI-HF-BR0p-gjp-f-08-0-UI.r1 NIH_MGC_5	1.78
	417967	BE244373	Hs.1119	nuclear receptor subfamily 4, group A, m	1.78
	405063			Target Exon	1.78
	405163			C5000561*:gij7513700[pir]T14151 Inv pro	1.75
75	402386			Target Exon	1.73
	406755	N80129	Hs.199263	metallothionein 1L	1.73
	409811	AW500896		gb:UI-HF-BP0p-air-a-03-0-UI.r1 NIH_MGC_5	1.70
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	1.70
	400489			Target Exon	1.70
80	428704	AA432007	Hs.192090	ESTs	1.69
	429307	AU076592	Hs.198951	jun B proto-oncogene	1.67
	400116			Eos Control	1.65
	404795			Target Exon	1.65
	408053	AW139474	Hs.246862	ESTs	1.65

5	414580	BE386918		gb:601275386F1 NIH_MGC_20 Homo sapiens c	1.63	
	428800	M57627	Hs.193717	Interleukin 10	1.63	
	451676	R84770	Hs.33538	ESTs, Weakly similar to oxygen-regulated	1.62	
	402394			Target Exon	1.61	
	404818			Target Exon	1.60	
10	436364	X06096		gb:Human macrophage alpha1-antitrypsin c	1.55	
	420369	U96769	Hs.97220	chondroadherin	1.54	
	405590			CX001497:gi4557543[re][NP_001384.1] ex	1.54	
	402448			Target Exon	1.53	
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	1.51	
15	409020	AA062549	Hs.21162	retbindin	1.51	
	405443			Target Exon	1.12	
	TABLE 37B:					
	Pkey:	Unique Eos probeset identifier number				
	CAT number:	Gene cluster number				
Accession:	Genbank accession numbers					
20	Pkey	CAT Number	Accession			
	409385	110758_1	T65940 T64515 AA071267 AA071334			
	442195	15007_1	U81984 NM_001430 BE907085 B1333232 A1021986 AU138476 C18601 U51626 AU100517 B1054387 AU076970 BE786454 BG010080 AW377189			
	25			BF998789 AA368139 R11396 T83613 BG006324 B1012404 BG001643 BF757957 AL549361 AL544018 BE002870 BE929314 BE090199 AL046650		
				B1053717 BE929315 B1054967 BF960055 BF925432 R05421 BF922073 T70331 B1004403		
439839		2594580_1	A1023587 AA889354 AA846791			
445493		423456_1	AV711317 A1809938 A1808768 A1240593 A1915771			
418056		286199_1	AW971347 AA524886 AA211537 BF903005 BF357120			
30	413164	1492512_1	BE068758 BE068745 BE068689 BE068778 BE068529 BE068683 BE068445 BE068392 BE068719 BE068473 BE068521 BE068628 BE068422			
			BE068618 BE068354 BE068390 BE068414 BE068433 BE068369 BE068384 BE068661 BE068324 BE068301 BE068436 BE068754 BE068329			
			BE068672 BE068494 BE068596 BE068332 BE068347 BE068588 BE068328 BE068493 BE068740 BE068685 BE068759 BE068307 BE068429			
			BE068303 BE068693 BE068374 BE0688295 BE068625 BE068302 BE068663 BE068675 BE068579 BE068311 BE068674 BE068547 BE068602			
			BE068605 BE068352 BE068306 BE068401 BE068537 BE068552 BE068450 BE068723 BE068393 BE068671 BE068748 BE068317 BE068447			
35			BE068568 BE068532 BE068357 BE068330 BE068498 BE068631 BE068540 BE068410 BE068626 BE068591 BE068522 BE068676 BE068499			
			BE068361 BE068598 BE068350 BE068299 BE068580 BE068567 BE068692 BE068321 BE068327 BE068739 BE068526 BE068538 BE068765			
			BE068340 BE068733 BE068293 BE068565 BE068480 BE068476 BE068761 BE068712 BE068706 BE068549 BE068419 BE068383 BE068434			
			BE068418 BE068525 BE068543 BE068752 BE068550 BE068623 BE068470			
			BG563152 BF846777 BF849354 BF849359 BF846636 BF849201 BF849356 C16931 AA056717 AW864542 AW882724 AA056567			
40	459330	105725_1	A1910738 AW139227 AA932891 AA622104			
	434038	630986_1	AF007191 AW820706 BG978594 BF872238			
	433291	73706_1	L13288 AA928785 A1008912 AW872978 AA565655 A1022915 A1304920 A1564366 A1668793 A1094557 T60038 R72302 H45409 AA508805 R46356			
	423387	2612_2	AA418798 BM129563 BM129126 BM129292 BM128865 A1808418 A1689932 A1806573 BF431808 AW872985 AW166269 H73241 T16182 A1264547			
			R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 A1797007 BE045543 BF110021 BF754250 T83923			
45			AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 B1022902 B1763932 B1910138			
	455674	1490762_1	BE065941 BE065997 BE066003 BE066070 BE066098			
	413861	1561647_1	BF352282 BE175424 BE175418 BE175383			
	409368	110612_1	AA071059 AA085201 AA085020			
	415405	1872126_1	W18191 R59141 R54142 R12130 F11362 Z42794 F08242 F07925 H21084 R54090 R59142			
50	409837	915621_1	AW501504 AW501656 AW503048 AW502449 AW502098			
	458637	395206_1	AV657752 AV657446			
	428193	430_1	AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 B1011351 AL575805 A1290876 A1014784 A1393429 A1266211			
			AW074303 AA620711 BF197792 AW008766 D25944 A1887397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201			
			AW874084 BE720622 A1127241 AA236239 A1579709 A1679135 A1572470 AA573434 A1568487 BE049325 AA687950 BG925989 A1338031			
55			A1365073 A1024576 AA298805 H04001 H45668 BG682146 AL552388 B1462361 BG547513 BG895863 B1256661			
	448793	3006936_1	A1936948 A1864581 A1570641			
	409859	916430_1	AW501926 AW502566 AW501927			
	409811	58948_2	AK057581 AW500982 AW500896 AW501105			
	400116	5269_1	D42041 NM_014610 AJ000332 B1758702 BG720650 AU141129 AU130711 AU141380 AU132402 BM048556 AU127520 BE259984 AU128952			
60			BE614151 AL601516 BM146777 AU128103 BM194094 BE937951 BE963936 AK026997 AK026567 BF969293 BE798100 B1086881 BG166248			
			BE877845 BG385414 AW886747 BF093789 AW390159 BF820311 AA421676 AW880845 AW404827 BF726465 BE161190 BE254102 AW406002			
			BE161223 A1912055 BF930228 AW374357 AW794531 BE720524 BE933982 BE933658 BE933694 BE933978 BE933654 BE933583 BE166557			
			BE933874 BE933641 BE933859 BE933626 BE933866 BE933633 BE933864 BE933631 BE933867 BE933634 BE933857 BE933624 BE933883			
			BE933650 BE720491 AA420426 BE720410 BE720458 BE720444 BE720411 AW368748 BF874616 BE933498 BE835979 BF926667 AW849921			
65			AW850026 AW850022 AW849977 AW849900 BG250251 W87689 A192825 A1692824 AA426263 A1090315 A1309537 AA877437 AA478438			
			A1538868 AW276162 A1279916 AA600318 A1188836 AW662284 A1262619 AA293457 BF347442 AA421677 AA56063 AA565510 AA937060			
			A1142684 AA788940 AA827426 AU152614 A1342784 AU148738 AA219564 AA047835 H99450 AA018563 A1073634 BM475120 BG875251			
			BG248778 U46372 AA383858 AU140356 BG821891 BF935049 B1760656 B1054103 BF982309 BE872215 B1257291 AU158469 AU160599			
			AU152469 AU152375 AU152059 AU148575 N32267 AU149554 A1627459 A1719840 AW773017 A1291493 AW304181 AW470055 A1086491			
70			A1311387 A1634232 A1151241 A1288848 AW050588 AW589580 A1241353 A1880219 AA039309 AA026517 AA016238 AA013444 H86822 R87530			
			AA058462 N27082 Z39679 BE544309 W52619 AA018076 A1813668 AW189907 A1418104 AU159878 AU150087 R21754 AA015932 H67274			
			AU153097 A1961344 AA018208 W32429 R45344 R77453 BM470129 AU130415 B1227374 BE298179 AW844963 AW844983 A1904066 AA379006			
			BF850571 AA355641 BG747156 AL547262 AW367941 BE560004 B1116061 BG899031 BE560318 BF174177 B1051456 BE001967 BE386446			
			BF969326 BF808765 BF684480 BG421617 A1940607 AW875483 BE789632 BF808711 B1192691 AW904249 B911430 BE265407 BE730343			
75			BE397808 B1226516			
	414580	623093_1	BG333973 BE385437 BE408833 BE387650			
	436364	1414_37	X05826 X06096 BG468890 AW951851 W23562 T28392 H56742 H58030 T69205			
	TABLE 37C:					
	80	Pkey:	Unique number corresponding to an Eos probeset			
Ref:		Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.				
Strand:		Indicates DNA strand from which exons were predicted.				

NT_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NT_position
5	402608	9910096	Plus	37495-37669
	404518	8151988	Plus	84494-84603
	401234	9929642	Plus	120173-120337
	402181	8575912	Plus	449746-450040
10	403479	7329292	Minus	148369-148533,150678-150809
	402911	7263904	Plus	142689-142979
	401540	8072433	Plus	105838-107310
	402328	4464283	Minus	13758-13922,14558-14752
	401590	9966320	Minus	33547-33649
15	403645	8599714	Minus	4433-4582
	403376	9369545	Minus	108698-108830
	401126	8699701	Minus	68290-68487
	401904	8871966	Plus	60959-61603,62670-62890,63778-63838
	401919	9502466	Plus	67536-67666
20	406443	9280765	Plus	85951-87327
	406016	8272661	Plus	41341-41940
	405938	6758795	Minus	166671-167411
	404231	8218035	Minus	61077-61322
	404102	7229900	Plus	97685-98018
25	403031	7768597	Minus	1308-1416
	406059	9103984	Minus	13856-14004
	402483	7574980	Minus	65578-66119
	405448	7582529	Plus	136347-136532
	404439	7139680	Plus	55316-55585
30	404026	7582549	Minus	79674-79968
	400881	2842777	Minus	91446-91603,92123-92265
	405429	7321905	Minus	51577-51723
	402642	9958129	Minus	125599-125756
	402217	9795981	Minus	21521-21757
35	405857	6758728	Plus	26564-26819
	405305	8575869	Plus	108239-108386,112216-112378,115388-11557
	403605	6862654	Plus	91614-91718
	402594	7705170	Plus	103082-103414
	402803	3287156	Minus	55923-56033
40	405156	9966228	Plus	146733-146860,147899-147961,153127-15325
	403591	8101229	Plus	4201-4833
	406193	7289992	Plus	30183-30662
	400703	8118859	Plus	63657-63857,64802-64905
	404975	3419864	Minus	86096-86605
45	400513	9796593	Plus	74613-74823
	402404	3970932	Plus	53154-53280
	406564	7711604	Minus	52788-53013
	403581	8101182	Plus	6794-7396
	403716	7239669	Plus	86899-87122
50	404758	7706327	Minus	130204-130806
	402051	8082020	Minus	19346-19480,20041-20119
	405063	7658414	Minus	111047-111666
	405163	9966267	Minus	161171-161299
	402386	9799769	Plus	22069-22303
55	400489	8954013	Plus	131475-131652
	404795	4826439	Plus	147501-147780
	402394	9929690	Plus	33308-33482
	404818	2769655	Plus	33671-33839
	405590	6960456	Plus	90492-90818
60	402448	9796640	Plus	112942-113069,114303-114521
	405443	7408143	Plus	90716-90887,101420-101577

65 TABLE 38A: About 207 genes upregulated in lung fibrosis relative to normal tissues

	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigenelD:	Unigene number		
70	Unigene Title:	Unigene gene title		
	R1:	90th percentile of lung fibrosis AIs divided by 70th percentile of normal tissue AIs, where the minimum value for the numerator and denominator was set to 50.		
	Pkey	ExAccn	UnigenelD	Unigene Title
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr
	407891	AA486620	Hs.41135	endomucin-2
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous
	410219	T98226	Hs.171952	occludin
80	434666	AF151103	Hs.112259	T cell receptor gamma locus
	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor I
	406617			Target Exon
	420568	F09247	Hs.247735	protocadherin alpha 10
	425873	NM_013390	Hs.160417	transmembrane protein 2
				R1
				4.28
				4.14
				4.07
				3.96
				3.88
				3.87
				3.76
				3.70
				3.69

5	438797	C16161	Hs.283040	hypothetical protein PR02543	3.68
	410315	A1638871	Hs.152519	Homo sapiens cDNA: FLJ22524 fis, clone H	3.65
	446714	W73818	Hs.110028	ESTs	3.64
	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	3.61
	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	3.58
10	412790	NM_014767	Hs.74583	KIAA0275 gene product	3.56
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	3.56
	412654	A1093480		hypothetical protein FLJ11896	3.56
	414386	X00442	Hs.75990	haploglobin	3.54
	451035	AU076785	Hs.430	plastin 1 (I isoform)	3.52
15	436473	A1193122	Hs.132275	ESTs	3.51
	406714	A1219304	Hs.266959	hemoglobin, gamma G	3.46
	414586	AA306160	Hs.16488	lymphocyte cytosolic protein 1 (L-plasti	3.45
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	3.45
	427527	A1809057	Hs.153261	immunoglobulin heavy constant mu	3.39
20	452813	U54727	Hs.191445	ESTs	3.36
	442831	A1798959	Hs.131686	ESTs	3.35
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	3.34
	445330	R52655	Hs.21691	ESTs	3.31
	436001	AW903849	Hs.173840	HUEL (C4orf1)-interacting protein	3.31
25	431681	AK000378	Hs.267566	hypothetical protein FLJ20371	3.29
	432314	AA533447	Hs.312989	ESTs	3.28
	435129	A1381659	Hs.267086	ESTs	3.28
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	3.24
	422607	Z45471	Hs.118684	stromal cell-derived factor 2	3.21
30	421205	AL137540	Hs.102541	netrin 4	3.20
	428582	BE336699	Hs.185055	BENE protein	3.20
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	3.19
	424880	NM_000328	Hs.153614	retinitis pigmentosa GTPase regulator	3.17
	421233	AA209534	Hs.284243	tetraspan NET-6 protein	3.17
35	429350	A1754634	Hs.131987	ESTs	3.16
	428727	AF078847	Hs.191356	general transcription factor IIH, polype	3.16
	434850	Z43161	Hs.283714	30 kDa protein	3.13
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	3.12
	446506	A1123118	Hs.15159	chemokine-like factor, alternatively spl	3.11
40	416114	A1695549	Hs.183868	glucuronidase, beta	3.10
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	3.09
	444212	AW503976	Hs.10649	basement membrane-induced gene	3.08
	422442	AA324998	Hs.147086	signal transducer and activator of trans	3.08
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	3.08
45	424456	AA341017	Hs.25549	hypothetical protein FLJ20898	3.07
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	3.07
	445107	A1208121	Hs.147313	ESTs, Weakly similar to I38022 hypoteti	3.06
	438828	AL134275	Hs.5434	hypothetical protein DKFZp761F2014	3.04
	428106	BE620016	Hs.182470	PTD010 protein	3.04
50	428403	A1393048	Hs.326159	leucine rich repeat (in FLII) interactin	3.04
	431830	Y16845	Hs.271387	small inducible cytokine subfamily A (Cy	3.03
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nimb	3.02
	423067	AA321355	Hs.285401	colony stimulating factor 2 receptor, be	3.01
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	2.96
55	415000	AW025529	Hs.239912	Homo sapiens serologically defined breas	2.96
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	2.96
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	2.96
	419660	BE280337	Hs.194693	solute carrier family 7 (cationic amino	2.96
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	2.95
60	414493	AL133921	Hs.76272	retinoblastoma-binding protein 2	2.94
	418883	AW140128	Hs.184902	ESTs	2.92
	417675	A1808607	Hs.3781	similar to murine leucine-rich repeat pr	2.92
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	2.92
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	2.92
65	429640	U83508	Hs.2463	angiotensin 1	2.91
	449843	R85337	Hs.24030	solute carrier family 31 (copper transpo	2.91
	401958			Target Exon	2.90
	416926	H03109	Hs.263395	HT018 protein	2.90
	433691	AA605012		ESTs	2.88
70	441892	AB028981	Hs.8021	KIAA1058 protein	2.87
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	2.87
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	2.87
	414291	A1289619	Hs.13040	G protein-coupled receptor 86	2.87
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	2.87
75	435913	W95006	Hs.269559	ESTs, Weakly similar to S65657 alpha-1C-	2.86
	422050	AA302741	Hs.25786	ESTs, Moderately similar to JC5238 galac	2.85
	451356	AA748418	Hs.164577	ESTs	2.85
	442085	AA975688	Hs.159955	ESTs	2.84
	427704	AW971063	Hs.292882	ESTs	2.83
80	427247	AW504221	Hs.174103	integrin, alpha L (antigen CD11A (p180),	2.83
	441965	AA972712	Hs.269737	ESTs	2.82
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	2.82
	450056	BE047394	Hs.8208	ESTs, Weakly similar to S71512 hypoteti	2.80
	407245	X90568	Hs.172004	tin	2.80
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	2.80
	446601	AJ12783	Hs.155772	Homo sapiens thymic stromal co-transport	2.80
	432195	AJ243669	Hs.8127	KIAA0144 gene product	2.80

	449088	AI654048	Hs.196556	ESTs	2.80
	416511	NM_006762	Hs.79356	Lysosomal-associated multispanning membr	2.80
	406648	AA563730	Hs.277477	major histocompatibility complex, class	2.79
5	412116	AW402166	Hs.784	Epstein-Barr virus induced gene 2 (lymph	2.78
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	2.78
	440255	AI932285	Hs.160569	ESTs	2.78
	410057	R66634	Hs.268107	multimerin	2.77
	417497	AW402482	Hs.82212	CD53 antigen	2.77
10	446733	AA863360	Hs.26040	ESTs, Weakly similar to fatty acid omega	2.76
	431884	AA521246	Hs.210792	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.75
	409969	AW514668	Hs.194258	ESTs, Moderately similar to ALU5_HUMAN A	2.75
	436729	BE621807		transmembrane 4 superfamily member 1	2.75
	431451	AA761378	Hs.192013	ESTs	2.74
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	2.74
15	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	2.74
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	2.74
	424673	AA345051	Hs.294092	ESTs, Weakly similar to I38022 hypotheti	2.74
	443194	AI954968		matrix Gla protein	2.71
20	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.71
	452870	AW502761	Hs.30909	KIAA0430 gene product	2.70
	430334	AI824719	Hs.143251	ESTs	2.70
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	2.70
	432279	N95104	Hs.274260	ATP-binding cassette, sub-family C (CFTR	2.70
25	413950	AA249096	Hs.32793	ESTs	2.70
	430016	NM_004736	Hs.227656	xenotropic and polytropic retrovirus rec	2.70
	431710	AI735482		ESTs	2.70
	448749	AW859679	Hs.21902	Homo sapiens clone 25237 mRNA sequence	2.69
	451154	AA015879	Hs.33536	ESTs	2.69
30	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	2.69
	446899	NM_005397	Hs.16426	podocalyxin-like	2.68
	418031	AA648744	Hs.269493	ESTs	2.68
	453902	BE502341	Hs.3402	ESTs	2.68
	405121			mitogen-activated protein kinase 8 inter	2.68
35	410163	AF151977	Hs.59260	NTT5 protein	2.67
	429632	AW195336	Hs.148910	ESTs	2.67
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	2.67
	455004	AW850303		gb:IL3-CT0219-191199-030-F09 CT0219 Homo	2.67
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	2.67
40	401113			solute carrier family 22 (organic cation	2.66
	419462	AF071076	Hs.112255	nucleoporin 98kD	2.66
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-fin	2.66
	419175	AW270037		KIAA0779 protein	2.66
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	2.66
45	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	2.66
	430592	AJ224864	Hs.9688	leukocyte membrane antigen (IRC1)	2.65
	446830	BE179030		Human DNA sequence from clone RP5-1174N9	2.64
	433327	AI674779	Hs.126744	ESTs	2.64
	424868	AI568170	Hs.96886	ESTs	2.64
	429854	R55608	Hs.99472	ESTs	2.63
50	427080	AW068287	Hs.301175	ras-related C3 botulinum toxin substrate	2.63
	455711	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	2.63
	419777	D60134	Hs.270975	ESTs	2.63
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	2.62
55	427596	AA449506	Hs.270143	extracellular glycoprotein EMILIN-2 prec	2.62
	452445	AB002438	Hs.29596	Homo sapiens mRNA from chromosome 5q21-2	2.62
	447482	AB033059	Hs.18705	KIAA1233 protein	2.62
	419110	AA234171	Hs.187626	ESTs	2.62
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	2.62
60	419828	T81422	Hs.14922	ESTs	2.62
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	2.62
	412491	W31589	Hs.73957	RAB5A, member RAS oncogene family	2.61
	436496	AA281959	Hs.5210	gila maturation factor, gamma	2.61
	435053	AW629386		ESTs	2.61
65	435029	AF167706	Hs.19280	cysteine-rich motor neuron 1	2.61
	425976	C75094	Hs.334514	NG22 protein	2.60
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	2.60
	430539	AK001489		ADP-ribosylation factor-like 1	2.60
	419825	AI754011	Hs.7326	ESTs	2.59
70	412577	Z22968	Hs.74076	CD163 antigen	2.58
	425894	AW954011	Hs.180711	ESTs	2.58
	410883	D43767	Hs.66742	CCL17 chemokine (TARC) (SCYA17)	2.58
	441028	AI333660	Hs.17558	Homo sapiens cDNA FLJ14446 fls, clone HE	2.58
	413949	AA316077	Hs.75639	Human TB1 gene mRNA, 3' end	2.58
75	434943	AI929819	Hs.92909	chromosome 21 open reading frame 50	2.58
	443605	H06865	Hs.134131	ESTs	2.57
	425017	AL119305	Hs.26409	ESTs	2.57
	440334	BE276112	Hs.7165	zinc finger protein 259	2.56
80	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.56
	425345	AI077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.56
	407174	T79938	Hs.77062	leukocyte immunoglobulin-like receptor,	2.56
	443834	AI741510	Hs.173548	ESTs	2.55
	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	2.55
	420539	AA282735	Hs.44004	AD031 protein	2.55

421177	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f	2.54
437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.54
422994	AW891802	Hs.296276	ESTs	2.54
411992	AW816214	Hs.143055	ESTs	2.54
451180	H61899	Hs.171937	steroid dehydrogenase-like	2.54
415775	H00747	Hs.29792	ESTs, Weakly similar to I38022 hypotheti	2.53
429752	H52348	Hs.36636	ESTs	2.53
414612	BE274552	Hs.76578	protein inhibitor of activated STAT3	2.53
453329	T97205	Hs.193400	ESTs, Weakly similar to 2109260A B cell	2.53
436503	AJ277750	Hs.183924	ubiquitin associated and SH3 domain cont	2.52
445911	AI985987	Hs.145645	ESTs, Moderately similar to ALU1_HUMAN A	2.52
433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	2.52
435943	R60194	Hs.31141	Homo sapiens mRNA for KIAA1568 protein,	2.52
452253	AA928891	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H	2.52
442506	BE566411	Hs.41726	ESTs	2.52
419972	AL041465	Hs.182982	golgin-67	2.52
431074	BE072772	Hs.8997	ESTs, Moderately similar to A46010 X-link	2.52
449129	AI631602	Hs.258949	ESTs	2.52
440524	R71284	Hs.16798	ESTs	2.51
419203	AA488719	Hs.190151	ESTs	2.51
404370			Target Exon	2.51
432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	2.51
439219	N33883	Hs.41322	ESTs	2.51
428044	AA093322	Hs.301404	RNA binding motif protein 3	2.50
433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.50
437644	AA748575	Hs.136748	lectin-like NK cell receptor	2.50
442568	R37337	Hs.12111	ESTs	2.50
409317	U20165	Hs.53250	bone morphogenetic protein receptor, type	2.50
450505	NM_004460	Hs.418	fibroblast activation protein, alpha	2.50
447484	AA464839	Hs.292566	hypothetical protein FLJ14697	2.50
415165	AW887604	Hs.78065	complement component 7	2.50
435284	AA879470	Hs.96849	Homo sapiens cDNA FLJ11492 fis, clone HE	2.50

TABLE 38B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
412654	1350_1	BG743181 AI830050 BE695688 AA126591 AI903503 R26045 N62894 N63950 AA131619 AI681480 N79626 AA461603 R78979 AW608865 N66622 BF448838 AA779000 AA460314 AI092721 AI870182 AI436284 AA94151 AI127704 AI127702 BE349350 AI093480 AA115264 AA131587 R26840 R78885
433691	2203511_1	AI223854 AI129852 AA605012
436729	6624_1	X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 B494959 AI240988 AI925554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H08983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI344860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741785 BI868522 AU135866 BI552770 BI259210 BI258520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556588 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG426896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AA446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA304736 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BI754027 BF696071 AI351939 BG151298 AI919334 AI041620 BI770165 W72057 T98158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA933445 AA916041 AA987847 AA983329 AA737219 AA916443 AW126994 AI492560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568954 BF725590 AI004210 AI809799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AA155854 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW023269 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA302459 BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI956165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI928079 D57214 BE045265 AA541785

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431710 1611592_1
455004 1089114_1
419175 35068_1

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46830 41421_1

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435053 124009_1
430539 31268_1

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BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 F27562 AA614749 D56645 F20774 F30660 F25646 AW023542
 AA827300 AA582214 AI701289 AA228293 AI906950 AA230156 AA384572 AW438988 AA742516 BI490938 AA731082 BF665869 BG190518
 AV704158 BE439643 AA910566 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258
 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553596 AA916094
 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215
 AI422419 AA514370 AI741678 AI735482 AI735081 AI371435
 AW850587 AW850589 AW850318 AW850303
 AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331
 AA885998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961064 AJ018062 H06018 BE221942 R52609 AI915164 AA365526
 Z44671 BI052776 BF882488 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H06052 AA360728 F10618
 AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634
 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572
 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA255551 AW044188 AI203159 N49403
 FQ2090 AI187299 AI609644 Z40516 AW952314
 BC020595 BI489430 BG168023 BE179030 AW294203 BF849776 AA459064 AI917452 AW403072 W27419 BF914568 BF798468 AW370558
 T35055 AW370623 AA399232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060705 AA194237
 T25074 C01285 BI489433
 AI332638 AA663215 AW629386
 AK001489 AU129447 BF959274 BG555452 AI245327 AU116848 BF358559 BF358554 BF358570 BG678119 AL515852 AU154607 AI357567
 AW874359 AI122554 AA406478 AI091013 AI866679 AI686163 AA662158 AA911580 D31095 AI302576 BF588761 AU151560 AU143828 AI291610
 AW169600 D31161 AA905362 C21179 BE327258 D31474 AW439053 D31309 BF756901 BI838626 BF979839 AU149562 BM142116 AU156455
 AA452028 AW473972 AW468490 AA410271 AI475944 BF821859 AA658188 AI360390 AA226320 F37355 F27660 F36093 AA152126 BF930021
 BF375775 AW821784 AW975085 W16475 D31031 BG696392 AW860676 AW752864 BI013705 BF965715 BF326604 AW821786

TABLE 38C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
406617	8439858	Plus	36430-36552
401958	3258613	Plus	108411-108629
405121	8102330	Minus	35816-36004, 36587-36684
401113	9965541	Minus	19419-19959
404370	7631003	Plus	127868-128244

TABLE 40A: 656 genes upregulated in fibrosis relative to normal body tissues

Table 40A lists about 656 genes upregulated in fibrosis relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 95th percentile of fibrosis AIs divided by the 50th percentile of normal tissue AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

442275; AW449467; Hs.54795; Homo sapiens secretoglobulin, family 3A, m; Uteroglobulin; TM=M; SS=Y; 39.47
 428434; AW363590; Hs.65551; Homo sapiens, Similar to DNA segment, Ch; LBP_BPL_CETP_C; TM=M; SS=Y; 32.35
 439335; AA742697; Hs.62492; NM_052863; Homo sapiens secretoglobulin, f; none; 28.49
 406964; M21305; ; FGENES predicted novel secreted protein; none, none; 27.90
 425211; M18667; Hs.1867; progastrin (pepsinogen C); asp; TM=M; SS=M; 27.90
 441835; AB038432; Hs.184; advanced glycosylation end product-specific homeobox, Acyltransferase, notch, EGF, ank, Acyltransferase; 27.23
 446921; AB012113; Hs.16530; small inducible cytokine subfamily A (C); IL8; 24.97
 428330; L22524; Hs.2256; matrix metalloproteinase 7 (matrilysin, ; Peptidase_M10; 24.38
 431723; AW058350; Hs.278966; Homo sapiens mRNA; cDNA DKFZp564B2062 (f; PMP22_Claudin, none; 23.35
 409153; W03754; Hs.50813; hypothetical protein FLJ20022; fibrinogen_C; 23.29
 431089; BE041395; Hs.374629; ESTs, Weakly similar to unknown protein; none, none; 18.23
 425371; D49441; Hs.155981; mesothelin; none; TM=M; SS=M; 18.17
 448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec, MIP; TM=M; SS=M; 17.64
 421502; AF111856; Hs.105039; solute carrier family 34 (sodium phospho; Ribosomal_L20, Na_P1_cotrans; TM=Y; SS=N; 17.33
 421798; N74880; Hs.355462; N-acylsphingosine amidohydrolase (acid c; SAPA, Surfactant_B, none; 16.81
 419556; U29615; Hs.91093; chitinase 1 (chitinotriosidase); Glyco_hydro_18, C8M_14; TM=M; SS=Y; 16.24
 419092; J05581; Hs.89603; mucin 1, transmembrane; SEA; TM=Y; SS=M; 16.06
 426174; AA547959; Hs.115838; Homo sapiens similar to Echinoidin (LOC1; none, none; 15.84
 406672; M26041; Hs.198253; major histocompatibility complex, class I; MHC_II_alpha; TM=M; SS=M; 15.42
 421110; AJ250717; Hs.1355; cathepsin E; asp; 15.08
 444342; NM_014398; Hs.10887; similar to lysosome-associated membrane ; Lamp; TM=Y; SS=M; 14.94

- 406621; X57809; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 14.36
 443709; A1082692; Hs.134662; ESTs; SNF,fn3,none; 14.05
 428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabo; 7tm_3;TM=Y;SS=M; 13.88
 457200; U33749; Hs.197764; thyroid transcription factor 1; homeobox;TM=M;SS=N; 13.86
 432519; A1221311; Hs.130704; ESTs, Weakly similar to BCUHIA S-100 pro; none,none; 13.82
 422355; AW403724; Hs.300697; coagulation factor VII [serum prothrombi; none,ig; 13.62
 430280; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 13.47
 415457; AW081710; Hs.7369; Homo sapiens testes specific A2 homolog ; MORN,sugar_lr;TM=Y;SS=M; 13.35
 431164; AA493650; Hs.94367; thyroid transcription factor 1; none,homeobox; 13.32
 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 12.83
 400269; ; Hs.253495; Eos Control; lectin_c,Collagen,Xlink; 12.30
 424310; AA338648; Hs.50334; testes development-related NYD-SP22; none;TM=M;SS=N; 11.81
 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1; ABC_tran,SRP54;TM=Y;SS=M; 11.79
 452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine ; none,none; 11.68
 445537; AJ245671; Hs.12844; EGF-like-domain, multiple 6; EGF,MAM; 11.56
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 11.41
 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 11.31
 430832; A1073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior ; none,none; 11.25
 407910; AA650274; Hs.41266; fibronectin leucine rich transmembrane p; fn3,LRR,LRRCT,LRRNT;TM=Y;SS=M; 11.15
 451497; H83294; Hs.284122; Wnt inhibitory factor-1; EGF,WIF; 11.07
 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none;TM=M;SS=N; 11.07
 411020; NM_006770; Hs.67726; macrophage receptor with collagenous str; SRCR,Collagen;TM=Y;SS=M; 11.05
 446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin ; Osteopontin; 11.01
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.97
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2,lectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 10.93
 432231; AA339977; Hs.274127; CLST 11240 protein; none;TM=M;SS=M; 10.81
 416402; NM_000715; Hs.1012; complement component 4-binding protein ; sushi;TM=M;SS=M; 10.77
 418156; W17056; Hs.83623; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 10.63
 436553; AW407157; Hs.181125; immunoglobulin lambda locus; ig,HSP70,Ppx-GppA;TM=M;SS=N; 10.58
 421071; AJ311238; Hs.104476; ESTs, Weakly similar to CGHU1E collagen ; none;TM=Y;SS=M; 10.57
 418007; M13509; Hs.83169; matrix metalloproteinase 1 (Interstitial; hemopexin,Peptidase_M10,Aslacin,PG_binding_1; 10.33
 419086; NM_000216; Hs.89591; Kellmann syndrome 1 sequence; fn3,wap; 10.30
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 10.28
 441384; AA447849; Hs.288660; retinoic acid induced 3; 7tm_3,none; 10.26
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPAse;TM=M;SS=N; 10.22
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 10.09
 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alph; vwa,CACHE;TM=M;SS=N; 10.03
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3,TPR;TM=M;SS=N; 10.02
 408562; A1436323; Hs.31141; roundabout (axon guidance receptor, Dros; ig,fn3;TM=M;SS=N; 10.02
 448782; AL050295; Hs.362806; KIAA0758 protein; 7tm_2,ig,GPS,SEA;TM=Y;SS=N; 9.86
 419235; AW470411; Hs.288433; neurotrimin; none,none; 9.79
 415992; C05837; Hs.145807; hypothetical protein FLJ13593; none;TM=Y;SS=M; 9.74
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metallophos;TM=M;SS=M; 9.70
 439018; AW300887; Hs.26638; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.69
 442652; A1005163; Hs.201378; Homo sapiens cDNA FLJ40427 fis; none;TM=M;SS=N; 9.68
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 9.64
 408380; AF123050; Hs.44532; diubiquitin; ubiquitin;TM=M;SS=N; 9.54
 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 9.52
 449494; AW237014; Hs.315369; aquaporin 4; MIP,none; 9.51
 456062; A1866286; Hs.71962; ESTs, Weakly similar to B36298 proline-r; none,none; 9.42
 446428; AW082270; Hs.12496; ESTs, Weakly similar to ALU4_HUMAN ALU S; none,none; 9.41
 421952; AA300900; Hs.98849; dynein light chain 2B (DNLC2B); none,none; 9.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell ; Ribosomal_S14,ank,pkinase,death,none; 9.16
 456034; AW450579; ; gb:UH-BI3-ala-a-12-O-UI.s1 NCL CGAP_Sur; none,none; 9.15
 407788; BE514982; Hs.38991; S100 calcium-binding protein A2; ehand,S_100,S_100,ehand; 9.15
 416965; N26223; Hs.160436; MDAC1; none,NA,NA; 9.03
 443324; R44013; Hs.184225; ESTs; none,none; 9.03
 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid; ig;TM=Y;SS=M; 9.00
 440273; A1805392; Hs.325335; Homo sapiens cDNA: FLJ23523 fis, clone L; none,none; 8.99
 424527; AW138558; Hs.334873; ESTs, Weakly similar to I54374 gene NF2 ; Zn_carbOpept,none; 8.80
 409203; AA780473; Hs.687; cytochrome P450, subfamily IVB, polypept; p450;TM=M;SS=Y; 8.76
 423387; AJ012074; Hs.348500; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 8.74
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding pro; none;TM=M;SS=Y; 8.73
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 8.68
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell ; ig;TM=Y;SS=M; 8.56
 421563; NM_006433; Hs.105806; granulysin; none; 8.55
 450726; AW204600; Hs.355462; HUMPSBPA Human pulmonary surfactant-asso; SAPA,Surfactant_B,none; 8.51
 419693; AA133749; Hs.301350; FXD domain-containing ion transport reg; ATP1G1_PLM_MAT8;TM=Y;SS=M; 8.51
 424450; AL137526; Hs.374425; dynein intermediate chain 2; WD40; 8.42
 402474; ; NM_004079;Homo sapiens cathepsin S (CTSS; Peptidase_C1; 8.41
 458079; A1796870; Hs.54277; Homo sapiens similar to RIKEN cDNA 28100; none;TM=M;SS=N; 8.40
 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 8.36
 453310; X70897; Hs.553; solute carrier family 6 (neurotransmitte; SNF,5HT_transporter;TM=Y;SS=N; 8.34
 448140; AF146761; Hs.20450; BCM-like membrane protein precursor; ig;TM=Y;SS=N; 8.33
 404240; ; NM_018950;Homo sapiens major histocompat; ig,MHC_I;TM=Y;SS=M; 8.28
 459702; A1204995; ; gb:an03cd3.x1 Stralagene schizo brain S1; none,none; 8.17
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.17
 442994; A1026718; Hs.16954; ESTs; ank,pkinase,death,Ribosomal_S14; 8.12
 446998; N99013; Hs.278966; Homo sapiens mRNA; cDNA DKFpZp564B2062 (f; PMP22_Claudin,none; 8.07
 420137; AA309478; Hs.95327; CD3D antigen, delta polypeptide (TTT3 co; ITAM;TM=Y;SS=M; 8.01
 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid; ig;TM=M;SS=M; 7.99
 432441; AW292425; Hs.163484; intron of hepatocyte nuclear factor-3 al; Fork_head,none; 7.99
 409208; Y00093; Hs.172631; integrin, alpha X (antigen CD11C (p150)); vwa,FG-GAP,Integrin_A,vwa,Integrin_A,FG-GAP; 7.94

- 432606; NM_002104; Hs.3066; granzyme K (serine protease, granzyme 3; trypsin; TM=Y; SS=M; 7.92
 442832; AW206560; Hs.253569; ESTs; none, none; 7.90
 412104; AW205197; Hs.240951; Homo sapiens, Similar to RIKEN cDNA 2210; none; TM=M; SS=N; 7.89
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, r; ig; TM=Y; SS=M; 7.86
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin, none; 7.84
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), ly; integrin_B, EGF, PSI; TM=Y; SS=M; 7.79
 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazero; none; TM=Y; SS=N; 7.78
 423961; D13666; Hs.136348; perlestin (OSF-2os); Fasciclin; TM=M; SS=M; 7.73
 424917; A1636208; Hs.96901; hypothetical protein FLJ23049; none; TM=M; SS=N; 7.72
 438564; AA381553; Hs.198253; major histocompatibility complex, class ; ig, MHC_II_alpha, none; 7.65
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, corn; none, PK, PK_C, myosin_head, RhoGAP; 7.64
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily; SRP14, TNFR_c6; 7.63
 436954; AA740151; Hs.130425; ESTs; none, none; 7.58
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain; SH2; 7.56
 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta; ASC; TM=Y; SS=M; 7.55
 417105; X60992; Hs.81226; CD6 antigen; SRCR; TM=Y; SS=M; 7.51
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, re; ig; TM=Y; SS=M; 7.46
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 7.40
 432222; AI204995; gbr:an03c03.x1 Stratagene schizo brain S1; none, none; 7.38
 422667; H25642; Hs.132821; ESTs; FMO-like, FMO-like; 7.37
 444527; NM_005408; Hs.11383; small inducible cytokine subfamily A (Cy; IL8; 7.36
 457411; AW085961; Hs.130093; iroquois-class homeobox protein IRX2; none, none; 7.32
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, kinase, Recep_L_domain, YLP, none; 7.32
 419231; AL046294; Hs.136245; ESTs, Weakly similar to T17227 hypothetical; none, none; 7.30
 438873; AJ302471; Hs.124292; Homo sapiens cDNA: FLJ23123 fis, clone L; none, none; 7.27
 424027; AW337575; Hs.201591; ESTs; 7tm_2, HRM, none; 7.26
 428927; AA441837; Hs.90250; Homo sapiens hypothetical protein FLJ231; none, none; 7.24
 432435; BE218886; Hs.282070; ESTs; none, none; 7.22
 428467; AK002121; Hs.184465; hypothetical protein FLJ11259; none; TM=Y; SS=M; 7.21
 416030; H15261; Hs.21948; ESTs; none, none; 7.20
 433293; AF007835; Hs.32417; hypothetical protein MGC2742; none; TM=M; SS=N; 7.18
 418741; H83265; Hs.8881; ESTs, Weakly similar to S41044 chromosome; kinase, Activin_rec, pkinase, Activin_rec; 7.16
 420656; AA279098; Hs.187636; ESTs; none, none; 7.14
 427698; AW972594; Hs.335499; ESTs; none, none; 7.11
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfurylase; TM=M; SS=N; 7.06
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT, none; 7.04
 430413; AW842182; Hs.241392; small inducible cytokine A5 (RANTES); IL8; TM=M; SS=Y; 7.04
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement comp; C1q, Collagen; 7.03
 421481; AW391972; Hs.104696; KIAA1324 protein; none; TM=M; SS=M; 7.01
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase, PLAT; TM=M; SS=N; 6.97
 452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide, TGF-beta, none; 6.96
 458124; AW005548; Hs.124590; ESTs; none, none; 6.94
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chr; SH3, PX; TM=M; SS=N; 6.93
 411027; AF072099; Hs.87846; leukocyte immunoglobulin-like receptor ; inositol_P; ig; TM=M; SS=N; 6.92
 428820; AA436187; Hs.172631; integrin, alpha M (complement component ; vva, integrin_A, FG-GAP; TM=Y; SS=M; 6.90
 423575; C18863; Hs.163443; intron of perlestin (OSF-2os); Fasciclin, none; 6.89
 419490; NM_006144; Hs.90708; granzyme A (granzyme 1, cytotoxic T-lymp; trypsin; TM=M; SS=M; 6.89
 450954; AJ904740; Hs.25691; receptor (calcitonin) activity modifying; none; TM=Y; SS=M; 6.87
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC; TM=Y; SS=M; 6.84
 425555; AA359291; Hs.130767; Homo sapiens cDNA: FLJ23553 fis, clone L; LRR; TM=M; SS=N; 6.81
 414991; C17898; Hs.104696; Homo sapiens up-regulated by BCG-CWS (LO; Zip, none; 6.80
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, rec; ITAM; TM=Y; SS=M; 6.80
 422163; AF027208; Hs.112360; prominin (mouse)-like 1; none; TM=Y; SS=M; 6.79
 445885; AI734009; Hs.127699; KIAA1603 protein; none, none; 6.77
 436576; AI458213; Hs.77542; ESTs; 7tm_1, DnaJ; 6.77
 417079; U85590; Hs.81134; Interleukin 1 receptor antagonist; IL1; 6.76
 424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2, HRM; TM=Y; SS=M; 6.75
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3; TM=M; SS=N; 6.73
 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54); ig, ICAM_N; TM=M; SS=M; 6.71
 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain; ig, abhydrolase; 6.70
 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 24; none, lectin_c; 6.70
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cy; IL8; TM=M; SS=Y; 6.68
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans_K_tetra, asp; 6.65
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C, IMPDH_N, CBS, integrin_B, Ricin_B_lectin; 6.62
 428582; BE336699; Hs.185055; BENE protein; none; TM=Y; SS=M; 6.60
 453142; AA033648; Hs.7473; Homo sapiens gap junction protein, alpha; connexin; TM=Y; SS=M; 6.60
 432374; W68815; Hs.301885; Homo sapiens cDNA FLJ11346 fis, clone PL; none, none; 6.56
 448569; BE382657; Hs.21486; signal transducer and activator of trans; SH2, STAT, STAT_bind, STAT_prot; TM=M; SS=N; 6.54
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2, SH3, pkinase; TM=M; SS=N; 6.51
 446932; AA961459; Hs.125644; ESTs; none, LRR, LRRNT; 6.50
 427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180); vva, integrin_A, FG-GAP; TM=Y; SS=M; 6.48
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; ig, pkinase; TM=M; SS=M; 6.47
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none; TM=M; SS=M; 6.46
 431745; AW972448; Hs.163425; Novel FGENSESH predicted cadherin repeat ; none, none; 6.43
 417370; Hs.374466; tryptophanyl-tRNA synthetase; WHEP-TRS, tRNA-synt_1b; 6.41
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3_Y_phosphatase; TM=M; SS=N; 6.40
 429610; AB024937; Hs.211092; LUNX protein; PLUNC (palate lung and nas; none; 6.39
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_P14_kinase, FAT, FATC, BoIA, RUN; TM=M; SS=N; 6.37
 413385; M34455; Hs.840; indoleamine-pyrrole 2,3 dioxygenase; IDO; TM=M; SS=N; 6.36
 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 6.34
 408369; R38438; Hs.118747; SLC15A2 Solute carrier family 15 (H+/-pep; PTR2; TM=Y; SS=N; 6.32
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysJg, FAD_Synth, Idh, Idh_C_kinase; 6.32

- 444090; S69115; Hs.10305; natural killer cell group 7 sequence; PMP22_Claudin; TM=Y;SS=M; 6.31
 416819; U77735; Hs.80205; pim-2 oncogene; pkinase; 6.30
 421659; NM_014459; Hs.106511; protocadherin 17; cadherin; TM=M;SS=M; 6.27
 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M;SS=N; 6.26
 424273; W40460; Hs.144442; phospholipase A2, group X; phospho; TM=M;SS=Y; 6.24
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M;SS=N; 6.23
 452194; AI694413; Hs.373599; olfactory receptor, family 2, subfamily : none,nons; 6.22
 424144; AA454033; Hs.41644; AKAP-associated sperm protein; Rila; 6.21
 414142; AW368397; Hs.334485; hemiscentin (fibulin 6); EGF,lg,isp_1,hormone4,squash,TIL,Adeno_E3_CR1; TM=M;SS=M; 6.21
 442006; AW975183; Hs.372210; ESTs, Weakly similar to S72482 hypotheti; none,none; 6.20
 420256; U84722; Hs.76206; cadherin 5, type 2, VE-cadherin (vascula; cadherin,Cadherin_C_term; TM=Y;SS=M; 6.19
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cy; IL8; TM=M;SS=Y; 6.17
 440452; AI925136; Hs.55150; ESTs, Weakly similar to CAYP_HUMAN CALCY; none;NA;NA; 6.17
 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y;SS=M; 6.16
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t_Y_phosphatase;none; 6.15
 410361; BE391804; Hs.62661; guanylate binding protein 1, interferon-; GBP,GBP_C; TM=Y;SS=M; 6.13
 415765; NM_005424; Hs.78824; tyrosine kinase with immunoglobulin and ; EGF,fn3,lg,pkinase,laminin_EGF; TM=M;SS=Y; 6.12
 430478; NM_014349; Hs.241535; apolipoprotein L 3; MolA_ExtB; TM=Y;SS=M; 6.12
 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; none; TM=Y;SS=M; 6.09
 446608; N75217; Hs.175622; ESTs; Armadillo_seg,HEAT_PBS; TM=M;SS=M; 6.08
 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfam; IL2; 6.08
 426116; AA868729; Hs.144694; ESTs; none,none; 6.06
 445033; AV652402; Hs.72901; cyclin-dependent kinase inhibitor 2B (p1; ank; 6.05
 426721; AF016495; Hs.288545; ESTs, Weakly similar to T29012 hypotheti; zf-C2H2; TM=M;SS=N; 6.05
 429228; AI553633; Hs.356828; ESTs; none,none; 6.05
 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase; 6.04
 437669; AJ358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA; none,pkinase,pkinase_C; 6.03
 419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane; TM=Y;SS=M; 6.02
 428667; AJ375550; Hs.346868; nucleolar protein p40; homolog of yeast ; none,none; 6.01
 432731; R31178; Hs.287820; fibronectin 1; fn1,fn2,fn3;none; 5.95
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=M; 5.95
 450656; AA010539; Hs.18912; unnamed protein product; zf-C2H2; 5.94
 418460; M26315; Hs.85258; CD8 antigen, alpha polypeptide (p32); ig; TM=Y;SS=M; 5.94
 424054; AA334511; Hs.26638; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=M; 5.94
 408048; NM_007203; Hs.42322; A kinase (PKA) anchor protein 2; Paralemm; TM=M;SS=N; 5.94
 438670; AJ275803; Hs.123428; ESTs; none;NA;NA; 5.91
 424238; AA337401; Hs.137635; ESTs; none; TM=M;SS=M; 5.90
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 throm; Bcl-2;none; 5.89
 423690; AA329648; Hs.23804; ESTs, Weakly similar to PN0099 son3 prot; ion_trans,IQ;none; 5.88
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase; TM=M;SS=N; 5.81
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, ; ig; TM=Y;SS=M; 5.81
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none; TM=Y;SS=M; 5.80
 420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TTT3 com; ITAM; TM=M;SS=M; 5.79
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr; TM=Y;SS=N; 5.79
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2,SH3; TM=M;SS=N; 5.79
 443257; AJ334040; Hs.11614; HSPC065 protein; trypsin; TM=M;SS=N; 5.76
 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity Iib, re; ig; TM=Y;SS=N; 5.70
 435299; AI745458; Hs.343026; ESTs, Weakly similar to T20593 hypotheti; none;NA;NA; 5.69
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X; TM=M;SS=N; 5.67
 436772; AW975688; Hs.348918; metallothionein 1E (functional); 7tm_2,HRM;none; 5.67
 431385; BE178536; Hs.11060; membrane-spanning 4-domains, subfamily A; none,none; 5.66
 419833; AA251131; Hs.220697; Homo sapiens tryptophanyl-tRNA synthetas; WHEP-TRS,tRNA-synt_1b;none; 5.66
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArlGap; 5.64
 407758; AA116021; Hs.38260; ubiquitin specific protease 18; UCH-1,UCH-2; 5.63
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y;SS=M; 5.63
 423533; NM_014339; Hs.129751; interleukin 17 receptor; none; TM=Y;SS=M; 5.63
 419577; L35531; Hs.91296; integrin, alpha 8; integrin_A,FG-GAP; TM=Y;SS=N; 5.61
 452561; AI692181; Hs.49169; KIAA1634 protein; TPR,PDZ,WW,Guanylate_kin; TM=M;SS=N; 5.61
 428677; AJ657119; Hs.351582; troponin I, cardiac; none; TM=M;SS=N; 5.60
 425509; AF079363; Hs.158213; sperm associated antigen 6; Armadillo_seg,HEAT_PBS; TM=M;SS=N; 5.58
 453852; AW961818; Hs.211592; MUM2 protein; pkinase,DAG_PE-bind,C2,pkinase_C;none; 5.57
 421924; BE154514; Hs.109606; coronin, actin-binding protein, 1A; WD40,kdh_C; TM=M;SS=N; 5.57
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none; TM=Y;SS=M; 5.55
 431630; NM_002204; Hs.265829; Integrin, alpha 3 (antigen CD49C, alpha ; FG-GAP,Rhabd_glycop,Integrin_A; TM=Y;SS=M; 5.53
 410257; BE244044; Hs.61469; hypothetical protein; none,none; 5.53
 441965; AA972712; Hs.269737; ESTs; pkinase,Activin_rec,TSPN,Collagen; 5.52
 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; Integrin_B,Glyco_hydro_56; 5.52
 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fts, clone MA; SH2,STAT,STAT_bind,STAT_prot;none; 5.50
 447357; AI375922; Hs.132821; ESTs; FMO-like,FMO-like; 5.46
 422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin,Defensin_propep; TM=M;SS=M; 5.46
 447033; AI357412; Hs.157601; Predicted gene: Eos cloned; secreted w/v; none,none; 5.45
 417412; X16896; Hs.82112; interleukin 1 receptor, type I; ig,TIR; TM=M;SS=M; 5.45
 436057; AJ004832; Hs.5038; neuropathy target esterase; cNMP_binding,Ion_trans,Patatin; TM=Y;SS=M; 5.41
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4; TM=Y;SS=M; 5.41
 439285; AL133916; Hs.47860; hypothetical protein FLJ20093; ig,pkinase,LRR,LRRNT,LRRCT;none; 5.40
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1; TM=Y;SS=M; 5.40
 443623; AA345519; Hs.9641; complement component 1, q subcomponent ; C1q,Collagen; 5.40
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrat; SH3,HS1_rep; TM=M;SS=N; 5.38
 437275; AW976035; Hs.292396; ESTs, Weakly similar to A47582 B-cell gr; none,Frizzled,Fz; 5.37
 419560; BE280337; Hs.194693; solute carrier family 7 (cationic amino ; aa_permeases; TM=Y;SS=M; 5.37
 449353; AF006823; Hs.24040; potassium channel, subfamily K, member 3; ion_trans; TM=Y;SS=M; 5.36
 442434; AA95787; Hs.129583; ESTs; IRK;none; 5.36
 428065; AI634046; Hs.157313; ESTs; ICE_p20,DED,ICE_p20,DED; 5.36

- 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to; ras, arl, TK; 5.33
- 425638; NM_012337; Hs.158450; nasopharyngeal epithelium specific prote; none; TM=M; SS=N; 5.32
- 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2, SH3, pkinase; TM=M; SS=N; 5.32
- 452416; AA026115; Hs.114777; ESTs; none; Porphobil. deam; 5.29
- 5 425205; NM_005854; Hs.155106; receptor (calcitonin) activity modifying; none; TM=Y; SS=N; 5.29
- 440475; A1807671; Hs.24040; potassium channel, subfamily K, member 3; ion_trans, none; 5.28
- 417355; D13168; Hs.82002; endothelin receptor type B; 7tm_1, zfc3HC4, fn3, SPRY, KRAB, zfc2H2, rve, zfb_box; TM=Y; SS=M; 5.28
- 436120; A1248193; Hs.119860; ESTs; hema_1, none; 5.27
- 10 418307; U70867; Hs.83974; solute carrier family 21 (prostaglandin); OATP_N, OATP_C; TM=Y; SS=M; 5.27
- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7tm_1, zfc3HC4, fn3, SPRY, KRAB, zfc2H2, rve, zfb_box; TM=Y; SS=M; 5.26
- 421554; AW137676; Hs.97775; ESTs; none, none; 5.23
- 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0452; none, none; 5.22
- 410434; AF051152; Hs.63668; toll-like receptor 2; LRR, LRRCT, TIR; TM=M; SS=M; 5.21
- 15 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2 ; 7tm_1; TM=Y; SS=M; 5.19
- 400261; ; Hs.1802; Eos Control; ig, MHC, II_beta; TM=Y; SS=M; 5.19
- 436856; A1469355; Hs.127310; ESTs; pkinase, rm; TM=M; SS=N; 5.18
- 408761; AA057264; Hs.238936; ESTs; Weakly similar to (define not ava; 7tm_1, none; 5.17
- 425023; AW956889; Hs.154210; EDG-1 (endothelial differentiation, sph; 7tm_1; TM=Y; SS=M; 5.16
- 20 452203; X57522; Hs.352018; transporter 1, ATP-binding cassette, sub; ABC, tran, ABC, membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 5.16
- 451220; AF124251; Hs.26054; novel SH2-containing protein 3; SH2; TM=M; SS=N; 5.15
- 417771; AA804698; Hs.82547; retinoic acid receptor responder (lazarus; none, none; 5.14
- 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation ant; PAAD, DAPIN, HIN; 5.14
- 451099; R52795; Hs.25954; interleukin 13 receptor, alpha 2; fn3; TM=Y; SS=M; 5.13
- 25 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm_1; TM=Y; SS=M; 5.12
- 423196; AK001866; Hs.125139; hypothetical protein FLJ11004; none; TM=M; SS=N; 5.12
- 433671; AW138797; Hs.132906; 19A24 protein; ig; TM=M; SS=M; 5.11
- 426457; AW894667; Hs.380138; chimera (chimera) 1; DAG, PE-bind, RhoGAP, SH2; TM=M; SS=N; 5.06
- 30 431890; X17033; Hs.271988; integrin, alpha 2 (CD49B, alpha 2 subunit; vva, integrin_A, FG-GAP; TM=Y; SS=M; 5.05
- 418185; AW958272; Hs.347326; intercellular adhesion molecule 2 (ICAM; none; TM=Y; SS=M; 5.05
- 437352; AL353957; Hs.284181; hypothetical protein DKFZp434P0531; DUF221; TM=Y; SS=M; 5.03
- 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M186; PLDc; TM=M; SS=N; 5.02
- 452924; AW580939; Hs.91799; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 5.02
- 426535; AU077012; Hs.288582; ESTs; Weakly similar to ubiquitous TPR rm; Kunitz_BPTI, Kunitz_BPTI, 7tm_2, HRM; 4.99
- 35 432805; X94630; Hs.3107; CD97 antigen; 7tm_2, EGF, GPS, FecCD; TM=Y; SS=M; 4.95
- 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3, PH, WW, RhoGAP; 4.95
- 414291; A1289619; Hs.13040; G protein-coupled receptor 86; 7tm_1; TM=Y; SS=M; 4.94
- 428981; BE313077; Hs.93135; ESTs; Weakly similar to ALU2_HUMAN ALU S; none, rm; 4.92
- 451154; AA015879; Hs.33536; ESTs; TIMP; none; 4.92
- 40 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase, TrkA-N, 2-Hacid_DH_C; TM=M; SS=N; 4.90
- 413011; AW068115; Hs.821; biglycan; LRR, LRRNT; 4.90
- 422732; AA577455; Hs.24937; transformer-2 alpha (htra-2 alpha); rm, ig; 4.89
- 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like, pyr_redox; TM=Y; SS=M; 4.88
- 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L OR; PLDc; TM=M; SS=N; 4.88
- 45 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein; 7tm_1, LRR; TM=Y; SS=N; 4.87
- 405102; ; C15001220; gij44695581gb|AAD21311.1| (AF; DAG, PE-bind, PH, RhoGEF, DC1; 4.86
- 422795; AB033109; Hs.375610; KIAA1283 protein; 7tm_1, kazal_A2M, A2M_N; TM=Y; SS=M; 4.84
- 432581; AU076465; Hs.278441; KIAA0015 gene product; PP2C; TM=M; SS=N; 4.83
- 414936; C14774; ; gb:C14774 Clontech human aorta poly A mRNA; ank, pkinase, death, none; 4.82
- 30 430152; AB001325; Hs.234642; aquaporin 3; MIP; TM=Y; SS=M; 4.82
- 444838; AV651680; Hs.208558; ESTs; integrin_A, FG-GAP; none; 4.81
- 410423; AW042432; Hs.63489; protein tyrosine phosphatase, non-recept; SH2, Y_phosphatase, DSPc; TM=M; SS=N; 4.81
- 55 453107; NM_016113; Hs.279746; vanilloid receptor-like protein 1; ank, ion_trans; TM=Y; SS=N; 4.80
- 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; 4.80
- 422010; A4302049; Hs.31181; Homo sapiens cDNA: FLJ23230 fs, clone C; none, SDF, sugar_br; 4.78
- 419542; AA366037; Hs.90911; solute carrier family 16 (monocarboxylic; none, none; 4.76
- 438899; AF085833; Hs.135624; ESTs; none, P13_P14_kinase, P13Ka, P13K_C2, P13K_rbd, P13K_p85B; 4.75
- 427418; AA02587; Hs.356667; LAT1-3TM protein; none, none; 4.75
- 431924; AK000850; Hs.272203; Homo sapiens cDNA FLJ20843 fs, clone AD; SH3; none; 4.73
- 424218; AF031824; Hs.143212; cystatin F (leukocystatin); cystatin; 4.72
- 60 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17; none; 4.72
- 416178; A1808527; Hs.192822; serologically defined breast cancer anti; none; TM=M; SS=N; 4.71
- 430037; BE409649; Hs.227789; mitogen-activated protein kinase-activat; pkinase; TM=M; SS=N; 4.71
- 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none, none; 4.71
- 65 453870; AW385001; Hs.8042; Homo sapiens cDNA: FLJ23173 fs, clone L; FG-GAP, integrin_A, NIF; 4.71
- 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fs, clone A; 7tm_3, none; 4.70
- 438543; AA810141; Hs.192182; ESTs; SH2, pkinase, none; 4.70
- 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank, pkinase, death, SPRY, SAP, Ribosomal_L24e, SRP54, dDENN, DENN, uDENN; TM=M; SS=N; 4.70
- 438113; A1467908; Hs.8882; ESTs; 7tm_1, none; 4.70
- 70 422164; NM_014312; Hs.112377; cortic al thymocyte receptor (X. laevis ; ig, Gemini_mov; TM=Y; SS=M; 4.69
- 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 4.69
- 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker; ; aldo_ket_red, none; 4.67
- 432314; AA533447; Hs.285173; ESTs; Xlink, none; 4.66
- 453518; AW503205; Hs.27268; gb:U1-HF-BNO-akt-g-03-0-U1.r1 NIH_MGC_50; SH3, PH, RhoGEF; TM=M; SS=N; 4.66
- 418813; AA744529; Hs.86575; mitogen-activated protein kinase kinase ; pkinase, CNH; TM=M; SS=N; 4.66
- 75 446063; A1702140; Hs.151079; ESTs; ISK_Channel, none; 4.65
- 454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member ; aldedh; 4.65
- 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC; TM=Y; SS=N; 4.65
- 443402; U77846; Hs.9295; elastin (supraaortic stenosis; ; none, PDZ_LIM, pkinase; 4.65
- 414809; A1434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; SS=N; 4.64
- 80 427535; R29543; Hs.2164; pro-platelet basic protein (includes pla; IL8; TM=M; SS=M; 4.64
- 437119; A1379921; Hs.177043; XP_171387 similar to rhotekin; none, none; 4.63
- 411779; AA292811; Hs.72050; non-metastatic cells 5, protein expresse; NDK; 4.63
- 429784; M89796; Hs.30; membrane-spanning 4-domains, subfamily A; none; TM=Y; SS=N; 4.62

- 415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phoslip; 4.61
 408873; AL046017; Hs.356216; calmodulin 2 (phosphorylase kinase, delta; none, none; 4.61
 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase; TM=M; SS=N; 4.59
 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase; WW, HECT, RNA_pol_A, none; 4.59
 408000; L11690; Hs.198689; bulky protein antigen 1 (230/240kD); ehfand, spectrin, GAS2, SH3, Plectin, RA, Xylose_isom, FliD, bZIP, Tropomyosin, Myc-LZ, Mjdh_C, CH, AIP3; TM=M; SS=N; 4.59
 431087; H12723; Hs.290791; ESTs; Ion_trans, none; 4.58
 425465; L18964; Hs.1904; protein kinase C, Iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; SS=N; 4.58
 422427; AA310514; Hs.96692; ESTs; PH, Ets, CH, spectrin, Ca_channel_B, none; 4.57
 441527; W19504; Hs.7884; solute carrier family 21 (organic anion); OATP_N, OATP_C; TM=Y; SS=N; 4.56
 416464; NM_000132; Hs.79345; coagulation factor VIII, procoagulant co; Cu-oxidase, F5_F8_type_C; 4.56
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4; TM=Y; SS=M; 4.56
 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; In3; TM=M; SS=N; 4.55
 444895; A1674383; Hs.22891; solute carrier family 7 (calcionic amino); ASC, death, TNFR_c6; 4.55
 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled); Nramp; TM=Y; SS=N; 4.55
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema, PSI, TIG, integrin_B; TM=Y; SS=M; 4.54
 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 4.54
 450086; AW016343; Hs.233301; ESTs; ank, death, ZU5, NMU, none; 4.54
 438209; AL120659; Hs.6111; aryl-hydrocarbon receptor nuclear trans; HLH, PAS, IL8; TM=M; SS=N; 4.54
 414788; X78342; Hs.77313; cyclin-dependent kinase (CDC2-like) 10; pkinase; TM=M; SS=N; 4.53
 429109; AL008537; Hs.195352; neutrophil cytosolic factor 4 (40kD); SH3, OPR, PX; TM=M; SS=N; 4.53
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; 4.53
 411213; AA676939; Hs.69285; neuropilin 1; MAM, F5_F8_type_C, CUB, CUB, MAM, F5_F8_type_C; 4.53
 434158; T86534; Hs.14372; ESTs; adenylate kinase, none; 4.52
 431941; AK000106; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone CO; pkinase, Furin-like, Recep_L_domain, none; 4.52
 447341; AF106941; Hs.18142; arrestin, beta 2; arrestin, arrestin_C, PX, PH, PLDc; 4.52
 447656; NM_003726; Hs.19126; src kinase-associated phosphoprotein of; SH3, PH; TM=M; SS=N; 4.51
 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related; SH2, SH3, pkinase; TM=M; SS=N; 4.51
 422893; X98411; Hs.380077; myosin IF; SH3, myosin_head, IQ; TM=M; SS=N; 4.51
 407202; N58172; Hs.109370; ESTs; F5_F8_type_C, pkinase, Ets, none; 4.51
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.s.a; zf-C2H2, zf-C3HC4, UIM; TM=M; SS=N; 4.51
 450747; A064821; Hs.129953; ESTs, Highly similar to 1818357A EWS gen; mm, zf-RanBP, GAS2; 4.50
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; Ig, pkinase; TM=Y; SS=M; 4.50
 453856; AA804789; Hs.379109; PDZ-LIM protein mystique; UIM, PDZ; TM=M; SS=N; 4.49
 432744; AA988835; Hs.38664; ESTs; none, none; 4.49
 419032; W81330; Hs.99877; ESTs, Highly similar to JAK3B [H.sapiens; pkinase, SH2, Insulin, pkinase, SH2; 4.48
 444009; A1380792; Hs.135104; ESTs; TNFR_c6, TIL, none; 4.48
 426416; AW612744; Hs.169824; killer cell lectin-like receptor subfam1; lectin_c; TM=Y; SS=M; 4.48
 412802; U41518; Hs.74602; aquaporin 1 (channel-forming integral pr; MIP; TM=Y; SS=M; 4.48
 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5_F8_type_C; TM=M; SS=M; 4.47
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed; ehfand, ion_trans_K_tetra, none; 4.47
 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none; TM=M; SS=N; 4.46
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin; 4.45
 423804; AW403448; Hs.1706; interferon-stimulated transcription factor IRF, zf-C3HC4, IIR, zf-RanBP; TM=M; SS=N; 4.45
 434308; N51517; Hs.47282; ESTs; pkinase, pkinase_C, none; 4.45
 434448; W25667; Hs.184581; Homo sapiens cDNA FLJ14821 fis, clone OV; pkinase, pkinase_C; 4.45
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, integrin_B; 4.44
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 4.44
 430259; BE550182; Hs.375142; RafGEF-like protein 3, mouse homolog; In3, RA, RasGEF; TM=M; SS=M; 4.44
 436001; AW903849; Hs.173840; HUEL (C4orf1)-interacting protein; Ig; TM=M; SS=M; 4.44
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; SS=N; 4.43
 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory su; SH2, none; 4.43
 410068; A1633888; Hs.58435; FYN-binding protein (FYB-120/130); SH3; TM=M; SS=N; 4.43
 449961; AW266534; Hs.133100; ESTs; pkinase, Furin-like, Recep_L_domain, none; 4.42
 451734; NM_008176; Hs.26944; neurogranin (protein kinase C substrate); IQ, 7tm_1; TM=M; SS=N; 4.42
 410598; A1817130; Hs.9195; Homo sapiens cDNA FLJ13698 fis, clone PL; RasGEF, PRK; 4.42
 439411; AA044876; Hs.58043; ESTs, Weakly similar to CYA2_HUMAN ADENY; guanylate_cyc; TM=Y; SS=M; 4.42
 433179; AW362945; Hs.162459; ESTs; Armadillo_seg, none; 4.42
 414849; AW372721; Hs.291623; ESTs, Weakly similar to unnamed protein; pkinase, none; 4.42
 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD, helicase_C, CARD; TM=M; SS=N; 4.41
 445903; A1347487; Hs.132781; class I cytokine receptor; In3; TM=Y; SS=N; 4.41
 438507; AA809052; Hs.356627; ESTs; none, none; 4.41
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfam1; TNF; TM=Y; SS=M; 4.40
 453037; AA045175; Hs.17914; ESTs; none; TM=Y; SS=M; 4.40
 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 4.40
 451035; AU076785; Hs.430; plasmin 1 (I isoform); ehfand, CH, Adaptin_N; 4.40
 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; 4.39
 408105; AW152207; Hs.270977; ESTs, Weakly similar to I38022 hypothet; Y_phosphatase, carb_anhydrase, DSPc; none; 4.39
 423099; NM_002837; Hs.123641; protein tyrosine phosphatase, receptor t; In3, Y_phosphatase, DSPc, COX6C; TM=M; SS=M; 4.39
 438330; AW450572; Hs.257316; ESTs; pkinase, zf-C4, ERM, CNH, none; 4.39
 433437; U20536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10, ICE_p20; 4.39
 429747; M87507; Hs.2490; caspase 1, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; 4.39
 426410; BE29446; Hs.305890; BCL2-like 1; Bcl-2, BH4, none; 4.38
 434511; R29892; Hs.18106; ESTs; pkinase, Glyco_hydro_39; 4.38
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; SS=N; 4.37
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor t; In3, Ig, Y_phosphatase, MAM; TM=Y; SS=M; 4.36
 432583; AW023624; Hs.162282; potassium channel TASK-4; potassium chan; ion_trans_X; TM=Y; SS=M; 4.36
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affi; SDF; TM=Y; SS=M; 4.36
 426828; NM_000020; Hs.172670; activin A receptor type II-like 1; pkinase, Activin_rec; TM=M; SS=M; 4.35
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none; TM=Y; SS=M; 4.35
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3_cotransp; TM=Y; SS=N; 4.36
 429670; L01087; Hs.211593; protein kinase C, theta; DAG_PE-bind, pkinase, pkinase_C, DNA_pol_viral_N, PHD, DC1; TM=M; SS=N; 4.35
 421195; BE464560; Hs.133017; ESTs; none, none; 4.35

- 415758; BE270465; Hs.78793; protein kinase C, zeta; pkinase,DAG_PE-bind,pkinase_C,OPR; 4.35
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metalloho_5;TM=M;SS=N; 4.34
 419150; T29618; Hs.89640; TEK tyrosine kinase, endothelial (venous); EGF,fn3,pkinase,ig,laminin_EGF,DSL;TM=Y;SS=M; 4.34
 440675; AW005054; Hs.279788; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase,none; 4.34
 429657; D13626; Hs.2465; KIAA0001 gene product; putative G-protein; 7tm_1;TM=Y;SS=M; 4.34
 414509; AW161311; Hs.76294; CD63 antigen (melanoma 1 antigen); transmembrane4;TM=Y;SS=M; 4.34
 425771; BE561776; Hs.159494; Bruton agammaglobulinemia tyrosine kinase; SH2,SH3,pkinase,PH,BTK;TM=M;SS=N; 4.34
 452124; AA454220; Hs.61170; ESTs; pkinase,none; 4.33
 407775; NM_004914; Hs.38772; RAB36, member RAS oncogene family; ras,arf;TM=M;SS=N; 4.33
 452688; AA721140; Hs.49930; ESTs, Weakly similar to putative p150 [H]; SH3,none; 4.33
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M;SS=N; 4.32
 445330; R52656; Hs.21691; ESTs; 7tm_1,none; 4.32
 437527; AI241019; Hs.145644; ESTs; PIP5K,none; 4.32
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP,pkinase,DAG_PE-bind,RBD; 4.31
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated); ig,ITAM,Zn_cis;TM=Y;SS=M; 4.31
 416269; AA177138; Hs.161671; ESTs; pkinase,DAG_PE-bind,RBD,none; 4.30
 425458; H89317; Hs.182889; ESTs; ion_trans,none; 4.30
 424206; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc); Cu_amine_oxid,Cu_amine_oxidN2,Cu_amine_oxidN3;TM=M;SS=M; 4.29
 451876; T63141; ; gbyb99a12.s1 Stratagene lung (937210) H; SH3,none; 4.29
 417801; AA417383; Hs.82582; integrin, beta-like 1 (with EGF-like rep; EGF; 4.29
 435240; AJ025435; Hs.117532; ESTs; GHMP_kinases,none; 4.27
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none,none; 4.26
 423523; AW299828; Hs.193580; ESTs; none,none; 4.26
 426274; D38122; Hs.2007; tumor necrosis factor (ligand) superfamily; TNF;TM=Y;SS=N; 4.26
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M;SS=N; 4.26
 448386; AB037750; Hs.21061; KIAA1329 protein; PKD,BNR;TM=Y;SS=M; 4.26
 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4;TM=Y;SS=M; 4.26
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; ig,pkinase;TM=Y;SS=M; 4.26
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; EGF,vwc,TSPN; 4.25
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.25
 436494; AA720997; Hs.128295; ESTs; none,CAP_GLY,HCO3_cotransp,Glyco_hydro_63,PH; 4.24
 439668; AI091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.24
 418255; AW135405; Hs.37251; ESTs; pkinase,none; 4.24
 400328; X87344; ; transporter 2, ATP-binding cassette, sub; none;TM=Y;SS=N; 4.24
 405121; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139; 4.24
 425795; AJ000479; Hs.159543; EDG-6 (endothelial differentiation, G-p; 7tm_1;TM=Y;SS=M; 4.23
 406786; AW161678; Hs.111334; ferritin, light polypeptide; ferritin;TM=M;SS=N; 4.23
 449843; R85337; Hs.24030; solute carrier family 31 (copper transp; none;TM=Y;SS=M; 4.23
 445657; AW612141; Hs.279575; Homo sapiens G-protein coupled receptor ; 7tm_1;TM=Y;SS=M; 4.23
 413795; AL040178; Hs.142003; ESTs; none,pkinase,LRR,LRRCT; 4.22
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran,MSMC_N,SMC_C,DUF164,none; 4.22
 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M;SS=N; 4.22
 417318; AW953937; Hs.240845; ESTs; SH3,PH,RhoGEF; 4.21
 424291; AL120051; Hs.144700; ephrin-B1; Ephrin;TM=Y;SS=M; 4.21
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, com; none,none; 4.20
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 4.20
 424618; L29472; Hs.1802; major histocompatibility complex, class ; ig,MHC_II_beta;TM=Y;SS=M; 4.19
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK,none; 4.19
 432882; NM_013257; Hs.279696; serum/glucocorticoid regulated kinase-ii; pkinase,PX,pkinase_C; 4.19
 425481; AW978162; Hs.372811; ESTs; none,Oxysterol_BP; 4.19
 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M;SS=N; 4.18
 401083; ; NM_016582; Homo sapiens peptide transp; PTR2;TM=Y;SS=M; 4.18
 420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 4.18
 424377; AF081675; Hs.146322; killer cell lectin-like receptor subfam; lectin_c;TM=Y;SS=M; 4.17
 424148; BE242274; Hs.1741; integrin, beta 7; integrin_B,EGF,metalho,PSI;TM=Y;SS=M; 4.17
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor tran; ig,none; 4.17
 452100; AI668668; Hs.379032; inositol polyphosphate-5-phosphatase, 75; Exo_endo_phos,RhoGAP,none; 4.17
 413969; X14034; Hs.75646; phospholipase C, gamma 2 (phosphatidylin; SH2,SH3,C2,PH,PI-PLC-Y,PI-PLC-X,PDG; 4.17
 422310; AA316622; Hs.98307; cytochrome P450, subfamily IIS, polypept; none,pkinase,fn3,ig; 4.17
 444034; AL181957; Hs.10177; pleckstrin homology domain interacting p; E1-E2,ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,Ribosomal_S15,bromodomain,WD40;TM=M;SS=N; 4.16
 450056; BE047394; Hs.502; ESTs, Weakly similar to S71512 hypothet; ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.16
 407245; X90568; Hs.172004; iitin; fn3,ig,SGXSG,pkinase;TM=M;SS=N; 4.16
 418962; AA714835; Hs.271863; ESTs; RhoGAP,SH2,pkinase,POLO_box,none; 4.15
 410590; BE615216; Hs.64746; chloride intracellular channel 3; none;TM=M;SS=N; 4.15
 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2;TM=Y;SS=N; 4.15
 446967; AI699629; Hs.156781; ESTs; none,none; 4.14
 432176; AW090386; Hs.112278; arrestin, beta 1; arrestin,arrestin_C,none; 4.14
 452571; W31518; Hs.34665; ESTs; none;TM=M;SS=N; 4.14
 425421; L11669; Hs.157145; tetracycline transporter-like protein; sugar_tr;TM=Y;SS=M; 4.14
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase; 4.14
 417871; AA521368; Hs.24252; ESTs; IBB,Armaddillo_seg,none; 4.13
 429819; AL133011; Hs.253920; Homo sapiens mRNA; cDNA DKFp434P201 (fr; none,none; 4.12
 424522; AL134847; Hs.149957; ribosomal protein S6 kinase, 90kD, polyp; pkinase,pkinase_C; 4.12
 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase,RGS;TM=M;SS=N; 4.12
 413019; BE281604; Hs.75140; low density lipoprotein-related protein-; none;TM=M;SS=Y; 4.12
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M;SS=N; 4.11
 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK;TM=Y;SS=N; 4.11
 449656; AA002008; Hs.188833; ESTs; PIP5K,none; 4.11
 406403; ; NM_002162; Homo sapiens intercellular ad; ig;TM=Y;SS=M; 4.10
 427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 4.10
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,RIO1,none; 4.10
 432885; AA595607; Hs.368129; ESTs, Weakly similar to ALU1_HUMAN ALU S; pkinase,pkinase_C,none; 4.10

- 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase,pkinase_C,HR1;TM=M;SS=N; 4.10
 418342; BE002723; Hs.334330; leptin receptor; ICE_p20,DED,ICE_p10,ICE_p20,DED; 4.10
 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese;; 4.10
 435905; AW97484; Hs.5003; KIAA0456 protein; SH3,RhoGAP,FCH;TM=M;SS=N; 4.10
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 4.10
 437952; D63209; Hs.5944; solute carrier family 11 (proton-coupled; none;TM=Y;SS=M; 4.10
 432827; Z68128; Hs.3109; Rho GTPase activating protein 4; FCH,RhoGAP,SH3;TM=M;SS=N; 4.09
 435140; AA668123; Hs.134170; ESTs; none,none; 4.09
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fascidin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.08
 428483; AI908539; Hs.184592; KIAA0344 gene product; none,none; 4.08
 446232; AI281848; Hs.194691; retinoic acid induced 3; 7tm_3,none; 4.07
 431674; AA098901; Hs.301642; G-protein coupled receptor; none,GCV_H; 4.07
 409686; AK000002; Hs.55879; Homo sapiens mRNA; cDNA DKFZp434L0827 (f; ABC_tran,ABC_membrane;TM=M;SS=M; 4.07
 441518; AW161697; Hs.294150; ESTs; Y_phosphatase,DSF;none; 4.07
 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M;SS=N; 4.06
 436982; AB018305; Hs.5378; spondin 1, (f-spondin) extracellular mat; tsp_1,Reeler; 4.05
 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP,7tm_1; 4.05
 439549; AW937885; Hs.137314; ESTs; SH2,none; 4.04
 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR;none; 4.04
 418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recpt,PDZ,ZU5,death; 4.04
 408806; AW847814; Hs.75608; Homo sapiens cDNA; FLJ21532 fis, clone C; SH3,PDZ,Guanylate_kin,none; 4.04
 432106; N58323; Hs.269098; ESTs; Weakly similar to RETROVIRUS-RELAT; SH3,PDZ,Guanylate_kin,none; 4.03
 426086; T94907; Hs.188572; ESTs; PH,ELs,CH,spectrin,Ca_channel_B,none; 4.03
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS;; 4.03
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M;SS=N; 4.03
 416350; AF188525; Hs.189507; phospholipase A2, group IID; phospho;TM=M;SS=Y; 4.02
 434457; AF141332; Hs.200333; apolipoprotein B48 receptor; none;TM=M;SS=N; 4.02
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M;SS=N; 4.02
 425694; U51333; Hs.159237; hexokinase 3 (white cell); hexokinase,hexokinase2;TM=M;SS=N; 4.02
 449943; AF104266; Hs.24212; latrophilin; 7tm_2,GPS,Gal_Lectin,OLF,Latrophilin,HRM;TM=Y;SS=M; 4.01
 408938; AA059013; Hs.22607; ESTs; tn3,Y_phosphatase,carb_anhydrase,none; 4.01
 426839; M74782; Hs.172689; interleukin 3 receptor, alpha (low affin; none;TM=M;SS=M; 4.00
 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExcB;TM=Y;SS=M; 4.00
 410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase,none; 4.00
 428318; BE300110; Hs.183842; ubiquitin B; lipocalin,aldehyd,ubiquitin,IRK;; 4.00
 440188; AK001812; Hs.7036; N-Acetylglucosamine kinase; ROK;TM=M;SS=N; 3.99
 429952; AF080158; Hs.226573; Inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 3.99
 414700; H63202; Hs.38163; ESTs; 7tm_1;TM=Y;SS=M; 3.99
 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met; pkinase,Sema,PSI,TIG,A4_EXTRA;TM=M;SS=M; 3.99
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M;SS=N; 3.98
 427541; AF798983; Hs.375835; solute carrier family 35 (CMP-static acid; none,none; 3.98
 440248; AA876138; Hs.369458; ESTs; SH2,none; 3.98
 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6,laminin_EGF;TM=Y;SS=N; 3.98
 425262; D87119; Hs.155418; GS3955 protein; pkinase; 3.98
 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (letr; transmembrane4;TM=Y;SS=M; 3.98
 437151; AA745618; Hs.380121; BANP homolog, SMAR1 homolog; none,none; 3.98
 443574; U83993; Hs.321709; purinergic receptor P2X, ligand-gated io; P2X_receptor;TM=Y;SS=M; 3.97
 449027; AJ271216; Hs.22890; dipeptidylpeptidase II; Peptidase_M49,EGF,Ig,Neuregulin;TM=M;SS=N; 3.97
 411574; BE242842; Hs.6780; protein tyrosine kinase 9-like (A6-relat; LRR,LRRCT,TIR,cofilin_ADF;TM=M;SS=N; 3.97
 432639; AW973785;; gb:EST385886 MAGE resequences, MAGM Homo; none,IRK; 3.97
 457675; AF119917; Hs.305574; Homo sapiens PRO3098 mRNA, complete cds; none; 3.97
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2,PH;TM=M;SS=N; 3.96
 437157; BE048860; Hs.17287; ESTs; IRK,none; 3.96
 453641; AA444140; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 3.96
 446714; W73818; Hs.110028; ESTs; 7tm_1,7tm_1; 3.96
 427648; AJ376722; Hs.180062; proteasome (prosome, macropain) subunit; proteasome;; 3.96
 453688; AL110326; Hs.304679; ESTs, Moderately similar to Z195_HUMAN Z; none,lectin_c,lig_chan; 3.96
 457718; F18572; Hs.22978; ESTs, Weakly similar to ALU4_HUMAN ALU S; pkinase,pkinase; 3.95
 428727; AF078847; Hs.78452; general transcription factor IIH, polype; PHO4,LIM;TM=M;SS=N; 3.95
 435411; AW444619; Hs.138211; ESTs; none,pkinase; 3.94
 440209; H05049; Hs.247837; neurexin 3; laminin_G,EGF,none; 3.94
 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic; none,none; 3.94
 435272; AA906415; Hs.110041; ESTs; none,pkinase; 3.93
 402550;; Target Exon; none,none; 3.93
 425233; Z17861; Hs.155218; E1B-55kDa-associated protein 5; SPRY,SAP,pkinase,fn3,Ig; 3.93
 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), a; Stathmin,Vinculin; 3.92
 453548; AL079983; Hs.116774; integrin, alpha 1; none,vwa,FG-GAP,Integrin_A; 3.92
 417226; AW505054; Hs.4283; ESTs; pkinase,RGS,PH,myosin_head,Myosin_tail; 3.92
 446755; AW451473; Hs.16134; serine/threonine kinase 10; pkinase,TYA;TM=M;SS=N; 3.92
 452344; AI264357; Hs.55405; hypothetical protein MGC16212; Sulfate_transp,STAS; 3.92
 418516; NM_006218; Hs.85701; phosphoinositide-3-kinase, catalytic, al; PI3_PI4_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85,none; 3.91
 423069; W15613; Hs.1613; adenosine A2a receptor; 7tm_1;TM=Y;SS=M; 3.91
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; lg,pkinase;TM=Y;SS=N; 3.91
 434392; AW983709; Hs.250824; Homo sapiens cDNA; FLJ23435 fis, clone H; pkinase,none; 3.91
 429615; AF258627; Hs.211562; ATP-binding cassette, sub-family A (ABC1; ABC_tran;TM=Y;SS=M; 3.91
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,trypsin,plant_thionins;; 3.91
 442831; AI798959; Hs.131686; ESTs; ABC_tran,PRK,ABC_tran; 3.91
 441657; BE314696; Hs.7936; BAI1-associated protein 2; SH3;TM=M;SS=N; 3.91
 438698; AW297855; Hs.361171; ESTs, Weakly similar to I38022 hypothetel; lipoxigenase,PLAT,none; 3.90
 447560; AF065214; Hs.18858; phospholipase A2, group IVC (cytosolic; PLA2_B;TM=M;SS=N; 3.90
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zf-DHHC,none; 3.89
 429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase,RIOT;TM=M;SS=N; 3.89
 410179; W27723; Hs.59498; cell division cycle 2-like 5 (cholinester; pkinase;; 3.89

- 428713; AA432057; Hs.268551; ESTs, Moderately similar to CYA4 RAT ADE; pkinase; 3.89
 456629; AW891965; Hs.357942; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD;none; 3.89
 425190; AW028302; Hs.155079; protein phosphatase 2, regulatory subunit; B56;TM=M;SS=N; 3.89
 426752; X69490; Hs.172004; iitin; fn3,ig,pkinase,SGXXSG;TM=M;SS=N; 3.89
 417767; BE242241; Hs.82542; acyltoxyacyl hydrolase (neutrophil); Lipase_GDSL;TM=M;SS=M; 3.88
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (calion dep; Man-6-P_recep;TM=M;SS=M; 3.88
 416140; AI918035; Hs.301198; roundabout (axon guidance receptor, Dros; none;none; 3.88
 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe co; fn3;TM=Y;SS=M; 3.88
 410011; AB020641; Hs.57856; PFTAIRE protein kinase 1; pkinase;TM=M;SS=N; 3.87
 406908; Z25437; ; gb:H.sapiens protein-tyrosine kinase gen; none;none; 3.87
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN; 3.87
 441859; AW194364; Hs.9877; Interleukin-4 induced gene-1 protein (FI; Amino_oxidase,FAD_binding_3,TBC;TM=M;SS=N; 3.87
 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triph; Ham1p_like;TM=M;SS=N; 3.87
 415392; Z44067; Hs.10957; ESTs; PIP5K;none; 3.86
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 3.86
 414543; AI672727; Hs.76753; endoglin (CD105 antigen) (ENG); none;TM=Y;SS=N; 3.85
 425729; L22647; Hs.159360; prostaglandin E receptor 1 (subtype EPI); 7tm_1;TM=Y;SS=M; 3.85
 414496; W73853; Hs.355424; ESTs; pkinase,F5_F8_type_C,adh_short;none; 3.84
 412204; AI125507; Hs.24937; ESTs; lg,rm;none; 3.84
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase,ATP-sulfurylase,PRK,Thymidylate_kinc; 3.84
 444981; AW855398; Hs.12210; hypothetical protein FLJ13732 similar to; SH2;TM=M;SS=N; 3.84
 412309; M23892; Hs.73809; arachidonate 15-lipoxygenase; lipoxygenase,PLAT; 3.84
 405545; ; Target Exon; ABC_tran,SRP54,ABC_membrane;TM=Y;SS=M; 3.84
 407143; C14076; Hs.332329; EST; none;TM=Y;SS=M; 3.84
 420593; AA280356; Hs.187634; ESTs; B56;none; 3.84
 413420; AW410235; Hs.75348; proteasome (prosome, macropain) activator; PA28_alpha,PA28_beta,biopterin_H; 3.83
 448253; H25899; Hs.201591; ESTs; 7tm_2,HRM;none; 3.83
 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHIT; ABC_tran,PRK,GBP;TM=Y;SS=N; 3.83
 430397; AI924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp;TM=Y;SS=N; 3.83
 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, bc; fn3;TM=Y;SS=M; 3.83
 458188; AW297226; Hs.137840; ESTs, Moderately similar to SIX4_HUMAN H; pkinase,WD40; 3.82
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (f; pkinase;none; 3.82
 428791; AA435661; Hs.264750; ESTs; zf-C3HC4;none; 3.82
 438068; AI927209; Hs.306210; Homo sapiens cDNA: FLJ23133 fis, clone L; NusG; 3.82
 453370; AI470523; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=N; 3.82
 419250; AW770185; Hs.356066; U5 snRNP-specific protein, 116 kD; 7tm_1,BAH,zf-CXXC,DNA_methylase; 3.82
 410017; AW959246; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none;none; 3.82
 420679; X57152; Hs.165843; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M;SS=N; 3.82
 417916; NM_006416; Hs.82921; solute carrier family 35 (CMP-sialic aci; DUF6;TM=Y;SS=M; 3.81
 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, de; none;none; 3.81
 417365; D50683; Hs.82028; transforming growth factor, beta receptor; pkinase,WD40;TM=Y;SS=N; 3.64
 4145817; D28124; Hs.76307; neuroblastoma, suppression of tumorigenit; DAN;TM=M;SS=M; 3.52
 422398; AI476149; Hs.334489; hypothetical protein FLJ21992; SH2,SH3; 3.51
 418432; M14156; Hs.85112; insulin-like growth factor 1 (somatomedin; Insulin; 3.50
 459705; BE082764; Hs.270252; ESTs, Weakly similar to androgen receptor, none, C2,WV,HECT; 3.48
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3,ig,Y_phosphatase,MAM;TM=Y;SS=M; 3.38
 415817; U88967; Hs.78867; protein tyrosine phosphatase, receptor-t; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 3.37
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2 (str; Fz,NTR; 3.24
 426125; X87241; Hs.166994; FAT tumor suppressor (Drosophila) homolog; EGF,cadherin,laminin_G;TM=Y;SS=M; 3.11
 419721; NM_001650; Hs.315369; aquaporin 4; MIP;none; 2.99
 433147; AF091434; Hs.43080; platelet derived growth factor C; PDGF,CUB; 2.91
 417976; BE565892; Hs.83077; interleukin 18 (interferon-gamma-inducin; none;TM=M;SS=N; 2.89
 439180; AI393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.59
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.23
 411089; AA458454; Hs.355702; cell division cycle 2-like 1 (PITSLRE pr; none;none; 2.07
 428800; M57627; Hs.193717; Interleukin 10; IL10; 1.10

TABLE 40B

60	Pkey:	Unique Eos probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
65	Pkey	CAT Number Accession
	458034	685586_1 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945
	459702	539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	432222	539529_1 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354
	414991	1785136_1 D78831 C17898 D78863
70	409745	MH1944_5 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625
		BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377
		AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
	414936	1782849_1 C14774 C17911 D79033
	451876	2328579_1 T63141 AI821021 BF370092 BF370127 BF370060 T62998
75	432639	1237887_1 AW973785 H60163 AA557608

TABLE 40C

80	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

5	Pkey	Ref	Strand	NL_position
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	404240	5002624	Minus	116132-116407,116653-116922
	405102	8076881	Minus	120922-121296
	405121	8102330	Minus	35816-36004,36587-36684
10	401083	3242744	Plus	33192-33360
	406403	9256305	Minus	151426-151680
	402550	7652009	Minus	80413-80673
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182

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TABLE 41A: 556 GENES UP-REGULATED IN PANCREATIC TUMORS OR PANCREATITIS RELATIVE TO NORMAL TISSUES

20 Table 41A lists about 556 genes up-regulated in pancreatic tumors or pancreatitis relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix HuO3 Genechip array.

25	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
	R1:	90th percentile of pancreatic cancer/median of normal pancreas			
	Pkey	ExAccn	UnigeneID	Unigene Title	R1
30	412228	AW503785	Hs.73792	complement component (3d/Epstein Barr vi	7.25
	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	1.64
	444995	AJ272265	Hs.12230	secreted phosphoprotein 2, 24kD	3.58
	453863	X02544	Hs.572	orosomucoid 1	114.18
	441031	A110684	Hs.7645	fibrinogen, B beta polypeptide	922.40
35	421344	AW631030	Hs.103665	villin-like	2.19
	416018	AW138239	Hs.78977	proprotein convertase subtilisin/kexin 1	61.10
	438091	AW373062	Hs.83623	nuclear receptor subfamily 1, group 1, m	607.40
	418888	AU076801	Hs.89436	cadherin 17, LI cadherin (liver-intestin	228.20
	418969	W33191	Hs.28907	hypothetical protein FLJ20258	4.97
40	443162	T49951	Hs.9029	DKFZP434G032 protein	38.01
	423096	AA732684	Hs.278428	progesterone induced protein	189.60
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	11.06
	448243	AW369771	Hs.52620	integrin, beta 8	116.90
	421044	AF061871	Hs.311736	Human DNA sequence from clone RP1-238D15	21.52
45	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.74
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (COM	3.11
	432467	T03667	Hs.239388	Human DNA sequence from clone RP1-304B14	307.70
	457059	BE561665	Hs.177677	exosome component Rrp40	33.60
	451945	BE504055	Hs.211420	ESTs	7.31
50	453354	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE	133.70
	443247	BE614387	Hs.333893	c-Myc target JPO1	349.10
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	330.00
	416984	H38765	Hs.80706	diaphorase (NADH/NADPH) (cytochrome b-5	3.78
	413835	A1272727	Hs.249163	fatty acid hydroxylase	3.53
55	433790	BE298215	Hs.288968	RAB22A, member RAS oncogene family	73.90
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.39
	410639	BE269047	Hs.65234	hypothetical protein FLJ20596	1.72
	410541	AA065003	Hs.64179	syntenin-2 protein	10.29
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	6.79
60	429612	AF062649	Hs.252587	pituitary tumor-transforming 1	4.62
	407604	AW191962	Hs.249239	collagen, type VIII, alpha 2	366.30
	431193	AW749505	Hs.296770	KIAA1719 protein	6.99
	442080	AW444761	Hs.44565	ESTs	118.00
	427670	BE612888	Hs.180224	myosin regulatory light chain	2.73
65	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	647.30
	419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	738.90
	441633	AW585544	Hs.112242	normal mucosa of esophagus specific 1	68.43
	407792	AU077715	Hs.39384	putative secreted ligand homologous to f	3.03
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	7.73
70	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	227.30
	418384	AW149266	Hs.25130	Homo sapiens cDNA FLJ14923 fis, clone PL	115.60
	452355	N54926	Hs.29202	G protein-coupled receptor 34	192.20
	419481	A1879195	Hs.90606	15 kDa selenoprotein	119.90
	407230	AA157857	Hs.182265	keratin 19	12.11
75	418526	BE019020	Hs.85838	solute carrier family 16 (monocarboxylic	6.63
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	592.10
	411498	NM_014210	Hs.70499	ecotropic viral integration site 2A	120.40
	445517	AF208855	Hs.12830	hypothetical protein	117.40
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	4.25
80	428385	AF112213	Hs.184052	putative Rab5-interacting protein	3.12
	448563	BE614599	Hs.106823	hypothetical protein MGC14797	135.20
	406867	AA157857	Hs.182265	keratin 19	11.32
	417426	NM_002291	Hs.82124	laminin, beta 1	406.20

	406366	AF026692	Hs.105700	secreted frizzled-related protein 4	0.62
	401201	#(NOCAT)		Target Exon	0.75
	420767	AF072711	Hs.99918	carboxyl ester lipase (bile salt-stimula	0.63
5	405556	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.75
	442776	AW959498	Hs.8709	chymotrypsin C (caldecrin)	0.67
	405555	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	0.83
	403207	#(NOCAT)		C2000960.gi 131432 sp P23132 LUTH_BOVIN	0.80
	427858	NM_001971	Hs.21	elastase 1, pancreatic	0.98
10	426004	AW600300	Hs.124123	ESTs, Moderately similar to SYNLRAT SYN	0.88
	401541	NA		Target Exon	0.91
	429793	AI417638	Hs.114648	estrogen regulated gene 1	0.85
	423068	M25629	Hs.123107	kalikrein 1, renal/pancreas/salivary	0.81
	433110	D56494	Hs.3191	rat regenerating islet-derived-like, hum	0.72
15	425988	BE045897	Hs.274454	ESTs, Weakly similar to 138022 hypotheti	0.95
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	0.87
	412470	M93283	Hs.73923	pancreatic lipase-related protein 1	0.89
	431969	AA366217	Hs.2879	carboxypeptidase A1 (pancreatic)	0.97
	419219	AW583139	Hs.89717	carboxypeptidase A2 (pancreatic)	0.95
20	412688	AW583062	Hs.74502	chymotrypsinogen B1	0.95
	427811	M81057	Hs.180884	carboxypeptidase B1 (tissue)	1.07
	420937	AW966719	Hs.1340	colipase, pancreatic	0.99
	418068	AW971155	Hs.293902	ESTs, Weakly similar to ISHUSS protein d	1.02
	410839	NM_006849	Hs.66581	protein disulfide isomerase	1.00
25	437986	AA774575	Hs.121776	testis expressed sequence 11	1.02
	415934	NM_000928	Hs.992	phospholipase A2, group IB (pancreas)	1.06
	427965	D00306	Hs.181289	elastase 3, pancreatic (protease E)	1.22
	406399	#(NOCAT)		NM_003122*:Homo sapiens serine protease	1.08
	426230	AA367019	Hs.241395	protease, serine, 1 (trypsin 1)	1.11
30	414061	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	1.22
	421243	AW873803	Hs.102876	pancreatic lipase	1.13
	419263	AW583874	Hs.89832	Insulin	1.12
	424208	AW583123	Hs.143113	pancreatic lipase-related protein 2	1.13
	408983	NM_000492	Hs.663	cystic fibrosis transmembrane conductanc	1.32
35	436217	T53925	Hs.107	fibrinogen-like 1	1.72
	435975	AL118990	Hs.41997	alpha-1-B glycoprotein	1.60
	431330	X69532	Hs.2777	Inter-alpha (globulin) inhibitor, H1 pol	2.02
	414463	T69078	Hs.76177	alpha-1-microglobulin/bikunin precursor	1.82
	415003	M11437	Hs.77741	kininogen	3.83
40	422281	M36803	Hs.1504	hemopexin	2.14
	414910	X12662	Hs.289057	arginase, liver	97.90
	417296	L36196	Hs.81884	sulfotransferase family, cytosolic, 2A,	236.70
	400836	#(NOCAT)		Target Exon	2.47
	452983	L32140	Hs.531	afamin	117.10
45	419768	T72104	Hs.93194	apolipoprotein A-I	4.87
	413841	M34276	Hs.75576	plasminogen	374.00
	400560	#(NOCAT)		NM_030878*:Homo sapiens cytochrome P450,	144.50
	419502	AU076704	Hs.90765	fibrinogen, A alpha polypeptide	266.50
50	425746	NM_001701	Hs.159440	bile acid Coenzyme A: amino acid N-acylt	77.80
	426205	D63521	Hs.167877	leukocyte cell-derived chemotaxin 2	169.80
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	3.60
	443614	AV655386	Hs.7645	fibrinogen, B beta polypeptide	400.40
	429023	NM_000312	Hs.2351	protein C (inactivator of coagulation fa	4.72
55	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	5.26
	425260	L47726	Hs.1870	phenylalanine hydroxylase	73.78
	443316	AI478463	Hs.18443	aldehyde dehydrogenase 8 family, member	182.20
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	335.00
	413829	NM_001872	Hs.75572	carboxypeptidase B2 (plasma)	173.40
	421126	M74587	Hs.102122	insulin-like growth factor binding prote	565.30
60	407731	NM_000066	Hs.38069	complement component 8, beta polypeptide	86.20
	413585	AI133452	Hs.75431	fibrinogen, gamma polypeptide	477.20
	452624	AU076606	Hs.30054	coagulation factor V (proaccelerin, labi	201.50
	416402	NM_000715	Hs.1012	complement component 4-binding protein,	426.10
	425573	AB006423	Hs.158308	serine (or cysteine) proteinase inhibito	1.10
65	421905	AI660247	Hs.32699	ESTs, Weakly similar to LIV-1 protein [H	0.62
	406672	M26041	Hs.198253	major histocompatibility complex, class	4.02
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (5.34
	421712	AK000140	Hs.107139	hypothetical protein	5.62
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	8.85
70	442896	R37725	Hs.261108	ESTs	157.70
	410566	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	137.70
	428486	AW583497	Hs.184604	pancreatic polypeptide	2.59
	457489	AI693815	Hs.127179	cryptic gene	3.23
	404866	NA		ENSP00000251112*:Sodium/potassium-transp	2.84
75	432874	W94322	Hs.279651	melanoma inhibitory activity	2.48
	445891	AW391342	Hs.199460	ESTs	70.38
	404682	NA		C9001188*.gi 12738842 ref NP_073725.1 p	1.38
	429547	AW009166	Hs.99376	ESTs	6.85
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	5.21
80	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	1.74
	446868	AV660737	Hs.135100	ESTs	102.10
	404287	NA		C6001909:gi 704441 dbj BAA18909.1 (D298	242.70
	443267	AW450630	Hs.133851	ESTs	98.90
	451635	AA018899	Hs.127179	cryptic gene	2.16

5	417801	AA417383	Hs.82582	integrin, beta-like 1 (with EGF-like rep	131.70
	414142	AW368397	Hs.150042	Homo sapiens cDNA FLJ14438 fis, clone HE	128.70
	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitte	92.90
	410309	BE043077	Hs.278153	ESTs	108.80
	425842	AI587490	Hs.159623	NK-2 (Drosophila) homolog B	170.10
10	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	75.70
	449592	AI655494	Hs.195718	ESTs	4.58
	414259	W44633	Hs.301296	Homo sapiens cDNA: FLJ23131 fis, clone L	188.50
	406585	M18728		gb:Human nonspecific crossreacting antig	1123.60
	411573	AB029000	Hs.70823	KIAA1077 protein	995.60
15	429201	X03178	Hs.198246	group-specific component (vitamin D bind	11.32
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	8.38
	428698	AA852773	Hs.334838	KIAA1866 protein	662.00
	444754	T83911	Hs.11881	transmembrane 4 superfamily member 4	4.00
	432596	AJ224741	Hs.278461	matrilin 3	283.50
20	428824	W23624	Hs.173059	ESTs	4.55
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.01
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.21
	418394	AF132818	Hs.84728	Kruppel-like factor 5 (intestinal)	4.80
	448844	AI581519	Hs.177164	ESTs	362.80
25	420908	AL049974	Hs.100261	Homo sapiens mRNA; cDNA DKFZp564B222 (fr	133.90
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	128.20
	428392	H10233	Hs.2265	secretory granule, neuroendocrine protei	13.83
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	316.00
	452571	W31518	Hs.34665	ESTs	245.50
30	443646	AI085198	Hs.164226	ESTs	189.40
	436032	AA150797	Hs.109276	latexin protein	291.10
	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	252.20
	422109	S73265	Hs.1473	gastrin-releasing peptide	278.20
	430407	H23551	Hs.30974	ESTs	6.20
35	419235	AW470411	Hs.288433	neurotrophin	423.50
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.01
	444301	AK000136	Hs.10760	asporin (LRR class 1)	499.90
	427333	AF067797	Hs.176658	aquaporin 8	1.05
	417931	W95642	Hs.82951	trefoil factor 3 (intestinal)	4.33
40	407777	AA161071	Hs.71465	squalene epoxidase	3.64
	435652	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	1.47
	421341	AJ243212	Hs.279611	deleted in malignant brain tumors 1	3.98
	453935	AI633770	Hs.42572	ESTs	2.08
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.84
45	439737	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN	14.21
	426227	U67058	Hs.168102	Human proteinase activated receptor-2 mR	315.70
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.53
	412104	AW205197	Hs.240951	Homo sapiens, Similar to RIKEN cDNA 2210	3.13
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	9.33
50	440484	BE328156	Hs.150356	ESTs	1.03
	447395	AI418412	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	1.09
	440099	AL080058	Hs.6909	DKFZP564G202 protein	14.74
	434665	AA642125		gb:nr60c01.s1 NCI_CGAP_Lym3 Homo saplens	0.98
	452194	AI694413	Hs.332649	olfactory receptor, family 2, subfamily	2.23
55	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	329.40
	424411	NM_005209	Hs.146549	crystallin, beta A2	1.71
	426575	M74826	Hs.170808	glutamate decarboxylase 2 (pancreatic is	2.69
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	1.70
	426322	J06068	Hs.2012	transcobalamin I (vitamin B12 binding pr	3.19
60	429010	Y18198	Hs.194725	one cut domain, family member 2	1.96
	414420	AA043424	Hs.76095	Immediate early response 3	2.54
	422565	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	3.30
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	312.80
	441350	AB020690	Hs.7782	paraneoplastic antigen MA2	177.80
65	406173	#(NOCAT)		ENSP00000250148*:Growth hormone variant	1.46
	403776	#(NOCAT)		ENSP00000226542*:Small inducible cytokin	121.80
	403574	NA		Target Exon	16.12
	428832	AA578229	Hs.324239	ESTs, Moderately similar to ZN91_HUMAN Z	3.94
	458449	H04482	Hs.29019	ESTs	71.60
70	409958	NM_001523	Hs.57697	hyaluronan synthase 1	1.77
	437100	AI761073	Hs.14535	Homo sapiens cDNA: FLJ22314 fis, clone H	3.13
	451181	AI796330	Hs.207461	ESTs	68.00
	440508	BE267911	Hs.196970	ESTs	38.00
	429636	AA455692	Hs.163232	ESTs	30.70
75	419570	W68738		gb:zd37g06.s1 Soares_fetal_heart_NbHH19W	1.02
	431779	AW971178	Hs.268571	apolipoprotein C-I	3.36
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	10.20
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (MMP7; uterin	3.94
	423961	D13666	Hs.136348	osteoblast specific factor 2 (fascidin	1171.10
80	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	809.50
	440482	AA886658	Hs.50873	ESTs	9.95
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	30.70
	423401	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	82.90
	425239	AW379378	Hs.170121	protein tyrosine phosphatase, receptor t	26.01
80	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	5.38
	409335	NM_001502	Hs.53965	glycoprotein 2 (zymogen granule membrane	0.54
	426876	AA918425	Hs.177744	ESTs	0.89

	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	0.94
	401732	#(NOCAT)		NM_001176*:Homo sapiens Rho GDP dissociation	1.13
	404142	NA		Target Exon	1.33
5	424165	AW582904	Hs.142255	islet amyloid polypeptide	2.95
	413880	AI660842	Hs.110915	interleukin 22 receptor	1.34
	407007	U22961		gb:Human mRNA clone with similarity to L	1.57
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	1.48
	432855	AF017888	Hs.279565	secreted frizzled-related protein 5	1.28
10	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	1.31
	445730	AI624342	Hs.170042	ESTs	2.14
	408666	V00495	Hs.184411	albumin	2.95
	435849	BE305242	Hs.16098	claudin 2	1.96
	426784	U03749	Hs.172216	chromogranin A (parathyroid secretory pr	2.49
	430272	X04898	Hs.237658	apolipoprotein A-II	3.29
15	412374	X01388	Hs.73849	apolipoprotein C-II	2.42
	419276	BE165909	Hs.306881	MSTP043 protein	83.40
	415448	T68645	Hs.952	solute carrier family 10 (sodium/bile ac	3.52
	423541	AA296922	Hs.129778	gastrointestinal peptide	3.16
	428355	BE256452	Hs.2257	vitronectin (serum spreading factor, som	6.24
20	425551	AA359252	Hs.126485	hypothetical protein FLJ12604; KIAA1692	14.67
	455630	AV655701	Hs.75183	cytochrome P450, subfamily IIE (ethanol-	4.30
	428786	Y16577	Hs.2314	mannose-binding lectin (protein C) 2, so	92.10
	420726	K02402	Hs.1330	coagulation factor IX (plasma thrombopla	203.30
	451253	H48299	Hs.26126	claudin 10	1.37
25	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	3.38
	413881	L00190	Hs.75599	serine (or cysteine) proteinase inhibitor	7.04
	431930	AB035301	Hs.272211	cadherin 7, type 2	5.84
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.65
30	419354	M62839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	9.28
	422237	M13149	Hs.1498	histidine-rich glycoprotein	34.26
	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	1.92
	414386	X00442	Hs.75990	haploglobin	8.32
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (MMP11; stro	1.74
35	452689	F33868	Hs.284176	transferrin	6.51
	436624	T64287	Hs.5241	fatty acid binding protein 1, liver	35.08
	409187	AF154830	Hs.50966	carbamoyl-phosphate synthetase 1, mitoch	170.30
	428874	W32133	Hs.194366	transferrin (prealbumin, amyloidosis I	2.34
	405849	#(NOCAT)		Target Exon	103.10
40	405281	#(NOCAT)		NM_002864:Homo sapiens pregnancy-zone pr	31.20
	419078	M93119	Hs.89584	insulinoma-associated 1	6.28
	422095	AI868872	Hs.282804	hypothetical protein FLJ22704	2.89
	425834	NM_001639	Hs.1957	amyloid P component, serum	3.80
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	1.82
45	407244	M10014	Hs.75431	fibrinogen, gamma polypeptide	13.15
	450400	AI894722	Hs.279744	ESTs	5.22
	413916	N49813	Hs.75615	apolipoprotein C-II	8.60
	444632	AI184027	Hs.146986	ESTs, Weakly similar to FATH_HUMAN CADHE	71.30
	415906	AI751357	Hs.288741	Homo sapiens cDNA: FLJ22256 fis, clone H	1.70
50	410197	NM_005518	Hs.59889	3-hydroxy-3-methylglutaryl-Coenzyme A sy	4.65
	417366	BE185289	Hs.1076	small proline-rich protein 1B (cornitin)	3.01
	436961	AW375974	Hs.156704	ESTs	164.60
	446319	AW207590	Hs.160711	ESTs	1.88
	427899	AA829286	Hs.332053	serum amyloid A1	6.98
55	419092	J05581	Hs.89603	mucin 1, transmembrane	2.12
	421515	Y11339	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I	132.20
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.23
	406319	NA		CX000780:gl[6579197]ref[NP_032800.1] pol	51.50
	404286	NA		C6001909:gl[704441]dbj[BAA18909.1] [D298	1.75
60	419183	U60669	Hs.89663	cytochrome P450, subfamily XXIV (vitamin	52.90
	406293	NA		Target Exon	68.30
	431912	AI660552	Hs.154903	ESTs, Weakly similar to A56154 Abl subst	102.43
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	206.30
	425200	BE255203	Hs.155101	ATP synthase, H transporting, mitochondr	5.76
65	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	200.10
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	97.70
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	3.96
	429921	AA526911	Hs.82772	collagen, type XI, alpha 1	30.00
	428758	AA433988	Hs.98502	hypothetical protein FLJ14303	4.66
70	446998	N99013	Hs.16762	Homo sapiens mRNA; cDNA DKFZp56482062 (f	193.80
	418478	U38945	Hs.1174	cyclin-dependent kinase inhibitor 2A (me	3.05
	420001	J05064	Hs.1282	complement component 6	159.00
	449038	AL133084	Hs.22908	Homo sapiens mRNA; cDNA DKFZp434J1027 (f	39.10
	423184	NM_004428	Hs.1624	eptin-A1	2.39
75	428505	AL035461	Hs.2281	chromogranin B (secretogranin I)	327.90
	444783	AK001468	Hs.62180	amitin (Drosophila Scars homolog), act	90.50
	445593	AW203963	Hs.150896	ESTs	49.20
	450701	H39960	Hs.283467	Homo sapiens cDNA FLJ12280 fis, clone MA	3.12
	424420	BE614743	Hs.146688	prostaglandin E synthase	1.93
80	408660	AA525775	Hs.292523	ESTs, Moderately similar to PC4259 ferri	39.90
	417940	R28205	Hs.24230	ESTs	57.20
	434206	AW136973	Hs.288516	ESTs, Weakly similar to S69890 mitogen i	2.51
	439920	H05430	Hs.288433	neurotrophin	1.91
	432542	AW083920	Hs.16098	claudin 2	3.47

	410418	D31382	Hs.63325	transmembrane protease, serine 4	3.82
	415989	AI257700	Hs.317584	ESTs	182.50
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.84
5	400024			AFFX control - HUMRGE/M10098_5	4.82
	418067	AI127958	Hs.83393	cystatin E/M	4.19
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	2.92
	405909	NA		Target Exon	71.80
	448811	AI590371	Hs.174759	ESTs	6.74
10	430044	AA464510	Hs.152812	ESTs	14.91
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	757.80
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	1.65
	423733	AA330281		gb:EST333985 Embryo, 12 week II Homo sapi	104.70
	450154	R15891	Hs.281587	Human (clone CTG-A4) mRNA sequence	143.00
15	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	311.80
	424902	NM_003866	Hs.153687	inositol polyphosphate-4-phosphatase, ty	63.00
	422330	D30783	Hs.115263	epiregulin	141.70
	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	2.59
	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	181.90
20	430691	C14187	Hs.103538	ESTs	95.80
	401682	NA		Target Exon	6.17
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	318.60
	431441	U81961	Hs.2794	sodium channel, nonvoltage-gated 1 alpha	2.51
	442560	AA365042	Hs.228598	ESTs, Weakly similar to 2004399A chromos	3.90
25	414812	X72755	Hs.77367	monokine induced by gamma Interferon	434.60
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	6.58
	421430	AW207555	Hs.97093	Homo sapiens cDNA: FLJ23004 fis, clone L	35.10
	419693	AA133749	Hs.301350	FXID domain-containing ion transport reg	2.45
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kafini	8.56
30	448437	AW470125		gb:wx60c04.x1 NCL_CGAP_Pan1 Homo sapiens	79.80
	406671	AA129547	Hs.285754	met proto-oncogene (hepatocyte growth fa	147.30
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	30.07
	424586	NM_003401	Hs.150930	X-ray repair complementing defective rep	55.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (CX	405.20
35	438746	AI885815	Hs.184727	ESTs	3.57
	456032	AW957446	Hs.301711	ESTs	136.80
	431808	M30703	Hs.270833	amphiregulin (schwannoma-derived growth	36.10
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	9.93
	439759	AL359055	Hs.67709	Homo sapiens mRNA full length insert cDN	146.40
40	442295	AB827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	20.60
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	1.58
	437157	BE048860	Hs.120655	ESTs	91.80
	404285	NA		C6001909:gi704441[dbj]BAA18909.1] (D298	123.80
45	424036	AA770688	Hs.28777	H2A histone family, member L	5.26
	422026	U80736	Hs.110826	trinucleotide repeat containing 9	130.40
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	48.80
	437935	AW939591	Hs.5940	mucin 13, epithelial transmembrane	3.15
	423575	C18863	Hs.163443	Homo sapiens cDNA FLJ11576 fis, clone HE	253.20
	422956	BE545072	Hs.122579	hypothetical protein FLJ10461	80.00
50	406722	H27498	Hs.293441	Homo sapiens SNC73 protein (SNC73) mRNA,	3.05
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	1.66
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	23.02
	434377	AW137148	Hs.306593	Homo sapiens cDNA FLJ11382 fis, clone HE	78.10
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	1.74
55	421298	AW172431	Hs.13012	ESTs	133.10
	422424	AI186431	Hs.296638	prostate differentiation factor	2.65
	421582	AJ910275	Hs.1406	trefol factor 1 (pS2)	5.17
	401480	NA		Target Exon	73.70
60	409269	AA576953	Hs.22972	hypothetical protein FLJ13352	137.70
	409757	NM_001898	Hs.123114	cystatin SN	9.36
	449722	BE280074	Hs.23960	cyclin B1	162.70
	452240	AJ591147	Hs.61232	ESTs	151.90
	415165	AW887604	Hs.78065	complement component 7	2.85
65	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	290.30
	428450	NM_014791	Hs.184339	KIAA0175 gene product	6.89
	409041	AB033025	Hs.50081	KIAA1199 protein	334.10
	453331	AJ240665	Hs.8895	ESTs	12.85
	400288	X06256	Hs.149509	integrin, alpha 5 (fibronectin receptor,	12.42
70	453160	AI263307	Hs.239884	H2B histone family, member L	156.40
	444015	AI472865	Hs.135534	ESTs	14.60
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	87.20
	448045	AJ297436	Hs.20166	prostate stem cell antigen	526.20
	422426	W79117	Hs.58559	ESTs	58.30
	450737	AW007152	Hs.203330	ESTs	281.00
75	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	31.25
	456553	AA721325	Hs.189058	ESTs, Highly similar to Similar to a C.e	78.00
	413281	AA861271	Hs.222024	transcription factor BMAL2	212.10
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	3.40
80	431630	NM_002204	Hs.265829	Integrin, alpha 3 (antigen CD49C, alpha	3.48
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	281.50
	431753	X76029	Hs.2841	neuromedin U	60.50
	428651	AF196478	Hs.188401	annexin A10	508.30
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	85.80
	433132	AB026264	Hs.284245	hypothetical protein IMPACT	55.30

	435039	AW043921	Hs.130526	ESTs	64.00
	447033	AI357412	Hs.157601	ESTs	123.20
	433578	BE336886	Hs.3416	adipose differentiation-related protein	9.22
5	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	525.70
	411274	NM_002776	Hs.69423	kallikrein 10 (KLK10) (PRSSL1) (nes1)	44.36
	452705	H49805	Hs.246005	ESTs	120.10
	428479	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	92.30
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	29.37
10	422562	AI962060	Hs.118397	AE-binding protein 1	3.84
	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	27.80
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	4.09
	440868	R79707	Hs.263339	ESTs, Moderately similar to I38022 hypot	76.30
	421493	BE300341	Hs.104925	ectodermal-neural cortex (with BTB-like	2.37
	410199	AW377424	Hs.205126	Homo sapiens cDNA: FLJ22667 fis, clone H	3.44
15	426320	W47595	Hs.169300	transforming growth factor, beta 2	138.10
	419290	AI128114	Hs.112885	spinal cord-derived growth factor-B	3.45
	459309	AA040620	Hs.5672	hypothetical protein AF140225	127.80
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	361.20
20	422553	AI697720	Hs.171455	ESTs, Weakly similar to T31613 hypothi	136.60
	432375	BE536069	Hs.2962	S100 calcium-binding protein P	6.87
	400534	#(NOCAT)		C22000015:gil12741327[ref]XP_008833.2] z	89.00
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.78
	423739	AA398155	Hs.97600	ESTs	135.60
25	450375	AA009647	Hs.8850	a disintegrin and metalloproteinase doma	148.50
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	87.70
	407001	U12471	Hs.247954	Human thrombospondin-1 gene, partial cds	76.80
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	110.60
	419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (234.60
30	428471	X57348	Hs.184510	stratifer	3.72
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	437.90
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothi	219.20
	419842	AA765489	Hs.104350	ESTs	3.80
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (MMP1; Inters	606.80
35	444207	AI565004	Hs.79572	cathepsin D (lysosomal aspartyl protease	2.62
	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	258.70
	413753	U17760	Hs.75517	laminin, beta 3 (nicellin (125kD), kalinin	304.80
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	8.78
	418327	U70370	Hs.84136	paired-like homeodomain transcription fa	10.95
40	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	199.70
	438199	AW016531	Hs.122147	ESTs	67.70
	422420	U03398	Hs.1524	tumor necrosis factor (ligand) superfam	107.20
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	3.59
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	3.45
45	421937	AI878857	Hs.109706	hematological and neurological expressed	3.17
	427961	AW293165	Hs.143134	ESTs	109.30
	422043	AL133649	Hs.110953	retinoic acid induced 1	2.98
	426711	AA383471	Hs.180669	conserved gene amplified in osteosarcoma	276.50
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	5.28
50	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	27.85
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	342.30
	424086	AI351010	Hs.102267	lysyl oxidase	213.50
	432731	R31178	Hs.287820	fibronectin 1	185.10
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	106.10
55	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	2.27
	417308	H60720	Hs.81892	KIAA0101 gene product	405.30
	438146	Z36842	Hs.57548	ESTs	8.38
	424800	AL035588	Hs.153203	MyoD family inhibitor	172.10
	416143	AI955650	Hs.79033	glutamyl-peptide cyclotransferase (glu	45.70
60	408380	AF123050	Hs.44532	diubiquitin	11.18
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	149.10
	422963	M79141	Hs.13234	ESTs	33.60
	409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	6.73
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	8.95
65	424897	D63216	Hs.153684	frizzled-related protein	312.40
	421110	AJ250717	Hs.1355	cathepsin E	790.80
	411789	AF245505	Hs.72157	DKFZP564I1922 protein	3.17
	421485	AA243499	Hs.104800	hypothetical protein FLJ10134	8.52
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	558.00
	406837	R70292	Hs.156110	immunoglobulin kappa constant	4.36
70	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	2.83
	421470	R27496	Hs.1378	annexin A3	242.90
	407242	M18728		gb:Human nonspecific crossreacting antig	36.91
	432101	AI918950	Hs.123642	EphA3	221.60
75	406687	M31126	Hs.272620	matrix metalloproteinase 11 (MMP11; stro	5.34
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	292.00
	408308	AL033377	Hs.44197	hypothetical protein DKFZp564D0462	184.90
	435202	AI971313	Hs.170204	KIAA0551 protein	64.80
	407216	N91773	Hs.102267	lysyl oxidase	73.70
80	409231	AA446644	Hs.692	GA733-2 antigen; epithelial glycoprotein	3.20
	407881	AW072003	Hs.40968	heparan sulfate (glucosamine) 3-O-sulfot	288.70
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	502.60
	420899	NM_001629	Hs.100194	arachidonate 5-lipoxygenase-activating p	6.13
	441020	W79283	Hs.35962	ESTs	178.90

	453857	AL080235	Hs.35861	DKFZP586E1621 protein	504.30
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	242.10
	413435	X51405	Hs.75360	carboxypeptidase E	7.30
5	436476	AA326108	Hs.33829	bHLH protein DEC2	247.20
	406747	AI925153	Hs.217493	annexin A2	110.00
	455800	R22479	Hs.167073	Homo sapiens cDNA FLJ13047 fis, clone NT	112.10
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	583.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subun)	6.56
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	460.90
	444665	BE613126	Hs.47783	B aggressive lymphoma gene	204.40
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	7.75
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	14.61
	424560	AA158727	Hs.150555	protein predicted by clone 23733	99.80
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	242.20
15	407137	T97307		glycyl-53hO5.s1 Soares fetal liver spleen	17.88
	410668	BE379794	Hs.65403	hypothetical protein	4.18
	427660	AI741320	Hs.114121	Homo sapiens cDNA: FLJ23228 fis, clone C	116.40
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	60.30
20	442577	AA292998	Hs.163900	ESTs	4.18
	416498	U33632	Hs.79351	potassium channel, subfamily K, member 1	334.20
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	8.16
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	375.30
	445133	AW157646	Hs.153506	ESTs	292.40
25	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	4.38
	431806	AF186114	Hs.270737	tumor necrosis factor (ligand) superfam	89.00
	437330	AL353944	Hs.50115	Homo sapiens mRNA: cDNA DKFZp761J1112 (f	322.10
	410687	U24389	Hs.65436	lysyl oxidase-like 1	9.10
	417409	BE272506	Hs.82109	syndecan 1	4.05
30	426471	M22440	Hs.170009	transforming growth factor, alpha	138.60
	458809	AW972512	Hs.20985	sln3-associated polypeptide, 30kD	250.50
	446625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.69
	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	11.76
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.79
35	408491	AI088063	Hs.7882	ESTs	8.25
	437802	AI475995	Hs.122910	ESTs	4.54
	408296	AL117452	Hs.44155	DKFZP586G1517 protein	175.10
	421155	H87879	Hs.102267	lysyl oxidase	170.10
	451310	AW250651	Hs.26213	Human DNA sequence from clone RP3-447F3	2.91
40	439867	AA847510	Hs.161292	ESTs	261.60
	417771	AA804698	Hs.82547	retinoic acid receptor responder (lazar	723.00
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	251.70
	431385	BE178536	Hs.11090	membrane-spanning 4-domains, subfamily A	155.50
	457180	R26022	Hs.194662	calponin 3, acidic	68.00
45	424408	AI754813	Hs.146428	collagen, type V, alpha 1	17.19
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	5.32
	425139	AW630488	Hs.325820	protease, serine, 23	371.90
	432978	AF126743	Hs.279884	DNAJ domain-containing	7.27
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	19.30
50	421991	NM_014918	Hs.110488	KIAA0990 protein	190.50
	421814	L12350	Hs.108623	thrombospondin 2	15.02
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	28.57
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	519.20
	413048	M93221	Hs.75182	mannose receptor, C type 1	240.60
55	404210	#(NOCAT)		NM_005936:Homo sapiens myeloid/lymphoid	404.60
	452862	AW378065	Hs.8687	ESTs	364.20
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	226.20
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	4.31
60	427390	AI432163	Hs.268231	Homo sapiens cDNA: FLJ23111 fis, clone L	10.41
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	22.46
	451295	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene	23.74
	448569	BE382657	Hs.21486	signal transducer and activator of trans	5.68
	417148	AA359896	Hs.293885	hypothetical protein FLJ14902	190.80
65	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	230.50
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	361.90
	422545	X02761	Hs.287820	fibronectin 1	8.81
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	7.30
	417412	X16896	Hs.82112	Interleukin 1 receptor, type I	267.20
70	422110	AI376736	Hs.111779	secreted protein, acidic, cysteine-rich	5.07
	431512	BE270734	Hs.2795	lactate dehydrogenase A	270.10
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	504.60
	426369	AF134157	Hs.169487	Kreisler (mouse) mal-related leucine zip	10.62
	437470	AL390147	Hs.134742	hypothetical protein DKFZp547D065	2.80
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	14.01
75	428797	AA496205	Hs.193700	Homo sapiens mRNA: cDNA DKFZp586I0324 (f	9.15
	434423	NM_006769	Hs.3844	LIM domain only 4	297.30
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	486.20
	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	9.73
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	762.90
80	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	7.81
	400133	NA		Eos Control	357.00
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1150.30
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.50
	446019	AI362520	Hs.279789	histone deacetylase 3	11.26

426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	459.50
422687	AW068823	Hs.119206	insulin-like growth factor binding prote	2.68
432401	NM_013330	Hs.274479	NME7	4.99
437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fls, clone HE	7.65

Table 41B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
419570	1860604_1	W68738 W68831
423733	231476_1	AA330281 OAA330232 AW962521
434665	390530_1	AA642125 AA654516
448437	763310_1	AW470125 AJ734872 AJ749559 AW856504 AI583942 AW779036 AW843429 AW844876 AI520713 AW847236

Table 41C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400534	6981826	Minus	278637-279292
400560	9843598	Plus	94182-94323,97056-97243,101095-101236,102824-103005
400836	8954179	Plus	677-1188
401201	9743387	Minus	138534-138629,139234-139294,140121-140335,142033-142479
401480	7321503	Plus	166120-166347,166451-166557,169651-169832
401541	8072607	Minus	50018-50158
401682	4755167	Plus	13022-13473
401732	1200312	Plus	19346-19525,19625-19708,19897-19973,20067-20130,20215-20414
403207	7630829	Plus	89914-90033,90729-90855,91131-91198
403574	8101156	Plus	5542-6176
403776	7770611	Minus	1414-1513,1624-1755
404142	9856692	Minus	80316-80459
404210	5006246	Plus	169926-170121
404285	2326514	Plus	32282-32416
404286	2326514	Plus	51086-51301
404287	2326514	Plus	53134-53281
404682	9797231	Minus	40977-41150
404866	9366919	Minus	11743-11929
405281	6139075	Minus	34202-34351,35194-35336,45412-45475,45731-45958,47296-47457,49549-49658,49790-49904,50231-50342,53583-53667,54111-54279
405849	7651817	Minus	17705-18287
405909	7705180	Minus	86985-87233
406173	7230224	Plus	12925-13213
406293	5686274	Minus	17646-17953
406319	9211730	Minus	82320-82561
406399	9256288	Minus	63448-63554

TABLE 42A: 574 genes upregulated in pancreatic cancer relative to normal body tissues

Table 42A lists about 574 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.Prol.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1: 90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
 R2: 90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prol.Domains; R1; R2

426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin, toxin_4; SS=M; 107.29; 1.07
 415934; NM_000928; Hs.992; phospholipase A2, group IB (pancreas); phospholipase; SS=M; 83.67; 1.06
 421996; AW583807; Hs.1460; glucagon; hormone; SS=M; 59.35; 1.61
 406399; ; NM_003122; Homo sapiens serine protease; kazal; SS=M; 55.49; 1.08
 444381; BE387335; Hs.283713; hypothetical protein BC014245; Collagen; TM=M; SS=M; 53.65; 43.61

- 406685; M18728; ; gb:Human nonspecific crossreacting anti; Ig; TM=M; SS=M; 52.73; 22.83
- 428698; AA852773; Hs.334838; KIAA1866 protein; none; NA; NA; 32.44; 13.11
- 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbon; HCO3_cotransp; TM=Y; 29.80; 1.46
- 428874; W32133; Hs.194366; transthyretin (prealbumin, amyloidosis t; Transthyretin; SS=M; 29.42; 1.94
- 444754; T83911; Hs.374341; transmembrane 4 superfamily member 4; none; TM=Y; SS=M; 28.78; 3.13
- 418068; AW971155; Hs.293902; ESTs, Weakly similar to ISHUS protein d; none; TM=M; SS=M; 28.61; 0.98
- 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group 1, m; hormone_rec_zf-C4; none; 25.38; 3.63
- 413719; BE439580; Hs.75498; small inducible cytokine subfamily A (Cy; IL8; SS=M; 24.64; 7.21
- 417771; AA804698; Hs.82547; retinoic acid receptor responder (Iazaro; none; none; 23.77; 6.74
- 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c; TM=Y; SS=M; 22.96; 4.57
- 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 22.31; 5.42
- 425573; AB006423; Hs.158308; serine (or cysteine) proteinase inhibitor; serpin; GCV_H; TM=M; SS=M; 21.91; 1.03
- 433110; D56494; Hs.3191; rat regenerating islet-derived-like, hum; lectin_c; TM=M; SS=M; 21.90; 0.60
- 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC; PAS; TM=M; 21.41; 19.89
- 453863; X02544; Hs.572; orosomucoid 1; lipocalin, aldedh, ubiquitin, IRK; SS=M; 20.80; 8.12
- 421126; M74587; Hs.102122; insulin-like growth factor binding prote; thyroglobulin_1; IGFBP; SS=Y; 20.60; 8.48
- 451035; AU076785; Hs.430; plastin 1 (I isoform); ehand, CH, Adeptin_N; SS=M; 19.26; 3.53
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kin; SAM_PNT; none; 18.38; 2.53
- 420332; NM_001756; Hs.1305; serine (or cysteine) proteinase inhibitor; serpin; TM=M; SS=M; 18.19; 2.29
- 438089; W05391; Hs.351546; nuclear receptor subfamily 1, group 1, m; hormone_rec_zf-C4; none; 17.67; 4.80
- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF; laminin_Nterm; Integrin_B; SS=M; 17.08; 6.37
- 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a; 7tm_1; TM=Y; SS=M; 16.89; 7.15
- 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C_G-alpha; arf; TM=M; SS=M; 16.59; 7.74
- 445033; AV652402; Hs.72801; cyclin-dependent kinase inhibitor 2B (p1; ank; 16.28; 9.22
- 431183; NM_005855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 15.96; 2.38
- 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodi; Somatomedin_B; Endonuclease, Phosphodiect; TM=Y; SS=M; 15.65; 1.33
- 408243; Y00787; Hs.624; interleukin 8; HLH; PAS; IL8; TM=M; 15.53; 4.34
- 419355; AA428520; Hs.90061; progesterone binding protein; hema_1; TM=Y; SS=M; 15.45; 10.50
- 426006; R49031; Hs.22627; ESTs; pkinase; TBC; 15.17; 0.58
- 433376; A1249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD; ICE_p10; ICE_p20; SS=M; 14.84; 3.04
- 422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c; SS=M; 14.71; 2.89
- 430260; AA361258; Hs.237868; interleukin 7 receptor; fn3; none; 14.26; 11.47
- 408993; NM_000492; Hs.663; cystic fibrosis transmembrane conductanc; ABC_tran; ABC_membrane; PRK; Bac_export_3; TM=Y; 13.98; 1.18
- 414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 13.81; 7.69
- 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese; DSPc_Y_phosphatase; Ribosomal_S3_N; TM=M; 13.59; 2.24
- 425988; BE045897; Hs.53985; ESTs, Weakly similar to I38022 hypotheti; none; none; 13.54; 0.95
- 409512; AW979187; Hs.293591; melanoma differentiation associated prot; DEAD; helicase_C; CARD; TM=M; 13.48; 3.59
- 429556; AW139399; Hs.98988; ESTs; none; TM=M; 13.20; 1.16
- 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1; SS=M; 12.83; 7.72
- 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway; SH3; TonB_boxC; TM=M; 12.72; 9.01
- 431912; A1605552; Hs.356183; ESTs, Weakly similar to A56154 Abl subst; none; Acyl-CoA_dh; Acyl-CoA_dh_M; Acyl-CoA_dh_N; 12.72; 6.72
- 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1; TM=Y; SS=M; 12.71; 12.56
- 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB; DNA_topoisolV; HATPase_c; SS=M; 12.52; 4.92
- 409142; A1136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran; M; SMC_N; SMC_C; DUF164; none; 12.38; 7.59
- 428157; A1738719; Hs.198427; hexokinase 2; hexokinase2; none; 12.34; 11.53
- 424273; W40460; Hs.144442; phospholipase A2, group X; phosph; TM=M; SS=Y; 12.32; 3.02
- 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia; re; Ig; TM=Y; SS=M; 12.29; 2.21
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chr; SH3; TPR; TM=M; 12.16; 4.14
- 427283; A1119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodi; Sulfatase; Somatomedin_B; Phosphodiect; Endonuclease; TM=M; SS=Y; 11.97; 5.93
- 434779; AF153815; Hs.50151; potassium inwardly-rectifying channel, s; IRK; TM=Y; 11.76; 1.58
- 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 11.75; 3.56
- 412228; AW503785; Hs.73792; complement component (3d/Epstein Barr vi; sushi; TM=Y; SS=M; 11.67; 3.77
- 450737; AW007152; Hs.63325; transmembrane protease, serine 4; trypsin; ktl_recept; none; 11.65; 4.52
- 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C; IMPDH_N; CBS; integrin_B; Rctn_B; lectin; 11.56; 5.46
- 431512; BE270734; Hs.2795; lactate dehydrogenase A; lch; kdh_C; SH3; pkinase; UBA; TM=M; 11.55; 5.11
- 429638; A1916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP; Tropomyosin; spectrin; LBP_BPI_CETP; B56; M; TM=Y; SS=M; 11.47; 4.65
- 445133; AW157648; Hs.198689; ESTs; ehand; spectrin; GAS2; SH3; Plectin; RA_Xylose_isom; FIID; bZIP; Tropomyosin; Myc-LZ; M; kdh_C; CH; AIP3; TM=M; 11.41; 12.62
- 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activa; SH2; SH3; C2; PH; Ras; GAP; TM=M; SS=M; 11.24; 9.95
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none; none; 11.19; 4.16
- 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS; AIRS_C; TM=M; 11.17; 5.98
- 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin; fn3; Y_phosphatase; TM=M; 11.14; 9.09
- 440594; AW445167; Hs.126038; ESTs; none; none; 11.05; 16.45
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD; DAPIN; HIN; SS=M; 11.05; 10.38
- 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese; DSPc; TM=M; 11.05; 4.70
- 448811; A1590371; Hs.199460; ESTs; none; TM=Y; 10.85; 9.69
- 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kin; SH2; SH3; pkinase; TM=M; 10.72; 8.65
- 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 10.51; 12.97
- 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys; Ig; FAD_Synth; kdh_C; pkinase; SS=M; 10.37; 6.35
- 436856; A1469355; Hs.127310; ESTs; pkinase; rm; TM=M; 10.36; 2.74
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb; r; Ig; TM=Y; SS=M; 10.34; 3.14
- 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related ; SH2; SH3; pkinase; TM=M; 10.34; 4.47
- 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; integrin_B; EGF; PSI; TM=Y; SS=M; 10.21; 4.58
- 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 10.18; 2.67
- 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2; lectin_c; Rctn_B; lectin; Xlink; TM=Y; SS=M; 10.17; 8.35
- 429752; H52348; Hs.36636; ESTs; pkinase; pkinase; 10.13; 12.35
- 452721; A1269529; Hs.301871; solute carrier family 37 (glycerol-3-pho; MORN; sugar_tr; TM=Y; SS=M; 10.08; 8.74
- 421462; AF016495; Hs.104624; aquaporin 9; MIP; TM=Y; SS=M; 10.05; 6.06
- 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1; TM=Y; SS=M; 9.98; 3.16
- 416389; AA180072; Hs.149846; Integrin, beta 5; Integrin_B; none; 9.85; 9.59
- 421044; AF061871; Hs.101302; Human DNA sequence from clone RP1-238D15; fn3; vwa; Collagen; TSPN; TM=M; SS=M; 9.78; 5.96
- 446620; AA128808; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 9.75; 2.64
- 405102; ; C15001220; gij4469558[gb]AAD21311.1 [AF; DAG_PE-bind; PH; RhoGEF; DC1; SS=M; 9.74; 1.88
- 418693; A1750878; Hs.87409; thrombospondin 1; EGF; ttp_1; vwa; TSPN; ttp_3; SS=M; 9.72; 6.94

- 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR m; Kunitz_BPTI,Kunitz_BPTI,7tm_2,HRM; 9.68; 10.58
 448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl_recept_a,trypsin;TM=Y;SS=M; 9.67; 4.06
 456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
 410240; AL157424; Hs.61289; synaptojanin 2; Exo_endo_phos,Syja_N,rm,Gram-ve_porins;TM=M; 9.62; 3.77
 457001; J03258; Hs.2062; vitamin D (1,25- dihydroxyvitamin D3) re; hormone_rec,zf-C4,Metalothio_5;TM=M; 9.60; 8.05
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A; none;TM=Y; 9.57; 3.77
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like do; SH3;TM=M; 9.56; 10.50
 437158; AW090198; Hs.348709; KIAA1150 protein; none;NA:NA; 9.55; 8.87
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M; 9.47; 5.67
 403344; ; NM_000341; Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 9.47; 1.42
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra,Ion_trans,none; 9.46; 3.12
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3,zf-C3HC4;TM=M; 9.42; 4.01
 444838; AV651680; Hs.208558; ESTs; Integrin_A,FG-GAP,none; 9.42; 1.87
 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none,none; 9.41; 5.55
 428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 9.38; 6.32
 432810; AA863400; Hs.374489; ESTs; none;Skp1,AAA; 9.38; 4.36
 427581; NM_014788; Hs.179703; KIAA0129 gene product; SPRY,zf-B_box;TM=M; 9.34; 8.26
 413109; AW389845; Hs.110855; ESTs, similar to leukemia virus receptor; PHO4,none; 9.34; 4.67
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M; 9.31; 4.24
 408113; TB2427; Hs.194101; Homo sapiens cDNA: FLJ20869 fis, clone A; 7tm_3,none; 9.24; 7.12
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A; none;TM=Y;SS=M; 9.23; 6.03
 437672; AW748265; Hs.5741; flavohemoprotein b57; heme_1,NAD_binding,lipoxigenase,FAD_binding_6;TM=M; 9.22; 10.72
 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1; ion_trans;TM=Y;SS=M; 9.20; 4.46
 409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;SS=M; 9.19; 16.46
 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-rel; none;START; 9.15; 2.18
 418838; AW385224; Hs.35198; ecdonucleotide pyrophosphatase/phosphodi; Phosphodiect;TM=Y;SS=M; 9.14; 3.03
 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor t Y_phosphatase,none; 9.14; 11.75
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; coflin_ADF;SS=M; 9.11; 4.29
 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG;TM=M; 9.06; 9.68
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M; 9.05; 5.61
 413367; NM_006517; Hs.75317; solute carrier family 16 (monocarboxylic; sugar_tr;TM=Y; 9.04; 5.79
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese,DSPc;TM=M; 9.02; 5.75
 418888; AU076801; Hs.89436; cadherin 17, LI cadherin (liver-intestine; cadherin;TM=Y;SS=M; 8.94; 5.01
 446406; AIS53681; Hs.348490; Arg/Abi-Interacting protein ArgBP2; Sorb,none; 8.91; 1.77
 428820; AA436187; Hs.172631; integrin, alpha M (complement component 1; vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 8.85; 4.74
 434398; AA121098; Hs.3838; serum-inducible kinase (SNK); pkinase,POLO_box;TM=M; 8.78; 4.54
 453902; BE502341; Hs.3402; ESTs; none,none; 8.72; 3.71
 433334; AI927208; Hs.231958; matrix metalloproteinase 28; Peptidase_M10,none; 8.71; 4.28
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 8.70; 3.71
 450247; AF123303; Hs.24713; hypothetical protein; ethand_mito_carr;TM=Y;SS=M; 8.68; 3.40
 432101; AI918950; Hs.123642; EphA3; fn3,pkinase,SAM,EPH_lbd;TM=Y;SS=M; 8.62; 5.62
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none,none; 8.61; 13.53
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 8.55; 4.82
 425465; L18964; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M; 8.50; 3.18
 419111; AA234172; Hs.137418; ESTs; none,IRK; 8.47; 7.51
 430024; AI808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 8.45; 3.46
 447574; AF162666; Hs.18895; tousled-like kinase 1; pkinase;TM=M; 8.45; 5.30
 447217; BE465754; Hs.17778; neuropilin 2; CUB,MAM,F5_F8_type_C;TM=M;SS=M; 8.44; 6.30
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,pkinase;TM=M; 8.43; 4.87
 405555; ; homeodomain-interacting protein kinase 3; trypsin;TM=M; 8.39; 0.68
 417412; X16898; Hs.82112; interleukin 1 receptor, type I; ig,TIR;TM=M;SS=M; 8.35; 4.74
 405556; ; homeodomain-interacting protein kinase 3; trypsin;TM=M; 8.31; 0.87
 407687; AK002011; Hs.37558; hypothetical protein FLJ11149; lys,lg,FAD_Synth,ldh,ldh_C,pkinase;SS=M; 8.28; 3.12
 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP,none; 8.27; 5.65
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.26; 5.49
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 dom; SH2;SS=M; 8.24; 8.91
 405204; ; NM_002086; Homo sapiens growth factor re; SH2,SH3;TM=M; 8.23; 6.43
 426806; T19228; Hs.172572; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 8.20; 6.11
 428428; AL033754; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase;TM=M; 8.18; 8.37
 450375; AA009647; Hs.352537; a disintegrin and metalloproteinase dom; Reprolysin,Pep_M12B_propep,disintegrin,Reprolysin,Pep_M12B_propep,disintegrin; 8.17; 12.24
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine pr; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 8.15; 4.61
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic; PKI;SS=M; 8.15; 11.12
 428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI,none; 8.13; 13.28
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 8.13; 1.15
 425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; per; none;TM=M; 8.12; 4.54
 425836; AW955698; Hs.90960; ESTs; Cbl_N,Cbl_N2,Cbl_N3,UBA,zf-C3HC4,none; 8.11; 7.47
 406366; ; secreted frizzled-related protein 4; trypsin;SS=M; 8.05; 0.69
 429663; M68874; Hs.211587; phosphatase A2, group IVA (cytosolic; C2,PLA2_B;TM=M; 8.04; 5.20
 458946; AA009716; Hs.42311; ESTs; none,DSPc,Y_phosphatase; 8.02; 1.93
 425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (sol; PEPCK;TM=M; 7.97; 19.33
 445800; AA126419; Hs.32944; inositol polyphosphate 4-phosphatase, ty; none,none; 7.90; 11.44
 449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg,HEAT_PBS; 7.83; 11.16
 400408; S75765; ; Homo sapiens delta CCK-B gene, partial c; 7tm_1,none; 7.81; 0.78
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0854 simil; sugar_tr;TM=Y;SS=M; 7.78; 7.02
 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substra; SH3;TM=M; 7.75; 2.63
 409799; D11928; Hs.76845; phosphoserine phosphatase-like; Hydrolase;TM=M; 7.72; 2.68
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M; 7.68; 2.40
 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg;SS=M; 7.49; 6.57
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HE; Nucleoside_tra2,none; 7.47; 2.53
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule; EGF,lectin_c,sushi;TM=M;SS=M; 7.38; 5.60
 436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78

- 428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3; TM=Y; SS=M; 7.26; 11.00
 426761; A1015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none; TM=Y; SS=M; 7.25; 7.22
 413880; A160842; Hs.110915; Interleukin 22 receptor; Tissue_fac; TM=Y; SS=M; 7.24; 0.98
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase; PLAT; TM=M; 7.22; 6.45
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3; TM=M; 7.20; 5.72
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like, pkinase, Recep_L_domain, Furin-like, pkinase, Recep_L_domain, Peptidase_M24; 7.13; 3.97
 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase; TM=M; 7.13; 5.43
 421582; A1910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil, Gastrin; SS=M; 7.08; 21.61
 449843; BE5337; Hs.24030; solute carrier family 31 (copper transpo; none; TM=Y; SS=M; 7.07; 6.18
 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PL; pkinase, Activin_rec; none; 6.94; 4.82
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase, DAG_PE-bind, pkinase_C, OPR; none; 6.92; 15.34
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU S; Y_phosphatase, Adaplin_N_Y_phosphatase; 6.88; 1.94
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG; 7tm_1, ldl_recept_L, LRR; SS=M; 6.86; 0.97
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxldase; SS=M; 6.83; 7.24
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor t; fn3, Ig_Y_phosphatase, MAM; TM=Y; SS=M; 6.83; 11.43
 400539; ; Target Exon; none; TM=M; 6.70; 1.19
 431113; AK000673; Hs.274337; hypothelical protein FLJ20666; pkinase; TM=M; 6.65; 2.21
 445280; AW055063; Hs.343220; v-erk avian sarcoma virus CT10 oncogene; SH2, SH3; none; 6.61; 10.66
 425834; NM_001639; Hs.1957; amyloid P component, serum; pentaxin; TM=M; SS=M; 6.57; 2.20
 435706; W31254; Hs.7045; GL004 protein; PDEase, GAF; none; 6.55; 11.44
 415906; A1751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone H; Ephrin; none; 6.45; 5.25
 408308; AL033377; Hs.44197; hypothelical protein DKFZp564D0462; none; none; 6.42; 9.14
 432336; NM_002759; Hs.274382; protein Kinase, Interferon-inducible dou; dsrm, pkinase; TM=M; 6.42; 4.12
 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase; TM=Y; 6.42; 2.26
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein c; 7tm_1; TM=Y; SS=M; 6.41; 4.54
 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a_PKD, MHC_1; TM=M; SS=Y; 6.38; 3.55
 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanesa, DSPc; SS=M; 6.35; 4.95
 422583; AA410506; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; 6.35; 3.56
 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; 6.32; 11.02
 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ ExbB; TM=Y; SS=M; 6.32; 5.15
 407235; D20569; Hs.189407; SAC2 (suppressor of actin mutations 2; y; none, Ribosomal_S13, Galactosyl_T_Zip, adh_short, zf-C3HC4; 6.30; 8.35
 428486; AW583497; Hs.184604; pancreatic polypeptide; monona3; TM=M; SS=Y; 6.29; 3.51
 408847; AW290997; Hs.30348; ESTs; pkinase, Ig; none; 6.28; 3.63
 428179; A112772; Hs.279696; serum/glucocorticoid regulated kinase-II; pkinase, PX, pkinase_C, SS=M; 6.28; 3.50
 443614; AV665386; Hs.7645; fibrinogen, B beta polypeptide; none; none; 6.26; 7.48
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1; TM=Y; SS=M; 6.25; 3.98
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 6.21; 4.10
 428180; A1129767; Hs.182874; guanine nucleotide binding protein (G pr; G-alpha, arf; TM=M; 6.18; 4.62
 409245; AA361037; Hs.356436; tRNA Isopentanylpurphosphate transferas; Armadillo_seg; TM=M; 6.17; 11.15
 417952; A1192838; Hs.372643; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; none; 6.17; 3.05
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; 6.16; 11.90
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 6.10; 2.96
 426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_B, SH3; 6.03; 3.17
 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPc; TM=M; 5.99; 2.55
 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone H; 7tm_3; none; 5.97; 13.12
 414217; A1309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none; NA; NA; 5.92; 6.47
 418506; AA084248; Hs.85339; Unknown protein for MGC:29643; none; none; 5.91; 1.94
 436345; AA873008; Hs.121572; ESTs; CARD, BIR, zf-C3HC4, CARD, BIR, zf-C3HC4; 5.90; 1.40
 414087; W19712; gbzb36d03.r1 Soares_parathyroid_tumor_N; pkinase; none; 5.85; 0.90
 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank, death, ZU5, EGF, kringle, bypsin, Nebulin, LIM; SS=M; 5.77; 1.24
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A; none; none; 5.71; 4.00
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase recepto; UPAR_LY6, ET, PLA2_inh; SS=M; 5.71; 3.83
 414171; AA360328; Hs.865; RAP1A, member of RAS oncogene family; pkinase, DAG_PE-bind, RBD, ras, DC1, GFP; TM=M; 5.69; 3.07
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1, 7tm_2; TM=Y; SS=M; 5.68; 12.92
 425317; AW205118; Hs.210546; interleukin 21 receptor; none; TM=Y; SS=M; 5.60; 5.45
 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 5.59; 4.19
 400151; ; Eos Control; AT_hook_DNA_mis_repair; HATPase_c, UOQ_con; TM=M; 5.53; 8.13
 450139; AK001838; Hs.355608; serum/glucocorticoid regulated kinase; none; none; 5.52; 8.61
 418203; X54942; Hs.83758; CDC28 protein Kinase 2; CKS; 5.52; 10.04
 433556; W55321; Hs.111460; calcitriol/calmodulin-dependent protein kin; pkinase; none; 5.51; 6.75
 424701; NM_005923; Hs.151988; mitogen-activated protein kinase kinase; pkinase; TM=M; 5.47; 4.58
 415875; AA894876; Hs.5687; protein phosphatase 1B (formerly 2C), ma; PP2C; TM=M; 5.43; 5.30
 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not avr; 7tm_1; none; 5.42; 2.59
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4, LIM; TM=M; 5.37; 8.69
 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20; pkinase, RIO1, APH, KOW; TM=M; 5.36; 3.32
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR, LRRCT, TIR; TM=M; SS=M; 5.36; 3.94
 429023; NM_000312; Hs.2351; protein C (inactivator of coagulation fa; EGF, bypsin, gla; SS=M; 5.31; 4.30
 421559; NM_014720; Hs.105751; Ste20-related serine/threonine kinase; pkinase, UVR; TM=M; 5.31; 3.26
 429922; Z97630; Hs.226117; H1 histone family, member 0; linker_histone; TM=M; 5.27; 3.12
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2; cyclin, bZIP; TM=M; 5.26; 4.82
 411558; AA102670; Hs.70725; gamma-aminobutyric acid (GABA) A recepto; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 5.25; 11.26
 428234; U93553; Hs.183123; nuclear receptor subfamily 5, group A, m; hormone_rec, zf-C4; SS=M; 5.20; 1.11
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos; TM=M; 5.19; 6.25
 408657; AA782601; Hs.173328; ESTs; B56; none; 5.18; 5.47
 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (m; transferrin, Guanylate_kin, PDZ, SH3; 5.17; 4.02
 438699; AW129785; Hs.361171; ESTs, Weakly similar to I38022 hypothel; lipoxygenase, PLAT; none; 5.16; 2.91
 442200; AW590572; Hs.235768; ESTs; none; none; 5.11; 4.22
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none; none; 5.08; 2.71
 419086; A1538323; Hs.367688; integrin, beta 8; integrin_B; none; 5.07; 3.53
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets); phoslip; TM=M; SS=Y; 5.05; 3.42
 408414; A114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell; fn3, Ig; TM=Y; SS=M; 5.05; 3.41
 430407; H23551; Hs.30974; ESTs; pkinase, PBD; none; 5.03; 1.63
 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 5.00; 5.14

- 452194; AI694413; Hs.373599; Ubiquitin-like protein FAT10777 - diubiq; none;none; 4.98; 2.65
- 410073; AW408163; Hs.58488; catenin (cadherin-associated protein), α ; Stathmin,Vinculin;SS=M; 4.97; 10.60
- 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 4.96; 2.87
- 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept Y_phosphatase;SS=M; 4.88; 21.69
- 433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
- 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filamenUbZIP,G-gamma,M,DUF164;TM=M; 4.79; 5.47
- 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm_1;TM=M; 4.75; 5.41
- 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPc,Y_phosphatase;TM=M; 4.74; 9.76
- 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none;TM=M;SS=M; 4.73; 4.68
- 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 4.66; 5.61
- 452239; AW379378; Hs.356289; protein tyrosine phosphatase, receptor t; none;none; 4.63; 6.62
- 427333; AF067797; Hs.176658; aquaporin 8; MIP;TM=Y;SS=M; 4.63; 0.80
- 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 4.58; 11.38
- 428065; AI634046; Hs.157313; ESTs; ICE_p20,DED,ICE_p10,ICE_p20,DED; 4.55; 4.51
- 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 4.54; 8.76
- 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding; efhand;SS=M; 4.54; 19.57
- 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypotheti; ABC_tran,ABC_membrane,Ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.49; 10.47
- 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 4.41; 7.27
- 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.41; 10.25
- 433208; AW002834; Hs.24095; ESTs; arf,Ca_channel_B,SH3; 4.39; 12.14
- 403208; ; Target Exon; lectin_c,none; 4.37; 0.76
- 440486; BE243513; Hs.7212; hypothetical protein PP1044; LRR,PAAD,DAPIN,AAA,CARD,NB-ARC,NA;NA; 4.36; 10.34
- 414278; AA330116; Hs.355877; Human glucose transporter pseudogene; none;none; 4.35; 7.95
- 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS;SS=M; 4.34; 6.23
- 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP,integrin_A,none; 4.32; 5.85
- 418721; NM_002731; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase,pkinase_C;SS=M; 4.31; 3.09
- 412330; NM_005100; Hs.788; A kinase (PRKA) anchor protein (gravin); none;TM=M; 4.25; 12.74
- 421939; BE169531; Hs.109727; TAK1-binding protein 2; KIAA0733 protein; zf-RanBP,CUE;TM=M; 4.25; 12.54
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle,lypsin,plant_thionins;SS=M; 4.24; 6.91
- 418528; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 4.22; 5.27
- 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, re; ig;TM=Y; 4.16; 7.22
- 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA;SS=M; 4.16; 9.27
- 445495; AB007860; Hs.12802; development and differentiation enhancin; SH3,ank,PH,ArtGap;TM=M; 4.15; 23.43
- 436075; BE090176; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 4.14; 3.76
- 414462; BE622743; Hs.301064; arfaplin 1; none;none; 4.08; 13.43
- 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase,TrkA-N,2-HadD_DH_C;TM=M; 4.06; 9.12
- 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_br;TM=Y; 4.04; 10.05
- 429379; NM_014840; Hs.200598; KIAA0537 gene product; pkinase,RIO1;TM=M; 4.00; 6.35
- 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M; 3.98; 5.66
- 405203; ; NM_002086; Homo sapiens growth factor re; SH2,SH3;TM=M; 3.95; 17.71
- 409335; NM_001502; Hs.53985; glycoprotein 2 (zymogen granule membrane; zona_pellucida;TM=M;SS=M; 3.94; 0.58
- 446008; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 3.89; 7.59
- 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens; SH3,PDZ,Guanylate_kin;TM=M; 3.84; 8.89
- 438000; AI825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none;TM=M; 3.83; 4.22
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 3.81; 6.45
- 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 3.78; 8.49
- 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 3.77; 4.22
- 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 3.68; 4.92
- 438113; AI467908; Hs.8882; ESTs; 7tm_1,none; 3.59; 12.12
- 414883; AA926960; Hs.348669; CDC28 protein kinase 1; CKS; 3.58; 10.93
- 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 3.57; 5.10
- 415088; AI077288; Hs.374374; serumglucocorticoid regulated kinase; none;none; 3.56; 4.60
- 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (ma; ank; 3.55; 4.52
- 448569; BE382857; Hs.21486; signal transducer and activator of trans; SH2,STAT,STAT_bind,STAT_prot;TM=M; 3.54; 8.19
- 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 3.52; 9.70
- 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor; Integrin_A,FG-GAP;TM=Y; 3.45; 6.44
- 445350; AF052112; Hs.12540; lysophospholipase 1; abhydrolase_2;TM=M; 3.41; 6.03
- 418255; AW135405; Hs.37251; ESTs; pkinase,none; 3.41; 13.97
- 408822; AW500715; Hs.57079; Homo sapiens cDNA FLJ13267 fis, clone OV; PIPSK,none; 3.40; 8.97
- 426432; AF001601; Hs.169857; paraoxonase 2; Arylesterase;TM=M; 3.39; 11.24
- 431629; AU077025; Hs.265827; Interferon, alpha-inducible protein (clo; none;TM=M;SS=Y; 3.39; 5.10
- 414291; AI289619; Hs.13040; G protein-coupled receptor 86; 7tm_1;TM=Y;SS=M; 3.38; 10.25
- 457329; AI634860; Hs.247043; type 1 tumor necrosis factor receptor sh; Peptidase_M1;SS=M; 3.38; 13.78
- 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 3.36; 4.17
- 443710; AI928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha,none; 3.32; 20.33
- 454294; AB000734; Hs.50640; JAK binding protein; SH2;TM=M; 3.31; 6.94
- 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg;TM=M;SS=M; 3.29; 3.07
- 426728; NM_007118; Hs.367689; triple functional domain (PTPRF interact; SH3,ig,pkinase,PH,spectrin,RhoGEF;TM=M; 3.27; 14.90
- 427202; BE272922; Hs.173936; interleukin 10 receptor, beta; Tissue_fac;TM=Y;SS=M; 3.24; 4.49
- 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M; 3.24; 12.27
- 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 3.23; 13.40
- 417534; NM_004998; Hs.82251; myosin IE; SH3,myosin_head,IQ;TM=M; 3.21; 15.21
- 458097; AW341135; Hs.58104; ESTs; none,SH3,PID; 3.21; 7.34
- 437928; NM_005476; Hs.5920; UDP-N-acetylglucosamine-2-epimerase/N-ac; hexokinase,FGGY,ROK,Epimerase_2;SS=M; 3.20; 8.38
- 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 3.19; 5.09
- 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none;none; 3.18; 4.17
- 453489; AA300057; Hs.102000; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Els,F5_F8_type_C,pkinase,Els; 3.17; 7.88
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_P14_kinase;TM=M; 3.16; 4.71
- 412767; AA233808; Hs.286241; protein kinase, cAMP-dependent, regulato; SH3,7tm_2,cadherin,GPS,laminin_E,EGF,laminin_EGF,Sulfata_transp,STAS,cNMP_binding,RJ1a; 3.16; 7.19
- 415662; AW972481; Hs.170610; ESTs, Highly similar to G01887 MEK kinase; pkinase,none; 3.16; 7.21
- 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 3.15; 22.66

- 437175; AW968078; Hs.87773; protein kinase, cAMP-dependent, catalytic; pkinase, pkinase_C, none; 3.14; 11.72
 409270; BE090051; Hs.23120; PIST; fn3, pkinase, PDZ, DUF139; TM=Y; SS=M; 3.09; 7.81
 419591; AF090900; Hs.91393; Homo sapiens cDNA: FLJ21887 fis, clone H; PDZ, L27; TM=M; 3.06; 5.46
 447225; R62676; Hs.17820; Rho-associated, coiled-coil containing p; PH, pkinase, HR1, none; 3.04; 13.05
 412692; AF044288; Hs.74515; aryl hydrocarbon receptor nuclear trans; HLH, PAS, PAC; TM=M; 2.95; 12.28
 409274; NM_003930; Hs.52644; SKAP55 homologue; SH3, PH; SS=M; 2.90; 14.62
 417707; AL035786; Hs.82425; actin related protein 2/3 complex, subunit; none; TM=M; 2.90; 11.00
 427045; H86504; Hs.173328; protein phosphatase 2, regulatory subunit; B56; TM=M; 2.89; 6.12
 431177; NM_003304; Hs.250687; transient receptor potential channel 1; Ion_trans, ank; TM=Y; 2.89; 6.53
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; 2.87; 9.18
 418546; AA224827; ; gb:nc32g04.s1 NCI_CGAP_P2 Homo sapiens ; vwa, Integrin_A, FG-GAP, none; 2.86; 9.94
 446668; W58353; Hs.285123; Homo sapiens mRNA full length insert cDN; NDK, PH, Oxysterol_BP; SS=M; 2.85; 14.25
 454080; AI199711; Hs.576; fucosidase, alpha-L-1, tissue; Alpha_L_fucos; TM=M; SS=M; 2.81; 28.84
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 433000; U26710; Hs.3144; Cas-Br-M (murine) ectropic retroviral tr; zf-C3HC4, UBA, Cbl_N, Cbl_N2, Cbl_N3; 2.77; 10.93
 444488; AW192879; Hs.355660; ancient conserved domain protein 4; none, none; 2.77; 12.58
 417904; AI707762; Hs.82911; protein tyrosine phosphatase type IVA, m; Y_phosphatase, DSPc; TM=M; 2.76; 12.78
 425204; NM_002436; Hs.1861; membrane protein, palmitoylated 1 (55kD); SH3, PDZ, Guanylate_kin; SS=M; 2.74; 5.71
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zf-C2H2, SET; 2.73; 12.50
 410793; AW581906; Hs.66392; Intersectin 1 (SH3 domain protein); SH3, ehfand, C2, PH, RhoGEF, M; SS=M; 2.73; 9.84
 446081; AA972412; Hs.13755; t-box and WD-40 domain protein 2; WD40, F-box, Ribosomal_L14; TM=M; 2.71; 12.29
 414443; AU077268; Hs.76144; platelet-derived growth factor receptor; lg, pkinase; TM=Y; 2.71; 10.53
 452683; AI089575; Hs.374574; progesterone membrane binding protein; homeobox, none; 2.69; 12.53
 423533; NM_014339; Hs.129751; interleukin 17 receptor; none; TM=Y; SS=M; 2.67; 8.59
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced; Fasciclin, ABC_tran, ABC_membrane, GTP_EFTU; TM=M; SS=M; 2.67; 12.22
 453915; AA588721; Hs.12284; ribosomal protein L44; none, T-box; 2.65; 6.38
 416810; AF035606; Hs.80019; programmed cell death 6; ehfand; TM=M; 2.61; 13.89
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none; TM=M; SS=M; 2.58; 10.19
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3, none; 2.56; 19.04
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C; MARCKS; SS=M; 2.55; 14.99
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell gr; Furin-like, pkinase, Recep_L_domain, YLP, none; 2.52; 14.71
 409098; AA132672; Hs.7984; pleckstrin homology, Sec7 and coiled/coi; PH, Sec7; TM=M; 2.51; 14.51
 413040; AA193338; Hs.12321; sodium calcium exchanger; Na_Ca_Ex; TM=Y; SS=M; 2.49; 9.28
 422070; AF149785; Hs.111126; pituitary tumor-transforming 1 Interact; TCPT; TM=M; SS=Y; 2.45; 12.49
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase; TM=M; 2.44; 6.68
 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none; TM=M; 2.43; 7.97
 446287; BE247683; Hs.14611; dual specificity phosphatase 11 (RNA/RNP; DSPc; SS=M; 2.41; 9.51
 410017; AW952426; Hs.109438; Homo sapiens clone 24775 mRNA sequence; none, none; 2.41; 14.01
 424756; AW504657; Hs.152931; lamin B receptor; ERG4_ERG24, FKBP; TM=Y; 2.40; 5.98
 447580; AJ953360; Hs.88201; ESTs; none, none; 2.36; 11.63
 426276; AW881411; Hs.169078; hypothetical protein FLJ23018; hormone_rec, zf-C4; TM=M; 2.34; 13.34
 424441; X14850; Hs.147097; H2A histone family, member X; histone, C8FD_NFYB_HMF; 2.33; 12.17
 429623; NM_005308; Hs.211569; G protein-coupled receptor kinase 5; pkinase, RGS; TM=M; 2.32; 15.80
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm, NTF2; TM=M; 2.32; 12.48
 453648; W21493; Hs.28329; hypothetical protein FLJ14005; none, none; 2.31; 13.19
 443951; F13272; Hs.356835; ferritin, light polypeptide; PMP22, Claudin, none; 2.31; 8.51
 453327; AW500180; Hs.356109; tryptophanyl-tRNA synthetase; rrm, vwa, FG-GAP; 2.30; 13.02
 439256; AA322302; Hs.183302; PCTAIRE protein kinase 2; none, none; 2.26; 10.38
 424467; AI929392; Hs.350026; Dnal (Hsp40) homolog, subfamily B, member; Dnal, pkinase, UBA, pkinase_C; SS=M; 2.26; 11.82
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 2.26; 12.54
 456607; AI660190; Hs.106070; cyclin-dependent kinase inhibitor 1C (p5; CDI; TM=M; 2.25; 13.11
 423960; AA164516; Hs.136309; SH3-containing protein SH3GLB1; SH3, none; 2.20; 20.05
 424058; AL121516; Hs.138617; thyroid hormone receptor Interactor 12; HECT, WWF; TM=M; 2.20; 13.38
 446644; NM_003272; Hs.15791; transmembrane 7 superfamily member 1 (up; none; TM=Y; SS=M; 2.18; 15.68
 411218; H46440; Hs.180628; dynamin 1-like; dynamin_2, dynamin, GED, none; 2.18; 13.83
 414721; X90392; Hs.77091; ribosomal protein L10; Exo_endo_phos, Ribosomal_L10a, Acyltransferase, SCP; TM=M; SS=M; 2.14; 11.24
 421759; AA027968; Hs.107979; small membrane protein 1; none; TM=Y; SS=M; 2.14; 14.03
 418240; NM_001981; Hs.79095; epidermal growth factor receptor pathway; ehfand, DUF164; TM=M; 2.13; 12.86
 435521; W23814; Hs.6361; mitogen-activated protein kinase kinase ; none, none; 2.12; 11.08
 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hock, DDT, PI3_P14_kinase, FAT, FATC, BclA, RUN; TM=M; 2.12; 14.05
 453064; R40334; Hs.89463; potassium large conductance calcium-act; none, none; 2.12; 8.96
 409223; AA312572; Hs.362852; phosphoinositide-3-kinase, regulatory su; SH2, SH3, RhoGAP, none; 2.08; 11.60
 414482; S57498; Hs.76252; endothelin receptor type A; 7tm_1; TM=Y; SS=M; 2.06; 14.23
 414496; W73853; Hs.355424; ESTs; pkinase, F5_F8_type_C, adh_short, none; 2.05; 13.45
 450455; AL117424; Hs.25035; chloride intracellular channel 4; none, TNF; 2.05; 19.04
 449905; NM_005638; Hs.24167; synaptobrevin-like 1; synaptobrevin, NTF2; TM=Y; 2.04; 13.34
 422112; BE540240; Hs.111783; Lsm1 protein; Sm, BAG; SS=M; 2.03; 12.60
 434935; BE561824; Hs.273369; uncharacterized hematopoietic stem/proge; none; TM=M; 2.02; 10.52
 433427; AI816449; Hs.171889; cholinephosphotransferase 1; SH2, CDP-OH_P_transf; TM=M; 2.02; 16.87
 410850; AW362867; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_transp, STAS, HMG_box; 2.02; 9.37
 440481; AA182907; Hs.7200; Homo sapiens, clone MGC:16714, mRNA, corr; pkinase, RCC1; TM=M; 2.02; 12.31
 434645; AF255303; Hs.112227; membrane-associated nucleic acid binding; zf-CCHC, gphd, Adeno_E1B_55K, zf-C3HC4; TM=M; 2.00; 9.15
 410113; AW998564; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone H; pkinase, none; 1.99; 10.64
 414636; AL120259; Hs.76691; stannin; none; TM=M; SS=Y; 1.95; 7.72
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase, none; 1.95; 14.95
 422690; AU077275; Hs.119222; suppression of tumorigenicity 13 (colon ; TPR; TM=M; 1.94; 10.91
 427881; BE538296; Hs.323834; cytochrome c oxidase subunit Va; none, GKAP; 1.93; 20.57
 433387; L76528; Hs.3260; presenilin 1 (Alzheimer disease 3); Presenilin, 7tm_3, oxidored_q5_N; TM=Y; 1.92; 12.58
 453938; AF082569; Hs.36794; D-type cyclin-interacting protein 1; B56; TM=M; 1.90; 12.74
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) ; none; TM=M; 1.89; 23.27
 447791; BE241859; Hs.19575; CGI-11 protein; V-ATPase_H, Armadillo_seg; TM=M; 1.88; 12.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone H; adenylatekinase, none; 1.88; 14.95

- 432650; D00860; Hs.56; phosphoribosyl pyrophosphatase synthetase ; none:none; 1.88; 12.70
 424250; AF073310; Hs.143648; insulin receptor substrate 2; PH,IRS;TM=M; 1.86; 19.50
 424482; BE268621; Hs.149155; voltage-dependent anion channel 1; Euk_gorin;SS=M; 1.85; 11.29
 425335; BE394327; Hs.296267; follistatin-like 1; ehand,kazal,arf,ras,7tm_1;TM=M; 1.85; 13.62
 5 426122; NM_006925; Hs.166975; splicing factor, arginine/serine-rich 5; rrm;SS=M; 1.83; 10.88
 451579; AW607731; Hs.26670; Human PAC clone RP3-515N1 from 22q11.2-q; kringle;TM=Y;SS=M; 1.83; 20.35
 428901; A1929568; Hs.146668; KIAA1253 protein; 7tm_2,UPF0073,TMS_TDE;TM=Y;SS=M; 1.83; 19.00
 453963; AA040311; Hs.28959; ESTs; pkinase,Activin_recpt;none; 1.82; 15.25
 417414; AA434589; Hs.367676; dUTP pyrophosphatase; dUTPase,KRAB; 1.81; 14.20
 10 414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 1.81; 22.29
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 14; Exo_endo_phos,SH2;TM=M; 1.80; 18.30
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown prot; none;NA;NA; 1.80; 6.28
 424805; AF230904; Hs.153260; C-Cbl-interacting protein; SH3;TM=M; 1.80; 11.99
 420747; BE294407; Hs.59910; phosphofructokinase, platelet; PFK;TM=M; 1.79; 25.25
 15 416819; U77735; Hs.80205; pim-2 oncogene; pkinase;SS=M; 1.78; 15.25
 437708; AB033020; Hs.5801; KIAA1194 protein; LRR,Exo_endo_phos;TM=M; 1.77; 11.11
 439877; H39685; Hs.258730; tryptase beta 1; pkinase;SS=M; 1.77; 21.91
 440256; U23841; Hs.18851; hypothetical protein FLJ10875; none,UBA,UBX; 1.76; 12.95
 20 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor t; none;TM=M;SS=Y; 1.76; 21.01
 414703; BE243877; Hs.374366; ATPase, Na⁺ transporting, beta 3 polypep; Na_K-ATPase;TM=Y;SS=M; 1.75; 20.03
 443693; AI344782; Hs.349261; DnaJ (Hsp40) homolog, subfamily C, member; rrm,DnaJ,TPR;TM=M; 1.75; 13.29
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,GTP_EFTU,ABC_membrane;none; 1.75; 8.75
 413796; AW406094; Hs.75545; Interleukin 4 receptor; fn3,granulin;TM=M;SS=M; 1.74; 14.73
 438438; AA257992; Hs.50651; Janus kinase 1 (a protein tyrosine kinase; pkinase,SH2,adenylatekinase;none; 1.73; 24.10
 25 429655; U48959; Hs.211582; myosin, light polypeptide kinase; pkinase,fn3,jg;none; 1.73; 31.59
 421456; AW579842; Hs.104557; hypothetical protein FLJ10697; zf-C2H2,DUF18,ehand,C2,PI-PLC-Y,PI-PLC-X;TM=M; 1.73; 16.87
 444252; R21135; Hs.54985; ESTs; none:none; 1.71; 10.40
 442819; BE622721; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; none,pkinase,PBD; 1.69; 14.02
 447918; AI129320; Hs.115175; ESTs, Highly similar to JC5818 gamma-act; pkinase,SAM;none; 1.69; 17.14
 30 429279; AB018271; Hs.198689; KIAA0728 protein; Myosin_tail,ehand,spectrin,GAS2,Myosin_tail; 1.68; 14.21
 450440; AB024334; Hs.25001; tyrosine 3-monooxygenase/tryptophan 5-mo; 14-3-3;TM=M; 1.67; 24.67
 413423; AU076684; Hs.75350; vinculin; Vinculin;none; 1.65; 29.28
 420972; AW814616; Hs.31431; hypothetical protein FLJ12171; Fructosamin_kin;SS=M; 1.65; 10.75
 416884; M60484; Hs.80350; protein phosphatase 2 (formerly 2A), cat; Metallophos;SS=M; 1.63; 24.55
 35 436719; Y11192; Hs.5299; aldehyde dehydrogenase 5 family, member ; lipocalin,aldedh,ubiquitin,IRK;SS=M; 1.61; 11.20
 419223; X60111; Hs.1244; CD9 antigen (p24); transmembrane4;TM=Y;SS=M; 1.61; 14.93
 414176; BE140638; Hs.75794; EDG-2 (endothelial differentiation, lys; 7tm_1,CRCB;TM=Y; 1.61; 8.03
 431476; BE612705; Hs.256697; histidine triad nucleotide-binding prote; HIT;SS=M; 1.60; 24.37
 412347; AW970026; Hs.73818; ubiquinol-cytochrome c reductase hinge p; UCR_hinge,G-alpha,arf;TM=M; 1.59; 18.09
 40 423804; AW030448; Hs.1708; Interferon-stimulated transcription fact; IRF,zf-C3HC4,IBR,zf-RanBP;TM=M; 1.59; 10.99
 426552; BE297660; Hs.170382; moesin; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmn,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 1.58; 25.97
 428216; M18468; Hs.183037; protein kinase, cAMP-dependent, regulator; cNMP_binding,Rlla;SS=M; 1.56; 10.58
 421251; Z28913; Hs.102948; enigma (LIM domain protein); LIM,PDZ;SS=M; 1.56; 13.51
 448581; NM_002709; Hs.21537; protein phosphatase 1, catalytic subunit; none:none; 1.55; 12.33
 45 417098; AB017365; Hs.173859; frizzled (Drosophila) homolog 7; Frizzled,Fz,7tm_2,loxin 2;TM=Y;SS=M; 1.55; 13.77
 437076; AA961260; Hs.5443; BCL2-associated athanogene 5; BAG,Hanta_nucleocap;TM=M; 1.54; 10.93
 426653; AA530892; Hs.171695; dual specificity phosphatase 1; Rhodanese,DSPc,Y_phosphatase;TM=M; 1.54; 11.88
 421143; AB024538; Hs.102171; Immunoglobulin superfamily containing la; ig,LRR,LRRNT,LRRCT;TM=M;SS=M; 1.53; 23.05
 414457; AW514320; Hs.76159; ATPase, H transporting, lysosomal (vacuo; pkinase,ATP-synt_C;none; 1.53; 32.59
 50 414382; AW380339; Hs.8068; hematopoietic PBX-interacting protein; M;TM=M; 1.52; 8.66
 450998; BE387614; Hs.25797; splicing factor 3b, subunit A, 49kD; rrm;TM=M; 1.52; 11.74
 402705; ; activator of S phase Kinase; AhpC-TSA;TM=M;SS=M; 1.51; 26.85
 426268; AF083420; Hs.168913; serine/threonine kinase 24 (Ste20, yeast; pkinase;SS=M; 1.50; 24.04
 414604; AU076649; Hs.76556; growth arrest and DNA-damage-inducible 3; none;TM=M; 1.50; 14.35
 55 445584; AF217518; Hs.8360; PTD012 protein; none;SS=M; 1.49; 12.00
 407232; X04526; ; gb:Human liver mRNA for beta-subunit sig; WD40;TM=M; 1.49; 19.32
 424206; NM_003734; Hs.198241; amine oxidase, copper containing 3 (vasc; Cu_amine_oxid,Cu_amine_oxidN3;TM=M;SS=M; 1.48; 13.21
 458761; AF090922; Hs.152738; mitochondrial ribosomal protein L11; ER_lumen_recept,Ribosomal_L11,N;TM=Y;SS=M; 1.48; 12.50
 426340; Z97989; Hs.169370; FYN oncogene related to SRC, FGR, YES; BNR,SH2,SH3,pkinase;TM=Y;SS=M; 1.48; 17.75
 60 414166; AW888941; Hs.75789; N-myc downstream regulated; DEAD,helicase_C,rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,JQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,DSPc,isp_1,Ribosomal_S21,rvp;TM=M; 1.46; 20.47
 452516; AA058630; Hs.29759; RNA POLYMERASE I AND TRANSCRIPT RELEASE ; none;SS=M; 1.46; 12.72
 414240; AL046742; Hs.75842; dual-specificity tyrosine-(Y)-phosphoryl; pkinase;SS=M; 1.45; 14.38
 420532; AA248016; Hs.194110; hypothetical protein PRO2730; pkinase,WD40;SS=M; 1.43; 13.92
 65 402575; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.43; 13.71
 414765; X07854; Hs.77269; guanine nucleotide binding protein (G pr; G-alpha,arf;TM=M; 1.41; 24.62
 448423; BE390905; Hs.21198; translocase of outer mitochondrial membr; TPR;TM=M;SS=M; 1.41; 10.70
 422587; AI879352; Hs.118625; hexokinase 1; hexokinase,hexokinase2;TM=M; 1.41; 19.31
 70 415995; NM_004573; Hs.355888; phospholipase C, beta 2; C2,PI-PLC-Y,PI-PLC-X;TM=M; 1.40; 11.21
 446108; AL036595; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemnin;TM=M; 1.40; 13.98
 427721; AI582843; Hs.180455; RAD23 (S. cerevisiae) homolog A; ubiquitin,UBA,integrin_B;SS=M; 1.39; 15.01
 417891; W79410; Hs.82887; protein phosphatase 1, regulatory (inhib; none;TM=M; 1.39; 15.97
 427373; AB007972; Hs.130760; myosin phosphatase, target subunit 2; ank;TM=M; 1.39; 14.49
 446334; U52427; Hs.14839; polymerase (RNA) II (DNA directed) polyp; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,catreticuln,7tm_2,rrm,PAP_assoc;TM=Y;SS=M; 1.38; 12.58
 75 447042; AB035863; Hs.182217; succinate-CoA ligase, ADP-forming, beta ; ligase-CoA,ATP-grasp,Zip,CPSase_L_D2,GARS_B;TM=Y;SS=M; 1.37; 11.37
 427705; AI870421; Hs.180394; signal recognition particle 14kD (homolo; SRP14,TNFR_c6;SS=M; 1.37; 22.05
 425989; AW576265; Hs.301763; KIAA0554 protein; SH3,FCH,HR1;TM=M; 1.37; 13.68
 433572; AL046859; Hs.3407; protein kinase (cAMP dependent, catalytic; PKI;SS=M; 1.35; 12.43
 80 410597; W16518; Hs.279518; amyloid beta (A4) precursor-like protein; Kunitz_BPTIA4_EXTRA,Coprogen_oxidase;TM=Y;SS=M; 1.35; 22.54
 418424; Y13622; Hs.85087; latent transforming growth factor beta b; EGF,TB,spidertoxin,granulin,ANF_receptor;SS=M; 1.34; 12.09
 442603; AL035719; Hs.303091; plectstrin homology, Sec7 and coiled/coi; PH,Sec7;TM=M; 1.34; 11.40
 418043; AW377752; Hs.83341; AXL receptor tyrosine kinase; fn3,jg,pkinase;TM=Y;SS=M; 1.31; 10.79

	439278; AF077046; Hs.6518; ganglioside expression factor 2; MAP1_LC3,aminotran_3;TM=M; 1.31; 15.89
	425875; AU077333; Hs.160483; erythrocyte membrane protein band 7.2 (s; PBP_Band_7;TM=M; 1.31; 17.93
	407744; AB020629; Hs.38095; ATP-binding cassette, sub-family A (ABC); ABC_tran,PRK;TM=Y;SS=M; 1.29; 10.95
5	420679; X57152; Hs.99853; fibrillarin; CK_II_beta,Fibrillarin,WD40;TM=M; 1.29; 18.69
	427397; AJ929685; Hs.177656; calmodulin 1 (phosphorylase kinase, delt; ehand,RmaAD;SS=M; 1.29; 15.68
	424661; M29551; Hs.151531; protein phosphatase 3 (formerly 2B), cat; Metallophos;TM=M; 1.28; 13.39
	428950; BE311879; Hs.194673; phosphoprotein enriched in astrocytes 15; DED;TM=M; 1.27; 11.15
	440820; AL031846; Hs.356416; plakophilin 4; none;none; 1.26; 10.65
10	448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevi; NusG;SS=M; 1.25; 12.07
	447386; NM_006289; Hs.375001; KIAA1027 protein; Band_41_LWEQ,Apolipoprotein,IRS;SS=M; 1.22; 10.65
	433053; BE301909; Hs.279952; glutathione S-transferase subunit 13 hom; HCCA_isomerase;TM=M; 1.20; 15.78
	440708; AF038962; Hs.7381; voltage-dependent anion channel 3; Euk_porin,Enterotoxin_A,PHO4;none; 1.20; 14.06
	417069; AA442192; Hs.374980; cytochrome c oxidase subunit VIII; COX8,SHMT,MIF,GST_C,EF1G_domain,GST_N,S1,Fz,Fizzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 1.18; 16.91
15	402559; ; Rho GTPase activating protein 1; PAP2;TM=Y;SS=M; 1.16; 15.49
	426536; BE242634; Hs.2055; ubiquitin-activating enzyme E1 (A1S9T an; ThiF,UBACT;TM=M; 1.14; 10.99
	428773; BE256238; Hs.193163; bridging integrator 1; BAR,SH3;SS=M; 1.14; 11.38
	406906; Z25424; ; gb.H.sapiens protein-serine/threonine kt; none;none; 1.13; 12.97
20	443932; AW888222; Hs.9973; tensin; SH2,WV,PID;none; 1.07; 15.41
	421996; AW583807; Hs.1460; glucagon; hormone2;SS=M; 59.35; 1.61
	414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin; lectin_c;TM=Y;SS=M; 22.96; 4.57
	442573; H93366; Hs.7567; branched chain aminotransferase 1, cytos; aminotran_4;none; 21.41; 1.15
	451035; AU076785; Hs.430; plastin 1 (i isoform); ehand,CH,Adaptin_N;SS=M; 19.25; 3.53
25	408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 15.53; 4.34
	421340; F07783; Hs.1369; decay accelerating factor for complement; sushit;SS=M; 14.84; 19.59
	422260; AA315993; Hs.105484; regenerating gene type IV; lectin_c;SS=M; 14.71; 2.89
	430280; AA361258; Hs.237868; Interleukin 7 receptor; fn3;none; 14.28; 11.47
	412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymph; 7tm_1;TM=Y;SS=M; 12.71; 12.56
30	451820; AW058357; Hs.199248; ESTs; 7tm_1;TM=Y;SS=M; 10.18; 2.67
	418693; AJ750878; Hs.87409; thrombospondin 1; EGF,isp_1,vwc,TSPN,isp_3;SS=M; 9.72; 6.94
	448105; AW591433; Hs.298241; Transmembrane protease, serine 3; ldl_recept_L,trypsin;TM=Y;SS=M; 9.67; 4.06
	456266; L29073; Hs.198726; cold shock domain protein A; 7tm_2,HRM,CSD;TM=Y;SS=M; 9.62; 2.36
	413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-ret; none;START; 9.15; 2.18
35	417933; X02308; Hs.82962; thymidylate synthetase; thymidylat_synt,MR_MLE,MR_MLE_N;SS=M; 8.97; 5.01
	433334; AJ927430; Hs.231958; matrix metalloproteinase 28; Peptidase_M10;none; 8.71; 4.28
	418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
	433437; AW0536; Hs.3280; caspase 6, apoptosis-related cysteine pr; ICE_p10,ICE_p20;SS=M; 8.31; 4.23
40	449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 8.26; 5.49
	428513; BE220806; Hs.184697; Homo sapiens clone 23785 mRNA sequence; PSI;none; 8.13; 13.28
	449444; AW818436; Hs.351306; solute carrier family 16 (monocarboxylic; none;TM=Y;SS=M; 7.89; 7.00
	453459; BE047032; Hs.257789; ESTs; none;none; 7.40; 0.60
	436729; BE621807; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 7.29; 5.78
	426761; AI015709; Hs.172089; PORIMIN Pro-oncosis receptor inducing me; none;TM=Y;SS=M; 7.25; 7.22
45	426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 7.13; 3.97
	419968; X04430; Hs.93913; interleukin 6 (interferon, beta 2); IL6;SS=Y; 6.93; 3.43
	457133; M54968; Hs.351221; v-K-ras2 Kirsten rat sarcoma 2 viral on; ras,ldh;SS=M; 6.90; 2.85
	420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 6.88; 3.10
	417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-recept; Y_phosphatase;TM=Y; 6.42; 2.26
50	427969; NM_001963; Hs.2230; epidermal growth factor (beta-urogastrin; EGF,ldl_recept_L,EB;TM=M;SS=M; 6.37; 1.07
	430396; X04942; Hs.241363; hyaluronan-binding protein 2; ank,death,ZU5,EGF,kringle,trypsin,Nebulin,LIM;SS=M; 5.77; 1.24
	427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptio; UPAR_LY6,ET,PLA2_inh;SS=M; 5.71; 3.83
	418283; S79895; Hs.83942; cathepsin K (pseudosclerosis); Peptidase_C1;SS=M; 5.59; 38.68
	458471; AV648609; Hs.194240; ESTs; none;none; 5.23; 1.05
55	433470; AW960564; Hs.351316; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.88; 4.60
	433293; AF007835; Hs.32417; hypothetical protein MGC4309; none;TM=M; 4.56; 4.96
	410857; X63556; Hs.750; fibrillin 1 (Marfan syndrome); EGF,TB,wnt,EB,TIL;SS=M; 4.32; 26.87
	417512; X76534; Hs.82226; glycoprotein (transmembrane) nmbl; PKD;TM=Y;SS=M; 4.26; 9.04
	414825; X06370; Hs.77432; epidermal growth factor receptor (avian ; Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 3.94; 1.16
60	439180; AJ393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 3.76; 2.21
	419508; AW997938; Hs.90786; ATP-binding cassette, sub-family C (CFTR; ABC_tran,ABC_membrane;TM=Y;SS=M; 3.47; 2.24
	419749; X73608; Hs.93029; sparclosteonectin, cwcv and kazal-like d; kazal,thyroglobulin_1;SS=M; 3.37; 7.10
	436576; AI458213; Hs.77542; ESTs; 7tm_1,DnaI; 3.15; 3.27
	428093; AW594506; Hs.104830; ESTs; none;none; 2.81; 3.40
65	459683; AI674906; Hs.199450; gb:wc73f02.x1 NCL CGAP_Pan1 Homo sapiens; none;TM=Y; 2.77; 1.36
	414443; AU077268; Hs.76144; platelet-derived growth factor receptor; ig,pkinase;TM=Y; 2.71; 10.53
	430451; AA836472; Hs.297939; cathepsin B; Peptidase_C1,pro_isomerase;SS=M; 2.28; 14.59
	428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 2.21; 6.33
	435496; AW840171; Hs.265398; PAR-6 beta; none;none; 2.17; 2.00
70	418641; BE243136; Hs.86947; a disintegrin and metalloproteinase dom; disintegrin,Repophysin,Pep_M12B_propep,EGF;TM=Y;SS=M; 1.91; 13.06
	414521; D28124; Hs.76307; neuroblastoma, suppression of tumorigen; DAN;TM=M;SS=M; 1.81; 22.29
	419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,pkinase;TM=Y;SS=M; 1.52; 8.40
	452795; AW392555; Hs.18878; hypothetical protein FLJ21620; 20G-Fell_Oxy;TM=M; 1.49; 3.29
	432199; AI693815; Hs.127179; cryptic gene; none;TM=M;SS=M; 1.23; 1.60
75	453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin,ldl_recept_a;none; 1.00; 3.92
	445418; AW139377; Hs.127179; cryptic gene; none;none; 1.00; 2.45
	451106; BE382701; Hs.25960; N-MYC oncogene; HLH,Myc_N_term;TM=M; 1.00; 1.87
	447993; AW139525; Hs.170362; ESTs; none;none; 1.00; 1.30

TABLE 42B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

5

Pkey	CAT Number	Accession
406685	Q_0	M18728
414087	1632850_1	W19712 BE247277
400151	9575_21	BC006850 U07418 NM_000249 U07343 AL574783 BI090482 BG684481 AA385302 BG196167 BI091720 BG195132 AI680106 AI457552 AA402478
418546	242836_1	BG249688 AA347119 BG755996 BG822578 T59708 AA224827 T59843 BE156903

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TABLE 42C

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Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

20

Pkey	Ref	Strand	Nt_position
406399	9256288	Minus	63448-63554
405102	8076881	Minus	120922-121296
403344	8569726	Plus	70823-70990
405555	1552511	Plus	153405-153564,154623-154876,155272-15540
405556	1552511	Plus	163497-163623,164715-164968,165369-16550
405204	7230116	Plus	126569-126754
406366	9256126	Minus	10639-10800,10890-11023,11113-11293
400539	7574902	Plus	8559-8721
403208	7630829	Minus	147706-147903,148667-148804
405203	7230116	Plus	125295-125463
402705	8782736	Plus	89961-90114,90773-90895,91131-91261
402575	9884830	Minus	109742-109883
402559	9864273	Plus	33539-33715

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TABLE 43A: 43 genes upregulated in pancreatic cancer relative to normal body tissues

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Table 43A lists about 43 genes upregulated in pancreatic cancer relative to normal body tissues that are likely to encode proteins particularly useful for diagnostic or prognostic applications. These genes were selected from 59680 probesets on the Eos/Altymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

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Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar accession number, GenBank accession number
UniGeneID:	UniGene number
Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).

50

UniGene Title:	UniGene gene title
R1	90th percentile of pancreatic cancer AIs divided by the 50th percentile of normal tissue AIs
R2	90th percentile of pancreatic cancer AIs divided by the 90th percentile of normal pancreas AIs, where the 15th percentile of all normal tissue AIs was subtracted from both the numerator and denominator

55

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1; R2

60

446619; AU076643; Hs.313; secreted phosphoprotein 1 (osteopontin); Osteopontin;SS=M; 44.95; 2.17
421552; AF026692; Hs.105700; secreted frizzled-related protein 4; Fz,NTR;SS=M; 35.40; 29.13
411274; NM_002776; Hs.69423; kallikrein 10; trypsin;TM=M; 30.10; 13.59
446921; AB012113; Hs.16530; small inducible cytokine subfamily A (C); IL8;SS=Y; 29.33; 16.08
413719; BE439580; Hs.75498; small inducible cytokine subfamily A (C); IL8;SS=M; 24.64; 7.21
452281; T93500; Hs.28792; Homo sapiens cDNA FLJ11041 fis, clone PL; TGFb_propeptide,TGF-beta:none; 23.81; 10.74
407811; AW190902; Hs.40098; cysteine knot superfamily 1, BMP antagonist; TGF-beta,DAN;SS=Y; 22.33; 10.20
404682; ; C9001188; gij12738842[ref]NP_073725.1] p; none;TM=M; 17.72; 1.40

65

413554; AA319146; Hs.75426; secretogranin II (chromogranin C); Granin;TM=M;SS=Y; 17.36; 2.01
428392; H10233; Hs.2265; secretory granule, neuroendocrine protei; none;TM=M;SS=M; 16.82; 1.70
408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 15.53; 4.34
419216; AU076718; Hs.164021; small inducible cytokine subfamily B (C); IL8;SS=M; 15.40; 3.70
428242; H55709; Hs.2250; leukemia inhibitory factor (cholineric); LIF_OSM;SS=M; 14.85; 6.58
421340; F07783; Hs.1369; decay accelerating factor for complement; sushi;SS=M; 14.84; 19.59

70

409757; NM_001898; Hs.123114; cystatin SN; cystatin;SS=M; 14.61; 12.75
425071; NM_013989; Hs.154424; deiodinase, iodothyronine, type II; T4_deiodinase;TM=M;SS=Y; 14.35; 17.22
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8;TM=M;SS=Y; 13.81; 7.69
409420; Z15008; Hs.54451; laminin, gamma 2 (nicel (100kD), kalin; laminin_B,laminin_EGF;SS=M; 13.05; 7.72

75

432596; AJ224741; Hs.278461; matrilin 3; EGF,vwa;SS=M; 12.80; 9.91
422109; S73265; Hs.1473; gastrin-releasing peptide; Bombesin,Defensin_propept;TM=M;SS=M; 12.79; 4.69
421379; Y15221; Hs.103982; small inducible cytokine subfamily B (C); IL8;TM=M;SS=Y; 11.36; 2.22
429547; AW009166; Hs.99376; FGENSEH predicted novel secreted protein; none:none; 10.25; 5.62
422424; AI186431; Hs.296638; prostate differentiation factor; TGF-beta;SS=M; 9.96; 1.88

80

428505; AL035461; Hs.2281; chromogranin B (secretogranin 1); Granin;SS=M; 9.40; 3.46
409956; AW103364; Hs.727; inhibin, beta A (activin A, activin AB a; TGF-beta,TGFb_propeptide,Tub;SS=M; 9.19; 16.46
418030; BE207573; Hs.83321; neuromedin B; Bombesin;TM=M;SS=Y; 8.38; 1.55
452401; NM_007115; Hs.29352; tumor necrosis factor, alpha-induced pro; Xlink,CUB;SS=M; 7.46; 4.96

- 421582; AI910275; Hs.350470; trefoil factor 1 (breast cancer, estroge; trefoil, Gastrin; SS=M; 7.08; 21.61
 423634; AW959908; Hs.1690; heparin-binding growth factor binding pr; none; TM=M; SS=M; 6.78; 12.19
 428486; AW583497; Hs.184604; pancreatic polypeptide; hormone3; TM=M; SS=Y; 6.29; 3.51
 443646; AI085198; Hs.164226; ESTs; EGF, tsp_1, vvc, TSPN, tsp_3, none; 6.17; 4.25
 457489; AI693915; Hs.127179; cryptic gene; none; TM=M; SS=M; 5.19; 2.79
 450983; AA305384; Hs.25740; ERO1 (S. cerevisiae)-like; none; SS=M; 5.01; 7.43
 422867; L32137; Hs.1584; cartilage oligomeric matrix protein (pse; tsp_3, EGF; SS=M; 4.87; 9.40
 426322; J05068; Hs.2012; transcobalamin I (vitamin B12 binding pr; Cobalamin_bind; SS=M; 4.71; 11.74
 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringle, trypsin, plasmin; SS=M; 4.24; 6.91
 428758; AA433988; Hs.98502; CA125 antigen; mucin 16; SEA; TM=Y; 3.52; 8.43
 422048; NM_012445; Hs.288126; spondin 2, extracellular matrix protein; tsp_1; TM=M; SS=M; 3.45; 7.69
 424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B; in2, hemopexin, Peptidase_M10; SS=M; 3.43; 10.37
 417931; W95642; Hs.82961; trefoil factor 3 (intestinal); trefoil; SS=M; 2.98; 9.65
 445417; AK001058; Hs.12680; Homo sapiens cDNA FLJ10196 fis, clone HE; tsp_1, Reprolysin, Pep_M12B_propep, none; 2.97; 5.74
 432874; W94322; Hs.279651; melanoma inhibitory activity; SH3; TM=M; SS=Y; 2.80; 10.53
 431462; AW583672; Hs.256311; granlin-like neuroendocrine peptide precu; none, none; 2.70; 1.99

TABLE 43C

- 20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 25 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
404682	9797231	Minus	40977-41150

TABLE 44A: 754 GENES UP-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

- 35 Table 44A lists about 754 genes up-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

- 40 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title

Pkey	ExAccn	UnigenID	Unigene Title
100042	M10098		AFFX control - HUMRGE/M10098_3
101577	M34353	Hs.1041	v-ras avian UR2 sarcoma virus oncogene h
103353	X89399	Hs.119274	RAS p21 protein activator (GTPase activa
104743	AA021157	Hs.33619	Homo sapiens cDNA FLJ20096 fis, clone CO
104996	AA112307	Hs.105894	hypothetical protein FLJ21919
105437	AA252191	Hs.25199	hypothetical protein
108258	AA063269		gb:zm02a09.s1 Stralagene corneal stroma
109086	AA166695	Hs.270737	tumor necrosis factor (ligand) superfam
109279	AA196625	Hs.86080	ESTs
109779	F10527	Hs.3353	beta-1,3-glucuronyltransferase 1 (glucur
111794	R32647	Hs.23545	ESTs
112531	R69798	Hs.29036	ESTs
112784	R96306	Hs.191290	ESTs
113293	T67026	Hs.187403	ESTs
115416	AA283893	Hs.337079	ESTs
116548	D20433		gb:HUMGS01407 Human promyelocyte Homo sa
116565	D45533	Hs.129691	hypothetical protein FLJ21603
118104	N55332	Hs.39785	ESTs
119243	T12603		gb:CHR90123 Chromosome 9 exon II Homo sa
119336	T55340	Hs.208238	ESTs
120101	W95414	Hs.55497	EST
120715	AA292700		gb:zs59a06.s1 NCL_CGAP_GCB1 Homo sapiens
120872	AA357993	Hs.96996	ESTs
121010	AA398355	Hs.97330	ESTs
121509	AA412092	Hs.97888	ESTs
121722	AA419482	Hs.98874	similar to proline-rich protein 48
122265	AA436838	Hs.98906	EST
123206	AA489681	Hs.102248	Homo sapiens cDNA: FLJ22105 fis, clone H
123490	AA599723		gb:ag11c07.s1 Gessler Wilms tumor Homo s
124198	H53099	Hs.198271	NADH dehydrogenase (ubiquinone) 1 alpha
124294	H90573	Hs.102298	EST
125067	T86429	Hs.111725	ESTs
125153	W38294		
125330	AA401804	Hs.114574	ESTs
125335	T86620	Hs.16230	hypothetical protein FLJ20619
125361	T90348	Hs.183404	ESTs
125439	AA826305		gb:PM0-LT0017-031299-001-c07 LT0017 Homo
125535	R17430	Hs.22215	secretogranin III
125583	R22272	Hs.86022	ESTs
125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
125742	H81181	Hs.261023	hypothetical protein FLJ20958

	125795	T98190	Hs.7756	prolactin (prolactin, macropain) 26S subu
	125858	H11549	Hs.31066	ESTs
	125865	H12876	Hs.283078	hOAT4
5	126039	AA160575	Hs.181102	p30 DBC protein
	126143	N29315	Hs.266331	hypothetical protein MGC4595
	126177	H93164	Hs.129750	hypothetical protein FLJ10546
	126219	N36368	Hs.293483	ESTs, Weakly similar to similar to C. el
	126221	AI248169	Hs.172965	ESTs
10	126262	C75147	Hs.143764	ESTs, Weakly similar to unknown [H.sapi
	126277	N39132	Hs.15441	Crm (Cramped Drosophila)-like
	126292	AA491328		gb:aa65d09.r1 NCI_CGAP_GC81 Homo sapiens
	126293	Z18870	Hs.248121	G protein-coupled receptor 22
	126353	AI243114	Hs.94031	ESTs
15	126556	AA491325	Hs.112227	membrane-associated nucleic acid binding
	126559	R15866	Hs.170263	tumor protein p53-binding protein, 1
	126609	W87435	Hs.186802	ESTs
	126616	AA348581	Hs.134605	ESTs
	126628	AI357886	Hs.170994	hypothetical protein MGC10946
20	126636	AA001527		gb:z156g09.r1 Soares retina N2b4HR Homo
	126861	AA742428	Hs.144432	ESTs
	126990	AA215510	Hs.191650	ESTs
	127017	AA740146	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I
	127049	AA235966	Hs.291811	ESTs
25	127209	AA305023	Hs.81964	SEC24 (S. cerevisiae) related gene famil
	127331	F20186		gb:HSPD05873 HM3 Homo sapiens cDNA clone
	127357	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	127368	AA434362	Hs.193326	fibroblast growth factor receptor-like 1
30	127374	AA448728	Hs.312110	ESTs, Weakly similar to 138022 hypothet
	127429	AA961490	Hs.293751	ESTs, Moderately similar to TPTE_HUMAN P
	127490	W52891	Hs.7278	cryptochrome 2 (photolyase-like)
	127502	AA614422	Hs.183502	ESTs
	127647	AI087279	Hs.148410	ESTs
35	127650	AA873776	Hs.261957	ESTs
	127676	D31237	Hs.279938	HSPC067 protein
	127746	AI239495	Hs.120189	ESTs
	127812	AA749094	Hs.291434	ESTs
	127824	AI208365	Hs.127811	ESTs
40	127933	AA811102	Hs.303581	ESTs, Moderately similar to ALU1_HUMAN A
	128006	AA058693	Hs.129908	KIAA0591 protein
	128011	AI347067	Hs.124636	ESTs
	128038	AA868782	Hs.137024	ESTs
	128058	AI126617	Hs.132449	ESTs
45	128199	AI073548	Hs.164597	ESTs
	128308	AI079496	Hs.134169	ESTs
	128389	AI142639	Hs.146662	ESTs
	128410	AA452788		gb:zv80d10.r1 Soares_total_fetus_Nb2HF8_
	129199	H90914	Hs.200332	hypothetical protein FLJ20651
50	130998	C00810	Hs.293981	guanine nucleotide binding protein (G pr
	134409	AA281600	Hs.164915	small nuclear RNA activating complex, p
	134578	AA194724	Hs.224137	hypothetical protein
	134644	S83308	Hs.87224	SRY (sex determining region Y)-box 5
	100262	D38500	Hs.278468	postmeiotic segregation increased 2-like
55	100676	HG3044-HT3742	Hs.287820	fibronectin 1
	100704	HG3242-HT3419	Hs.166110	calcium channel, voltage-dependent, alph
	100787	HG3872-HT4142	Hs.302063	immunoglobulin heavy constant mu
	100873	HG4333-HT4603	Hs.17364	zinc finger protein 79 (pT7)
	100943	HG880-HT880		gb:PMO-SN0019-280300-001-D11 SN0019 Homo
60	100996	J03909	Hs.14623	interferon, gamma-inducible protein 30
	101046	K01160		
	101371	M13232	Hs.36989	coagulation factor VII (serum prothrombi
	101461	M22430	Hs.76422	phospholipase A2, group IIA (platelets,
	101697	M64358		gb:Human rhom-3 gene, exon.
	101909	S69265		
65	102199	U21128	Hs.79914	lumican
	102275	U30998	Hs.17752	phosphatidylserine-specific phospholipas
	102295	U32581	Hs.168052	KIAA0421 protein
	102319	U34587	Hs.66576	corticotropin releasing hormone receptor
	102383	U40622	Hs.150930	X-ray repair complementing defective rep
70	102470	U49835	Hs.154138	chiuinase 3-like 2
	102544	U57721	Hs.169139	kynureninase (L-kynurenine hydrolase)
	102649	U68133		gb:U68133 Human cell line PCI-06A Homo s
	102798	U88898		gb:Human endogenous retrovirus H proteas
	102804	U89942		lysyl oxidase-like 2
75	102851	V00532	Hs.83354	interferon, alpha 14
	102852	V00571	Hs.93907	corticotropin releasing hormone
	102860	X00368	Hs.75294	gb:Human prolactin gene 5' region.
	103262	X78565	Hs.289114	hexabrachion (tenascin C, cytolactin)
	103484	Y08374	Hs.75184	chiuinase 3-like 1 (cartilage glycoprote
80	103559	Z19585	Hs.75774	thrombospondin 4
	103658	Z74615	Hs.172928	collagen, type I, alpha 1
	103719	AA054109	Hs.4273	hypothetical protein FLJ13159
	103876	AA226865	Hs.8203	endomembrane protein emp70 precursor iso
	103897	AA248870	Hs.55058	EH-domain containing 4

5	103906	AA249437	Hs.317403	hypothetical protein MGC2744
	103985	AA313880	Hs.99872	fetal Alzheimer antigen
	104056	AA397529	Hs.58297	CLLL8 protein
	104209	AB000221	Hs.16530	small inducible cytokine subfamily A (Cy
	104386	H41895	Hs.144164	ESTs, Moderately similar to ALU8_HUMAN A
10	104398	H53555	Hs.36790	ESTs, Weakly similar to putative p150 pH
	104422	H86858	Hs.132909	ESTs
	104561	R60100	Hs.323817	DKFZP547E1010 protein
	104593	R81267	Hs.98640	hypothetical protein FLJ21069
	104643	AA004701	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K
15	104673	AA007633	Hs.20010	ESTs
	104681	AA009832	Hs.34500	ESTs
	104711	AA017254	Hs.32794	ESTs
	104812	AA034111	Hs.124187	ESTs
	104877	AA047437	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
20	104886	AA053348	Hs.339699	growth differentiation factor 11
	104924	AA058532	Hs.28774	ESTs, Weakly similar to I38022 hypotheti
	105071	AA136532	Hs.29475	ESTs
	105105	AA151872	Hs.87016	hypothetical protein FLJ22938
	105203	AA195660	Hs.7882	ESTs
25	105317	AA233926	Hs.52620	Integrin, beta 8
	105617	AA280687	Hs.4069	glucocorticoid modulatory element bindin
	105707	AA291012	Hs.37617	ESTs, Weakly similar to A53933 myosin I
	105754	AA302657	Hs.192028	ESTs
	105770	AA347964	Hs.269873	Homo sapiens clone IMAGE:297403, mRNA se
30	105882	AA400292	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	105883	AA400490	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com
	105890	AA400766	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,
	106080	AA418046	Hs.35124	ESTs
	106090	AA418909	Hs.169333	hypothetical protein DKFZp761E2110
35	106096	AA419609	Hs.170121	protein tyrosine phosphatase, receptor t
	106124	AA423987	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106308	AA436186	Hs.30662	ESTs
	106438	AA449199	Hs.21342	ESTs
	106660	AA460936	Hs.27056	KIAA1284 protein
40	106731	AA465657	Hs.29205	alpha integrin binding protein 63
	106880	AA488889	Hs.32425	ESTs
	107055	AA600152	Hs.29419	ESTs
	107151	AA621169	Hs.8687	ESTs
	107183	C20974	Hs.12114	vanin 1
45	107231	D59299	Hs.34727	ESTs, Moderately similar to I38759 zinc
	107490	W74158	Hs.103189	lipopolysaccharide specific response-68
	107572	AA001903	Hs.59962	ESTs
	107620	AA005039	Hs.60171	ESTs
	107801	AA019433	Hs.285803	Homo sapiens cDNA FLJ10674 fis, clone NT
50	107817	AA020781	Hs.60847	ESTs
	107823	AA021057	Hs.60836	ESTs
	107857	AA024687	Hs.61208	ESTs
	107882	AA025630	Hs.231967	ALL1 fused gene from 5q31
	108005	AA037769	Hs.194293	ESTs, Weakly similar to I54374 gene NF2
55	108092	AA045961	Hs.184029	hypothetical protein DKFZp761A052
	108115	AA047291	Hs.165216	ESTs
	108214	AA058661	Hs.60764	ESTs
	108382	AA074885	Hs.67726	macrophage receptor with collagenous str
	108409	AA075578		gb:zm88h03.s1 Stratagene ovarian cancer
60	108435	AA078801		gb:zm94a09.s1 Stratagene colon HT29 (937
	108625	AA101993	Hs.283022	triggering receptor expressed on myeloid
	108631	AA102553	Hs.334337	ESTs
	108763	AA127539	Hs.281397	hypothetical protein AD034
	108852	AA133131		gb:zm25d03.s1 Stratagene pancreas (93720
65	108931	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
	108976	AA151480	Hs.91202	ESTs
	109026	AA157811		gb:zo35d07.s1 Stratagene colon (937204)
	109170	AA180352	Hs.191472	ESTs, Weakly similar to ALU1_HUMAN ALU
	109303	AA206126	Hs.269291	ESTs
70	109326	AA210719		gb:zr68e04.s1 NCI_CGAP_GCB1 Homo sapiens
	109345	AA213774	Hs.203396	ESTs
	109404	AA224594	Hs.86941	ESTs
	109473	AA233151	Hs.81796	ESTs
	109725	F10003	Hs.79658	casein kinase 1, epsilon
75	109794	F10684	Hs.23687	ESTs
	109835	H00815	Hs.170044	ESTs
	109896	H04794	Hs.30489	ESTs
	109918	H05641	Hs.216701	Homo sapiens mRNA; cDNA DKFZp56410816 (f
	109950	H08200	Hs.268770	ESTs, Weakly similar to 2004399A chromos
80	110078	H15054	Hs.318773	KIAA1836 protein
	110182	H20402	Hs.31746	hypothetical protein DKFZp547F072
	110213	H23216	Hs.86905	ATPase, H ⁺ -transporting, lysosomal (vacu
	110310	H38209	Hs.32728	EST
	110354	H41280	Hs.22586	ESTs
	110413	H48124	Hs.279454	ESTs
	110422	H48467	Hs.36094	EST
	110433	H49425	Hs.301062	UDP-N-acetyl-alpha-D-galactosamine:polyp

	110434	H49446	Hs.26299	ESTs
	110553	H58934	Hs.124990	ESTs
	110750	N20522	Hs.30981	ESTs
	110827	N30077	Hs.14855	ESTs
5	110829	N30198	Hs.28625	ESTs
	110917	N46363	Hs.5170	ESTs
	111100	N62522	Hs.20450	BCM-like membrane protein precursor
	111112	N63281	Hs.35452	ESTs
10	111179	N67239	Hs.10760	asporin (LRR class 1)
	111185	N67551	Hs.12844	EGF-like-domain, multiple 6
	111223	N68921	Hs.334838	KIAA1866 protein
	111275	N70970	Hs.35006	ESTs
	111443	R01901		gb:Homo sapiens endogenous retrovirus W
	111573	R10305	Hs.185683	ESTs
15	111590	R11157	Hs.75425	ubiquitin associated protein
	111671	R19368	Hs.229084	Homo sapiens cDNA FLJ11666 fis, clone H
	111732	R25153	Hs.163813	ESTs
	111809	R33616	Hs.24688	EST
20	111829	R36070		gb:Homo sapiens full length insert cDNA
	111944	R40606	Hs.21263	suppressor of potassium transport defect
	112015	R42836	Hs.23198	ESTs
	112023	R43020	Hs.236223	EST
	112055	R43621	Hs.26139	ESTs
25	112334	R56239	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S
	112340	R56602	Hs.8904	Ig superfamily protein
	112353	R58986	Hs.26613	Homo sapiens mRNA; cDNA DKFZp586F1323 (f
	112467	R65706		gb:yl16g12.s1 Soares placenta Nb2HP Homo
	112478	R66067	Hs.28664	ESTs
30	112533	R69886		gb:yl47f03.s1 Soares placenta Nb2HP Homo
	112588	R77302		gb:yl75h08.s1 Soares placenta Nb2HP Homo
	112595	R77783	Hs.22404	protease, serine, 12 (neurotrypsin, moto
	112676	R86976	Hs.34060	ESTs
	112744	R93206	Hs.293762	ESTs, Weakly similar to I38022 hypothetical
35	112777	R95869	Hs.35467	EST
	112817	R98491	Hs.14584	ESTs
	112902	T09262	Hs.129190	Human DNA sequence from clone RP5-1046G1
	113009	T23699	Hs.7246	ESTs
	113151	T51620	Hs.9326	EST
40	113297	T67161	Hs.13059	ESTs
	113398	T82280	Hs.87016	hypothetical protein FLJ22938
	113484	T87795	Hs.187543	ESTs
	113769	U55966	Hs.22985	alpha2,8-sialyltransferase
	113794	W37382	Hs.11090	membrane-spanning 4-domains, subfamily A
45	113971	W86760	Hs.269172	ESTs
	114066	Z38152	Hs.26920	ESTs
	114178	Z39063	Hs.17930	chromosome 6 open reading frame 11
	114206	Z39294	Hs.27339	EST
	114371	Z41835	Hs.27810	ESTs
50	114428	AA017130	Hs.84790	KIAA0225 protein
	114466	AA026970	Hs.135150	lung type-I cell membrane-associated gly
	114625	AA084362		gb:zn05b10.r1 Stratagene hNT neuron (937
	114662	AA235174	Hs.106432	Homo sapiens cDNA FLJ13410 fis, clone PL
	114908	AA236545	Hs.54973	cathecin-like protein VR20
55	114973	AA250845	Hs.87762	ESTs
	115009	AA251561	Hs.48689	ESTs
	115055	AA253005	Hs.61753	ESTs
	115098	AA256161	Hs.161729	ESTs
	115321	AA280805	Hs.191540	ESTs
60	115385	AA282540	Hs.109694	KIAA1451 protein
	115466	AA287008	Hs.285655	ESTs
	115479	AA287596	Hs.278188	ESTs, Moderately similar to I54374 gene
	115653	AA405838	Hs.40507	ESTs
	115689	AA410645	Hs.199014	ESTs, Moderately similar to ALU7_HUMAN A
65	115748	AA418835	Hs.90286	ESTs
	115810	AA426026	Hs.187615	ESTs
	115827	AA427890	Hs.83583	actin related protein 2/3 complex, subun
	115881	AA435577	Hs.184942	G protein-coupled receptor 64
	116148	AA460708	Hs.62905	hypothetical protein FLJ14834
70	116257	AA481493	Hs.88537	ESTs
	116365	AA521080	Hs.46765	ESTs
	116941	H77395	Hs.39749	ESTs
	116982	H81933	Hs.312582	ESTs
	116995	H83928		gb:ys64b03.s1 Soares retina N2b4HR Homo
75	116997	H84214	Hs.40594	ESTs
	117016	H87171	Hs.52170	ESTs
	117097	H93608	Hs.41919	EST
	117101	H94043	Hs.24341	transcriptional co-activator with PDZ-bl
	117238	N20815	Hs.173337	ESTs
80	117303	N22776	Hs.264079	ESTs
	117399	N26480	Hs.43805	lipoma HMGIC fusion partner-like 3
	117503	N31963	Hs.44286	ESTs
	117544	N33222	Hs.44451	ESTs
	117594	N34929	Hs.171984	ESTs

5	117627	N36113	Hs.44789	ESTs, Weakly similar to B34087 hypothel
	117653	N38970	Hs.194214	ESTs
	117695	N40953	Hs.45093	EST
	117697	N40976		gb:yy80b06.s1 Soares_multiple_sclerosis_
	117766	N47807	Hs.46767	EST
10	117807	N48701	Hs.46523	EST
	117816	N48872		gb:yy77a05.s1 Soares_multiple_sclerosis_
	117882	N50101	Hs.301406	hypothetical protein PP3501
	117987	N51935	Hs.47374	Homo sapiens cDNA FLJ13561 fis, clone PL
	118074	N54188	Hs.130323	Homo sapiens, clone IMAGE:3960432, mRNA
15	118114	N56875	Hs.143212	cystatin F (leukocystatin)
	118151	N58276	Hs.229119	EST
	118270	N52868	Hs.48653	ESTs
	118291	N63076	Hs.138746	EST
	118358	N64017	Hs.144633	hypothetical protein DKFZp434F2322
20	118383	N64529	Hs.49001	EST
	118412	N64856	Hs.97437	centrosomal protein 1
	118433	N66248	Hs.141609	EST
	118600	N69222	Hs.238936	ESTs, Weakly similar to (define not av
	118641	N70298	Hs.49829	ESTs
25	118643	N70324	Hs.49840	ESTs
	118695	N71781	Hs.50081	KIAA1199 protein
	118915	N91481	Hs.54713	ESTs
	119041	R02591	Hs.284294	Breakpoint cluster region protein, uteri
	119069	R27619	Hs.231046	EST
30	119105	R42357	Hs.91453	ESTs
	119154	R61293		gb:yh07a05.s1 Soares infant brain 1N1B H
	119241	T12559		gb:CHR90079 Chromosome 9 exon II Homo sa
	119269	T16367	Hs.65327	EST
	119310	T40427		gb:ya01a06.s2 Stratagene lung (937210) H
35	119345	T63474	Hs.90696	EST
	119353	T66867	Hs.187402	ESTs
	119390	T89122	Hs.249712	ESTs, Weakly similar to ALU1_HUMAN ALU
	119423	T99544	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU
	119428	W02129	Hs.55242	EST
40	119529	W38053		
	119795	W73370	Hs.339722	ESTs, Highly similar to S03917 fibronect
	119817	W74257	Hs.159690	ESTs
	119831	W78050	Hs.58419	DKFZP586L2024 protein
	119930	W86471	Hs.151624	hypocretin (orexin) receptor 2
45	120039	W92548	Hs.94985	ESTs
	120256	AA169801	Hs.98710	hypothetical protein
	120284	AA182626		gb:zp54e11.s1 Stratagene NT2 neuronal pr
	120350	AA211300	Hs.108614	KIAA0627 protein; Drosophila multiple as
	120379	AA227849		gb:DKFZp434B1822_r1 434 (synonym: hles3)
50	120383	AA228030	Hs.123122	FSH primary response (LRPR1, rat) homolo
	120420	AA236031	Hs.112885	spinal cord-derived growth factor-B
	120437	AA243427	Hs.104311	novel protein with MAM domain
	120461	AA251301	Hs.293369	ESTs
	120594	AA282054	Hs.5094	ring finger protein 10
55	120611	AA284178	Hs.110637	homeo box A10
	120626	AA285064	Hs.104485	EST
	120696	AA291503	Hs.97249	ESTs
	120747	AA302976	Hs.96672	ESTs
	120749	AA303235		gb:EST14544 Testis tumor Homo sapiens cD
60	120752	AA311972	Hs.22895	hypothetical protein FLJ23548
	120851	AA349662	Hs.174248	ESTs
	120866	AA350718	Hs.291272	ESTs
	120949	AA397830	Hs.98347	ESTs, Weakly similar to JC5308 testis-sp
	120996	AA398281	Hs.308114	ESTs
65	121038	AA398536	Hs.97365	ESTs
	121065	AA398658	Hs.97300	ESTs
	121067	AA398662	Hs.97302	ESTs
	121071	AA398678	Hs.139355	ESTs
	121082	AA398722		gb:z175h07.s1 Soares_testis_NHT Homo sap
70	121172	AA400013	Hs.97750	EST, Weakly similar to MPL3 RAT MICROTUB
	121191	AA400205	Hs.104447	ESTs
	121354	AA405384	Hs.193737	ESTs
	121393	AA405981	Hs.262643	ESTs
	121399	AA406059	Hs.332700	EST
75	121479	AA411911	Hs.98110	ESTs
	121498	AA412033	Hs.178045	ESTs
	121704	AA418743	Hs.98306	KIAA1862 protein
	121736	AA421131	Hs.148515	Human clone 23564 mRNA sequence
	122198	AA435892	Hs.97541	ESTs
80	122220	AA436011	Hs.98187	ESTs
	122250	AA436692	Hs.98892	EST
	122279	AA437209	Hs.234016	ESTs
	122286	AA437259	Hs.104944	ESTs
	122330	AA442870	Hs.98628	Homo sapiens, clone IMAGE:4214491, mRNA,
	122338	AA443311	Hs.98998	ESTs
	122355	AA443789	Hs.19978	CGI-30 protein
	122590	AA453264	Hs.99310	ESTs

	122746	AA458791		gb:aa88c02.s1 Stratagene fetal retina 93
	122805	AA460702	Hs.82772	collagen, type XI, alpha 1
	122841	AA461536	Hs.288908	WAS protein family, member 2
5	122899	AA469960	Hs.178420	ESTs, Highly similar to WASP interacting
	122933	AA476728	Hs.107537	chromosome 7 open reading frame 2
	123005	AA479726	Hs.52620	Integrin, beta 8
	123142	AA487504	Hs.105718	EST
	123153	AA488349	Hs.334808	hypothetical protein MGC4189
10	123168	AA488881	Hs.105218	EST
	123188	AA489092	Hs.177726	ESTs
	123276	AA491270	Hs.187946	ESTs
	123305	AA496133		gb:zv51e12.s1 Soares_testis_NHT Homo sap
	123328	AA496968		gb:aa42g03.s1 Soares_NhHMPu_S1 Homo sapi
15	123450	AA598913	Hs.111207	ESTs
	123464	AA599014	Hs.153321	Homo sapiens cDNA FLJ10577 fis, clone NT
	123650	AA609332	Hs.180696	ESTs
	123700	AA609606	Hs.191956	ESTs
	123858	AA620821	Hs.112911	EST
20	123863	AA620873	Hs.112916	ESTs
	124046	F10243		gb:HSC3GC122 normalized infant brain cDN
	124059	F13673	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124196	H52617	Hs.144167	ESTs
	124197	H52921		gb:yq76c09.s1 Soares fetal liver spleen
25	124229	H62793	Hs.268945	ESTs
	124230	H63111	Hs.6655	Homo sapiens EST from clone 208499, full
	124241	H65947	Hs.165355	ESTs, Moderately similar to ZN91_HUMAN Z
	124251	H68286	Hs.107924	ESTs
	124400	N30597	Hs.179152	tol-like receptor 7
30	124416	N34042	Hs.271674	ESTs
	124570	N67117	Hs.102808	ESTs
	124575	N68168		gb:za11c01.s1 Soares fetal liver spleen
	124588	N69197	Hs.191361	ESTs, Weakly similar to I38022 hypotheti
	124598	N70294	Hs.269137	ESTs, Weakly similar to A56194 thromboxa
35	124655	N93176	Hs.102914	ESTs
	124706	R07499	Hs.193612	ESTs, Weakly similar to ALU8_HUMAN ALU
	124848	R60135	Hs.203498	EST
	124882	R74041	Hs.101539	ESTs
	124898	R82846	Hs.273789	ESTs
40	125086	T91161	Hs.173880	interleukin 1 receptor accessory protein
	125145	W38001		
	125216	W73409	Hs.103185	ESTs
	125342	AI055916	Hs.133552	ESTs
	125351	T96520	Hs.324746	alpha-2-HS-glycoprotein
45	125419	AI076822	Hs.134544	ESTs
	125424	T99667	Hs.18564	ESTs
	125526	R14487	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f
	125539	R17870	Hs.248120	G protein-coupled receptor 21
	125633	AA908225	Hs.15463	Homo sapiens, clone IMAGE:2959994, mRNA
50	125689	R48940	Hs.108043	Friend leukemia virus integration 1
	125707	C14616	Hs.284122	Wnt inhibitory factor-1
	125790	AA868325	Hs.99962	proteoglycan 2, bone marrow (natural kil
	125876	AA324967	Hs.7298	biphenyl hydrolase-like (serine hydrolas
	125969	R94247	Hs.88414	BTB and CNC homology 1, basic leucine zi
55	125970	AI000964	Hs.177516	high density lipoprotein binding protein
	125975	AA495891	Hs.152290	ESTs, Highly similar to JC2463 vasoactiv
	125985	H54857	Hs.35981	ESTs
	126018	H54866	Hs.167583	ESTs
	126032	H59735	Hs.269065	ESTs, Highly similar to KIAA0349 [H.sapi
60	126059	H66582	Hs.308486	ESTs
	126107	H79155	Hs.93361	ESTs
	126154	AI004105	Hs.190488	Homo sapiens, Similar to nuclear localiz
	126199	AI000492	Hs.125829	ESTs
	126207	W77936	Hs.83583	actin related protein 2/3 complex, subun
65	126227	N27236	Hs.269034	ESTs
	126269	AA830432	Hs.44701	ESTs
	126373	F11806	Hs.6079	B cell RAG associated protein
	126378	AA347842		gb:yy62a11.s1 Soares_multiple_sclerosis_
70	126383	AA885594	Hs.6298	KIAA1151 protein
	126403	N73388	Hs.125976	ESTs, Weakly similar to S71949 metallopr
	126525	AA884833	Hs.166432	ESTs
	126527	AA548559	Hs.103853	hypothetical protein FLJ20043
	126566	W67245	Hs.103142	ESTs
	126583	W92895	Hs.279746	vanilloid receptor-like protein 1
75	126610	AA460338	Hs.191391	ESTs
	126622	AA699443	Hs.193213	ESTs
	126633	AA206993	Hs.315367	Homo sapiens, Similar to hypothetical pr
	126727	AA037230	Hs.135084	cystatin C (amyloid angiopathy and cereb
	126762	AA064671		gb:zm13b04.s1 Stratagene pancreas (93720
80	126775	S86382	Hs.957	putative opioid receptor, neuromedin K (
	126783	AA126047		gb:zn09d10.s1 Stratagene hNT neuron (937
	126882	AA761143	Hs.250581	SWI/SNF related, matrix associated, acti
	126945	R51877	Hs.25845	ESTs
	126968	AI311457	Hs.99472	ESTs

5	127070	AA641812	Hs.190037	ESTs
	127087	AA380418	Hs.88012	SHP2 interacting transmembrane adaptor
	127187	AA297138	Hs.207422	ESTs, Weakly similar to S71949 metallopro
	127215	AI246377	Hs.127675	ceroid-lipofuscinosis, neuronal 8 (epile
	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of
10	127278	AA342715		gb:EST48309 Fetal spleen Homo sapiens cD
	127299	AA360710	Hs.158480	ESTs
	127325	AA393073	Hs.126099	ESTs
	127347	AA428350	Hs.58389	hypothetical protein MGC4090
	127401	AA921944	Hs.127639	ESTs
15	127420	AA699582	Hs.82171	Homo sapiens clone 19187 placenta expres
	127438	AI224421	Hs.77100	general transcription factor IIE, polype
	127441	AA835684	Hs.287601	Homo sapiens cDNA FLJ13830 fis, clone TH
	127449	AI421866	Hs.75722	ribophorin II
	127493	AA808081	Hs.291701	ESTs
20	127505	AA594244	Hs.292245	ESTs, Weakly similar to ALU1_HUMAN ALU S
	127620	AI025699	Hs.116200	ESTs
	127623	AA773234	Hs.271877	angiotensin-like 2
	127633	AI339609	Hs.268538	potassium voltage-gated channel, Isk-rel
	127701	AA935466		gb:zfb4c06.s1 Soares_pineal_gland_N3HPG
25	127713	AA688322	Hs.150683	ESTs
	127722	AA700444	Hs.189186	ESTs, Weakly similar to ALUD_HUMAN !!!!
	127733	AA704680	Hs.189005	ESTs
	127816	AA743646	Hs.120504	ESTs, Weakly similar to YA02_HUMAN HYPOT
	127966	AI493406	Hs.292514	ESTs
30	127973	AI336794	Hs.129117	ESTs
	127989	AA909267	Hs.132413	ESTs
	127997	AI281549	Hs.311054	Homo sapiens mRNA full length insert cDN
	128016	N92597	Hs.82689	tumor rejection antigen (gp96) 1
	128037	AA868394	Hs.181129	ESTs, Weakly similar to S18968 cyritesti
35	128053	T65605	Hs.65377	ESTs, Moderately similar to KIAA1399 pro
	128066	AA884838	Hs.189171	ESTs
	128071	AA889398	Hs.189241	ESTs
	128091	AA904559	Hs.129329	ESTs
	128113	AI341423	Hs.288433	neurotrophin
40	128145	AI498467	Hs.166669	solute carrier family 4, sodium bicarbon
	128167	AA932961	Hs.85752	uncharacterized hematopoietic stem/proge
	128195	AI143866	Hs.127778	ESTs
	128265	T96851	Hs.17691	ESTs
	128283	AI076570	Hs.134053	ESTs
45	128309	AI457235	Hs.166479	ESTs
	128313	AI051250	Hs.157775	ESTs
	128346	AI088907	Hs.160189	ESTs
	128359	AI096526	Hs.270244	ESTs, Weakly similar to I38022 hypotheti
	128369	F12681	Hs.30445	Homo sapiens cDNA FLJ14687 fis, clone NT
50	128371	H12876	Hs.283078	hOAT4
	128421	T77876	Hs.268589	ESTs
	128453	X02761	Hs.287820	fibronectin 1
	128496	T83496	Hs.32944	inositol polyphosphate-4-phosphatase, ty
	128514	H84261	Hs.301893	Homo sapiens, clone IMAGE:3638994, mRNA,
55	128551	H09058	Hs.278398	KIAA1117 protein
	128683	AA316862	Hs.9605	cleavage and polyadenylation specific fa
	128731	AF005271	Hs.104555	neuropeptide FF-amide peptide precursor
	128843	AA234141	Hs.275675	katanin p80 (WD40-containing) subunit B
	128988	AA411040	Hs.294140	ESTs
60	129016	W84524	Hs.184194	transmembrane 4 superfamily member 5
	129021	AA426406	Hs.173081	KIAA0530 protein
	129095	L12350	Hs.108623	thrombospondin 2
	129171	AA234048	Hs.7753	calumenin
	129188	M30257	Hs.109225	vascular cell adhesion molecule 1
65	129410	U25987	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	129467	AA410311	Hs.44208	hypothetical protein FLJ23153
	129518	AA369807	Hs.112238	ESTs
	129534	R73640	Hs.11260	hypothetical protein FLJ11264
	129632	L27213	Hs.1176	solute carrier family 4, anion exchanger
70	129691	X06700	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl
	129681	AA458952	Hs.181406	hypothetical protein FLJ22301
	129990	N30316		gb:yrw75b05.s1 Soares_placenta_8to9weeks_
	130049	V01515	Hs.1460	glucagon
	130171	AA454177	Hs.245257	ESTs, Weakly similar to A46010 X-linked
75	130411	AA505009	Hs.169910	KIAA0173 gene product
	130479	R44163	Hs.12457	hypothetical protein FLJ10814
	130511	L32137	Hs.1584	cartilage oligomeric matrix protein (pse
	130521	U92971	Hs.194351	coagulation factor II (thrombin) recepto
	130645	AA020942	Hs.17200	STAM-like protein containing SH3 and ITA
80	130655	N92934	Hs.17409	cysteine-rich protein 1 (Intestinal)
	130656	Z20481	Hs.330988	Homo sapiens, Similar to Bicaudal D (Dro
	130889	D57622	Hs.20985	sin3-associated polypeptide, 30kD
	131064	AA598441	Hs.22583	DKFZP434K2235 protein
	131070	F13694	Hs.22607	ESTs
	131189	L16782	Hs.240	M-phase phosphoprotein 1
	131318	X51899	Hs.2558	bone gamma-carboxyglutamate (gla) protei
	131506	W47579	Hs.5801	KIAA1194 protein

5	131551	AA127867	Hs.28608	Homo sapiens cDNA: FLJ22115 fis, clone H
	131553	C20547	Hs.302810	Novel human gene mapping to chromosome 20
	131830	U33054	Hs.32959	G protein-coupled receptor kinase 2 (Dro
	131879	AA017161	Hs.33782	ESTs
	132017	W67251	Hs.267659	vav 3 oncogene
10	132025	U58516	Hs.3745	milk fat globule-EGF factor 8 protein
	132096	AA131410	Hs.3964	Homo sapiens clone 24877 mRNA sequence
	132159	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi
	132164	U84573	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132180	AA405569	Hs.418	fibroblast activation protein, alpha
15	132223	R77451	Hs.4245	chromosome 11 hypothetical protein ORF3
	132238	AA453446	Hs.42673	ESTs
	132406	F09979	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
	132945	N40559	Hs.6129	ATP-binding cassette, sub-family B (MDR/
	133185	AA481404	Hs.6686	hypothetical protein DKFZp564O1664
20	133193	C14015	Hs.303075	EST
	133370	AA156897	Hs.72157	DKFZP564I1922 protein
	133406	U22172	Hs.179697	Human DNA damage repair and recombination
	133409	U65918	Hs.73078	deleted in azoospermia-like
	133591	T82292	Hs.75111	protease, serine, 11 (IGF binding)
25	133899	X00588	Hs.77432	epidermal growth factor receptor (avian
	134137	F10045	Hs.79347	KIAA0211 gene product
	134339	AA478971	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	134421	AA122386	Hs.82985	collagen, type V, alpha 2
	134462	U11037	Hs.181300	sel-1 (suppressor of lin-12, C.elegans)-
30	134515	C20737	Hs.84469	ESTs
	134527	T40835	Hs.322978	EST
	134711	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro
	134824	S78723	Hs.298623	5-hydroxytryptamine (serotonin) receptor
	134854	J03464	Hs.179573	collagen, type I, alpha 2
35	134921	W60186	Hs.125511	Homo sapiens mRNA; cDNA DKFZp434P1530 (f
	135003	H42527	Hs.26102	trichorhinophalangeal syndrome I
	135210	W90522	Hs.93589	hypothetical protein DKFZp564B1162
	135348	AA442054	Hs.268177	phospholipase C, gamma 1 (formerly subty
	100547	HG2149-HT2219		gb:Homo sapiens mucin (mucin) mRNA, part
40	100572	HG2271-HT2367	Hs.73995	filaggrin
	100687	HG3115-HT3291		gb:Human Golli-mbp gene, exon 2
	100695	HG315-HT315	Hs.272620	pregnancy specific beta-1-glycoprotein 9
	101447	M21305		gb:Human alpha satellite and satellite 3
	102329	U35407	Hs.158084	peroxisome receptor 1
45	102892	X05232	Hs.83326	matrix metalloproteinase 3 (stromelysin
	103036	X54925	Hs.83169	matrix metalloproteinase 1 (interstitial
	103206	X72755	Hs.77367	monokine induced by gamma interferon
	103260	X78416	Hs.3155	casein, alpha
	103751	AA082824		gb:zo08b08.s1 Stratagene neuroepithelium
50	104113	AA427510	Hs.181202	hypothetical protein FLJ10038
	104316	D61871	Hs.330821	EST
	104453	M19169	Hs.123114	cystatin SN
	104668	AA007312		gb:EST376458 MAGE resequences, MAGH Homo
	104916	AA056588	Hs.155489	NS1-associated protein 1
55	105151	AA424958	Hs.294132	ESTs
	106899	AA490107	Hs.21763	JM5 protein
	107379	U93868	Hs.333861	polymerase (RNA) III (DNA directed) (32k
	107412	W26105	Hs.287797	integrin, beta 1 (fibronectin receptor,
	107652	AA010195	Hs.52642	ESTs, Weakly similar to ALUF_HUMAN !!!!
60	107754	AA017462	Hs.269244	ESTs
	107897	AA026240		gb:zo77a05.s1 NCI_CGAP_AA1 Homo sapiens
	108238	AA059473	Hs.66783	EST
	108497	AA083070		gb:zm85a05.r1 Stratagene ovarian cancer
	108710	AA121960		gb:zm24g09.r1 Stratagene pancreas (93720
65	109012	AA156576	Hs.5947	mel transforming oncogene (derived from
	109043	AA159605	Hs.72580	ESTs
	109560	F01778	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H
	110572	H60523	Hs.37844	EST
	110687	H93005	Hs.177311	ESTs
70	111418	R01084	Hs.19081	ESTs
	111507	R07728	Hs.268668	ESTs
	111644	R16539	Hs.223649	EST, Moderately similar to Cd-7 Melallo
	111919	R39926	Hs.21031	ESTs, Weakly similar to I78885 serine/th
	112102	R44840	Hs.326475	ESTs
75	112229	R50938	Hs.24949	ESTs
	112309	R55021		gb:yyf76d05.s1 Soares breast 2NbHBst Homo
	112368	R59371	Hs.26653	ESTs
	112397	R60822	Hs.26805	ESTs, Weakly similar to putative p150 [
	112532	R69824	Hs.28313	ESTs
80	112858	T02963	Hs.4454	ESTs
	113170	T54342	Hs.270373	ESTs, Weakly similar to S65657 alpha-1C
	113321	T70580	Hs.13759	RAB3A interacting protein (rab3)-like
	113404	T82323	Hs.70337	immunoglobulin superfamily, member 4
	113420	T83964	Hs.15400	ESTs, Weakly similar to S65824 reverse
	113613	T93337	Hs.17167	ESTs, Highly similar to LRR FLI-I intera
	113663	T95909		gb:ye47g07.s1 Soares fetal liver spleen
	113790	W33178	Hs.26912	ESTs

113889	W72720		gb:zd61c03.s1 Soares_fetal_heart_NbHH19W
114016	W90671	Hs.11087	ESTs
114251	Z39898	Hs.21948	ESTs
115187	AA261805	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,
115722	AA417297	Hs.59609	ESTs
115775	AA424030	Hs.46627	ESTs
116380	AA598455	Hs.66817	ESTs
116551	D20458	Hs.229071	EST
117009	H85422	Hs.108556	ESTs
117329	N23680	Hs.93670	Homo sapiens cDNA: FLJ22664 fis, clone H
117523	N32626	Hs.145532	ESTs, Weakly similar to FV1 MOUSE FRIEND
118387	N64579		gb:yz51d11.s1 Morton Fetal Cochlea Homo
118456	N65580		gb:yy69f01.s1 Soares_multiple_sclerosis_
118741	N74042	Hs.50421	KIAA0203 gene product
118771	N74690	Hs.50547	ESTs
119075	R35451	Hs.287820	fibronectin 1
119217	R95778	Hs.237309	EST
119306	T26914	Hs.132785	EAP30 subunit of ELL complex
119347	T64349		gb:yc10d08.s1 Stratagene lung (937210) H
120006	W90108	Hs.10848	KIAA0187 gene product
120441	AA243588	Hs.190035	ESTs
120651	AA287286	Hs.99657	ESTs
120811	AA346854	Hs.52788	fragile X mental retardation, autosomal
121186	AA400156	Hs.339808	hypothetical protein FLJ10120
121599	AA416770	Hs.98255	EST
122146	AA435584	Hs.250173	hypothetical protein FLJ13158
122261	AA436830	Hs.98902	ESTs
122352	AA443725	Hs.159677	ESTs
122433	AA447417	Hs.285491	ESTs
122489	AA448342	Hs.178551	ribosomal protein L8
122554	AA451886	Hs.154654	cytochrome P450, subfamily I (dioxin-ind
122857	AA463879	Hs.99606	EST, Weakly similar to STK2_HUMAN SERIN
122889	AA465704	Hs.287687	Homo sapiens cDNA: FLJ21960 fis, clone H
123399	AA521274	Hs.105516	EST
123662	AA609385	Hs.112703	ESTs, Moderately similar to AF171102.1 r
123762	AA610013		gb:af18d04.s1 Soares_testis_NHT Homo sap
123792	AA620333	Hs.112857	ESTs
123900	AA621223	Hs.112953	EST
123981	C20797	Hs.95481	ESTs
124126	H18517	Hs.164568	fibroblast growth factor 7 (keratinocyte
124404	N31998	Hs.164256	hypothetical protein FLJ20657
124557	N66025	Hs.141604	ESTs, Moderately similar to ALU1_HUMAN A
124703	R07294	Hs.300076	solute carrier family 22 (organic cation
124867	R68971	Hs.168500	ESTs
125092	T92544	Hs.137548	CD84 antigen (leukocyte antigen)
125111	T96240	Hs.178658	RAD23 (S. cerevisiae) homolog B
125331	AI422996	Hs.161378	ESTs
125349	T87826	Hs.164480	ESTs, Weakly similar to T50609 hypotheti
125426	R43963	Hs.184029	hypothetical protein DKFZp761A052
125436	R64472	Hs.16131	hypothetical protein FLJ12876
125465	AI375276	Hs.158732	ESTs
125515	R13353		gb:yl76c04.r1 Soares infant brain 1NIB H
125626	AI038854	Hs.180789	S164 protein
125656	AA040118	Hs.78687	neutral sphingomyelinase (N-SMase) activ
125743	H17151		gb:ym37a05.r1 Soares Infant brain 1NIB H
125757	AI274906	Hs.166835	ESTs, Highly similar to 1814460A p53-ass
125760	W03020	Hs.40300	calpain 3, (p94)
125804	R79519	Hs.16899	ESTs
125967	AI341206	Hs.173770	ESTs
126058	AI190171	Hs.144413	ESTs
126081	AI346024	Hs.227835	KIAA1049 protein
126150	AA018427	Hs.64616	chromosome 12 open reading frame 3
126171	AA704771	Hs.191942	ESTs
126198	AI469355	Hs.127310	ESTs
126224	AI097280	Hs.44493	Human DNA sequence from clone 462023 on
126289	AA194603	Hs.73451	ESTs, Weakly similar to S55024 nebulin,
126343	AA628890	Hs.158701	ESTs
126406	AA034096		gb:yyv41h02.r1 Soares fetal liver spleen
126419	AA451775	Hs.129064	Homo sapiens chromosome 19, cosmid F2216
126479	T78141	Hs.12285	ESTs, Weakly similar to I55214 salivary
126500	AA885306	Hs.184376	synaptosomal-associated protein, 23kD
126520	AA292988	Hs.72071	hypothetical protein FLJ20038
126701	AA515212	Hs.339670	ESTs, Weakly similar to AF147790.1 trans
126718	AA322718	Hs.309435	ESTs, Weakly similar to KIAA0927 protein
126739	AF160709	Hs.269047	Homo sapiens cDNA FLJ14059 fis, clone HE
126745	AA057506		gb:zf49g04.r1 Soares retina N2b4HR Homo
126846	AA663527	Hs.116910	ESTs
126872	AA136653		gb:LI-H-B13-ala-a-12-Q-UI.s1 NCL_CGAP_Su
126952	AA195575	Hs.85962	hyaluronan synthase 3
127036	AI468598	Hs.276916	nuclear receptor subfamily 1, group D, m
127039	AA233366	Hs.168103	prp28, U5 snRNP 100 kd protein
127067	F06732		gb:HSC1JA051 normalized infant brain cDN
127083	Z44079	Hs.91608	otoferlin

5	127116	AA278492	Hs.288304	Homo sapiens cDNA FLJ11529 fis, clone HE
	127282	AA347547	Hs.185780	ESTs
	127349	AA412108	Hs.269350	ESTs
	127352	AA416577	Hs.189105	ESTs, Weakly similar to NBR13 [H.sapiens
	127482	AI337294	Hs.105352	GalNAc alpha-2, 6-sialyltransferase I, I
	127543	AI364367	Hs.157392	Homo sapiens cDNA FLJ20780 fis, clone CO
	127553	AA282433		gb:aa63g02.r1 NCI_CGAP_GCB1 Homo sapiens
10	127556	AA679831	Hs.190228	ESTs
	127859	AA806837	Hs.291559	ESTs
	127993	AA847856	Hs.124565	ESTs
	128277	AI018275	Hs.269791	ESTs
	128285	AA634569	Hs.13351	LanC (bacterial lantibiotic synthetase c
	128317	AI051960	Hs.303754	ESTs
15	128334	AI080130	Hs.134207	ESTs
	128428	AI185718	Hs.143900	ESTs
	128582	U22963	Hs.101840	major histocompatibility complex, class
	128592	AA470056	Hs.113994	Homo sapiens cDNA FLJ20796 fis, clone CO
	128751	AA442274	Hs.183176	ESTs
20	129105	AA224351	Hs.108681	Homo sapiens brain tumor associated prot
	129161	N27334	Hs.181780	hypothetical protein FLJ20241
	129246	N99174	Hs.206063	ESTs
	129361	X64229	Hs.110713	DEK oncogene (DNA binding)
	129577	AA424952	Hs.82906	CDC20 (cell division cycle 20, S. cerevi
25	129600	N78980	Hs.271599	hypothetical protein MGC10500
	129989	AF005887	Hs.247433	activating transcription factor 6
	130024	U15197	Hs.113271	ABO blood group (transferase A, alpha 1-
	130292	U70136	Hs.218791	proteoglycan 4, (megakaryocyte stimulati
	130589	AA234308	Hs.16441	DKFZP434H204 protein
30	130736	T99385		gb:ow89g07.s1 Soares_fetal_liver_spleen_
	131238	R82327	Hs.24625	ESTs
	131378	AA463886	Hs.203910	small glutamine-rich tetratricopeptide r
	131601	M31165	Hs.29352	tumor necrosis factor, alpha-induced pro
	131605	AA256220	Hs.29383	Homo sapiens mRNA; cDNA DKFZp434E2321 (f
35	131676	C20785	Hs.30514	ESTs
	131861	D11925	Hs.184245	KIAA0929 protein Mx2 interacting nuclea
	131873	H39997	Hs.166852	KIAA1683 protein
	132023	F01927	Hs.3743	matrix metalloproteinase 24 (membrane-in
	132273	AA489716	Hs.43658	DKFZP586L151 protein
40	132770	AA425647	Hs.56406	Homo sapiens cDNA FLJ13549 fis, clone PL
	132858	D20925	Hs.69235	transportin-SR
	133052	R40166	Hs.106826	KIAA1696 protein
	133373	S72487	Hs.73946	endothelial cell growth factor 1 (platelet
	133446	M25322	Hs.73800	selectin P (granule membrane protein 140
45	134693	N70361	Hs.8854	Human transcription unit PVT gene, exons
	134733	U03644	Hs.89421	CBF1 interacting corepressor
	134865	J05480	Hs.272458	protein phosphatase 3 (formerly 2B), cat
	135327	AA477989	Hs.98800	ESTs
	135377	C21382	Hs.99766	Homo sapiens mRNA; cDNA DKFZp564J0323 (f
50	135398	AA194075	Hs.287270	ret proto-oncogene (multiple endocrine

TABLE 44B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

60	Pkey	CAT number	Accessions
65	108497	110079_2	AA074897 AA113914 AA064871 AA079329 AA071309 AA084710 AA129030 AA075042 AA074794 AA071453 AA078803 AA148628 AA122204 AA074159 AA125185 AA079117 AA127089 AA070912 AA079280 AA131372 AA078833 AA071087 AA076131 AA071047 AA079401 AA083070 AA102076 AA115163 AA074198 AA134725 AA113889 AA121103 AA075041 AA065148 AA071310 AA101144 AA079659 AA078931 AA079209 AA070928 AA068994 AA069817 AA076187 AA069053 AA131489 AA071308 AA063317 AA070156 AA071430 AA076056 AA075684 AA070053 AA126283 AA126078 AA075895 AA079208 AA074583 AA071086 AA079623 AA070627 AA078802 AA076622 AA055051 AA079143 AA071110 AA079434 AA148748 AA079230 AA085188 AA074485 AA070560 AA076151 AA083166 AA085118 AA079450 AA085044 AA120938 AA079200 AA100188 AA081472 AA122355 AA129031 AA085362 AA069220 AA070940 AA075968 AA074563 AA084027 AA115929
70	107897	91776_1	AA604872 AA026240
	130736	611414_1	AI168326 T99385
	108710	133560_1	AA121959 AA121960
	100943	45976_1	AW864944 L07517 AW865606
75	124575	1666649_1	N68168 N69188 N90450
	125439	465590_1	AW635829 AA826305 R01759
	117697	499877_1	N40976 AA902795
	125515	181_2	R13353 R13890 H11359
	118387	65081_5	N64579
80	126292	327512_1	AA491328 N42312
	102798	34624_4	U88896 U88898 AA916056 T03285 AI341594 AI359534 AI634031 U88897
	126378	244444_1	N58924 AA347842
	125743	5025_5	H17151 H11956
	126406	95703_1	N76683 AA034096 AA034082

127067	1534978_1	F06732 Z43705
119243	1774795_1	T12603 T12604
111443	31528_18	AF072503 AF208161 AA613238 H12439 N76991 D78692 BE019603 AA776439 R37932 T93615 AF072508 R00744 R01948 R68685
5		AI128496 AA865193 AI797629 H13302 AF072506 NM_014590 AF072505 R00743 T93661 T39519 R68740 H13097 N58614 N77302
		H01372 N41878 H04136 AA426511 AW971553 AW900030 R76136 T52094 AI598135 AA781423 R76086 R77278 AI393478 AA837267
		AI570707 R01901 R27412 N53177 AI379210 AI128526 AA250958 R79323 R27389 H01325 N55091 T69704 AA868777 T47345 R27591
		AA860368 AA729556 H04137 T87297 C17420 AA293243 AA419144
10	127278 240640_1	AA342715 AA367634
	103751 118557_1	AA131367 AA082824
	126636 80804_1	AA067531 AA001527
	127331 379388_1	F20186 AA622352
	127357 288073_1	AA424107 AA452788
	126745 104479_1	AA047854 AA057506 AA053841
15	126762 110350_1	AA064613 AA064671
	126783 113388_1	AA083531 AA125047 AA074915 AA148649
	112309 1576900_1	R55021 H26613
	126972 142696_1	AW450979 AA136653 AA136656 AW419381 AA984358 AA492073 BE168945 AA809054 AW238038 BE011212 BE011359 BE011367
20	120284 158963_1	BE011368 BE011362 BE011215 BE011365 BE011363
	111829 46636_1	AA179656 AA182626 AA182603
	104668 82752_1	AF074991 R36070
	127553 202308_2	AW964385 AA007312 AI081711 AA318253 AW891655 T99192
	120379 34624_3	AA505046 AW969109 AA505047
25		AL042725 BE063316 AW975610 AA457591 BE062092 AI655202 AA714296 AI267264 AI075321 AA223286 AA071122 AA227849
		AA216700 AI696002 AA101867 AA099426 AA135997 AL041698 T02815 T51824 AA207189 T59230 T51868 AA663341 BE165757
		AW818104 AW392886 AA584918 AA099408 AW856396 AW861859 AA053045
30	127701 405284_1	AA679064 AA935466
	128410 288073_1	AA424107 AA452788
	114625 111686_1	AA081507 AA070071 AA070840 AA084362
	109026 150431_1	AA157811 AA836869
	108409 113869_1	AA075631 AA075578
	100687 tigr_HT3291	L18862
35	109326 genbank_AA210719	AA210719
	123762 genbank_AA610013	AA610013
	116548 genbank_D20433	D20433
	125145 entrez_W38001	W38001
	125153 entrez_W38294	W38294
40	116995 genbank_H83928	H83928
	102649 genbank_U68133	U68133
	118456 genbank_N66580	N66580
	102860 entrez_X00368	X00368
	120715 genbank_AA292700	AA292700
	120749 genbank_AA303235	AA303235
	113663 genbank_T95909	T95909
45	113889 genbank_W72720	W72720
	108258 genbank_AA063269	AA063269
	101046 entrez_K01160	K01160
	129990 genbank_N30316	N30316
	122746 genbank_AA458791	AA458791
50	124046 genbank_F10243	F10243
	108436 genbank_AA078801	AA078801
	124197 genbank_H52921	H52921
	101447 entrez_M21305	M21305
	108852 genbank_AA133131	AA133131
55	101697 entrez_M64358	M64358
	108931 genbank_AA147186	AA147186
	101909 entrez_S69265	S69265
	117816 genbank_N48872	N48872
60	119154 genbank_R61293	R61293
	119241 genbank_T12559	T12559
	119310 genbank_T40427	T40427
	119347 genbank_T64349	T64349
	119529 entrez_W38053	W38053
	112467 genbank_R65706	R65706
65	112533 genbank_R69886	R69886
	112588 genbank_R77302	R77302
	121082 genbank_AA398722	AA398722
	123305 genbank_AA496133	AA496133
	123328 genbank_AA496968	AA496968
70	100547 tigr_HT2219	M57417
	123490 genbank_AA599723	AA599723

75 TABLE 45A: 90 GENES DOWN-REGULATED IN RHEUMATOID ARTHRITIS COMPARED TO NORMAL BODY

Table 45A lists about 90 genes down-regulated in rheumatoid arthritis. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip.

80 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title

	Pkey	ExAccn	UnigenelD	Unigene Title
5	100137	D13627	Hs.15071	chaperonin containing TCP1, subunit 8 (i
	100240	D31767	Hs.75416	DAZ associated protein 2
	100289	D45248	Hs.179774	proteasome (prosome, macropain) activato
	100658	HG2855-HT2995	Hs.75452	heat shock 70kD protein 2
	100763	HG3597-HT3800		gb:Human major histocompatibility comple
10	100779	HG3731-HT4001	Hs.302063	immunoglobulin heavy constant mu
	101091	L06132	Hs.149155	voltage-dependent anion channel 1
	101155	L13972	Hs.301698	sialyltransferase 4A (beta-galactosidase
	102223	U24685		gb:Homo sapiens immunoglobulin heavy cha
	102282	U31383	Hs.79126	guanine nucleotide binding protein 10
15	102378	U40369	Hs.28491	spermidine/spermine N1-acetyltransferase
	102386	U40998	Hs.81728	unc119 (C.elegans) homolog
	102389	U41371	Hs.75916	splicing factor 3b, subunit 2, 145kD
	102480	U50327	Hs.1432	protein kinase C substrate 80K-H
	102566	U59752	Hs.303091	pleckstrin homology, Sec7 and coiled/coi
20	102605	U64444	Hs.181369	ubiquitin fusion degradation 1-like
	102693	U73824	Hs.183684	eukaryotic translation initiation factor
	102710	U77827	Hs.113207	G protein-coupled receptor 30
	102920	X12451	Hs.78056	cathepsin L
	102929	X13238	Hs.74649	cytochrome c oxidase subunit VIc
25	103166	X67951	Hs.180909	peroxiredoxin 1
	103283	X80199	Hs.83422	MLN51 protein
	103463	Y00281	Hs.2280	ribophorin I
	103835	AA172215	Hs.93748	Homo sapiens cDNA FLJ14676 fis, clone NT
	104796	AA029368	Hs.33026	hypothetical protein PP2447
30	105714	AA291429	Hs.12211	GDP-fucose transporter 1
	105927	AA402968	Hs.332040	hypothetical protein MGC13010
	105945	AA404512	Hs.14453	interferon consensus sequence binding pr
	106001	AA410986	Hs.8963	Homo sapiens mRNA full length insert cDN
	106027	AA412119	Hs.234799	breakpoint cluster region
35	106227	AA429262	Hs.19613	ESTs
	106295	AA435664	Hs.8583	similar to APOBEC1
	106417	AA448008	Hs.261828	G protein-coupled receptor kinase 7
	107391	W02877	Hs.284294	Breakpoint cluster region protein, uter
	109107	AA169180	Hs.269280	ESTs
40	109685	F09325	Hs.28102	ESTs
	110021	H11252	Hs.31037	ESTs
	110738	H99370	Hs.139848	kinesin family member 1C
	112746	R93237	Hs.74170	metallothionein 1E (functional)
	113059	T26925	Hs.172684	vesicle-associated membrane protein 8 (a
45	113822	W47350	Hs.17466	retinoic acid receptor responder (tazaro
	113859	W67225	Hs.13273	KIAA0592 protein
	113909	W78127	Hs.9956	hypothetical protein FLJ20259
	114693	AA122158	Hs.300683	Homo sapiens cDNA FLJ12825 fis, clone NT
	115399	AA283182	Hs.92023	core histone macroH2A2.2
50	116606	D80217	Hs.259842	protein kinase, AMP-activated, gamma 2 n
	116633	F02702	Hs.268726	ESTs, Highly similar to ZN91_HUMAN ZINC
	119254	T15837	Hs.279009	matrix Gla protein
	119493	W35384	Hs.50477	RAB27A, member RAS oncogene family
	120108	W95696	Hs.16803	LUC7 (S. cerevisiae)-like
55	120886	AA365566	Hs.301342	hypothetical protein MGC4342
	120953	AA397911	Hs.97499	ESTs, Weakly similar to unknown [H.saple
	121303	AA402441	Hs.303197	B-cell CLL/lymphoma 7C
	121547	AA412448	Hs.104777	ESTs
	123495	AA599850	Hs.106747	serine carboxypeptidase 1 precursor prot
60	123608	AA609144	Hs.112651	ESTs
	123749	AA609949	Hs.112790	EST
	124763	R39610	Hs.76288	calpain 2, (mII) large subunit
	125366	H60192	Hs.76853	Homo sapiens mRNA; cDNA DKFZp434N1728 (i
	125657	AA481719	Hs.150540	Homo sapiens, clone IMAGE:3954961, mRNA,
65	125670	AI432621	Hs.82685	CD47 antigen (Rb-related antigen, Integr
	125882	H45538	Hs.101448	metastasis associated 1
	126541	AA204913	Hs.7854	zinc/iron regulated transporter-like
	126715	R70160	Hs.241552	KIAA0268 protein
	126817	AA478642	Hs.291623	ESTs, Weakly similar to unnamed protein
70	127112	AI143906	Hs.125103	ESTs
	127273	AA335263	Hs.144950	ESTs
	127615	AA718919		gb:zv88a04.s1 Soares_NhHMPu_S1 Homo sapi
	127635	AA766903	Hs.116346	ESTs, Highly similar to A46297 beta-1,6-
	128528	R39234	Hs.251699	ESTs, Weakly similar to IDN4-GGTR14 [H.s
75	129398	AA437374	Hs.234573	Homo sapiens mRNA for TL132
	129621	AA489459	Hs.301005	purine-rich element binding protein B
	131037	AA256171	Hs.22391	chromosome 20 open reading frame 3
	131328	V01512	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131631	AA486868	Hs.29802	stII (Drosophila) homolog 2
80	132079	H67964	Hs.38694	ESTs
	132455	T15774	Hs.4892	Homo sapiens clone 24841 mRNA sequence
	132582	AA318547	Hs.278712	eukaryotic translation initiation factor
	132610	AA443114	Hs.5326	amino acid system N transporter 2; porcu
	132755	AA609201	Hs.182635	ESTs
	133192	AA393804	Hs.67052	vacuolar protein sorting 26 (yeast homol

133437	R57419	Hs.7370	phosphatidylinositol transfer protein, b
133449	AA094989	Hs.7381	voltage-dependent anion channel 3
133649	AA479139	Hs.75393	acid phosphatase 1, soluble
133814	M33882	Hs.76391	myxovirus (influenza) resistance 1, homo
134378	AF006088	Hs.82425	actin related protein 2/3 complex, subun
134419	L08044	Hs.82961	trefoil factor 3 (intestinal)
134548	U41515	Hs.333495	Deleted in split-hand/split-foot 1 regio
134776	J05582	Hs.89603	mucin 1, transmembrane
135032	AA243497	Hs.173685	hypothetical protein FLJ12619

TABLE 45B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT number	Accessions
127615	380951_1	AA626215 AA718919
100763	tigr_HT3800	X12432 Y08693
102223	221_265	AF013616 AA300945 X65907 AF062264 AF062250 Z47228 Z75389 Z75374 AF062152 AF062146 Z75398 X64153 AF062101 AF062218 S59161 Z75392 AF062196 AF062192 X65904 U24685 AF062181 Z47241 Z75376 AF062217 Z47234 X64152 AF062187 AF062158 Z47229 M74018 M74021 X54441 M84512 L29115 M84508 Z75384 AJ245240 AJ245030 AJ245042 M26998 L03635 S64473 AJ244997 AJ245013 AJ279535 U89766 AF174049 AF174085 AF174086 U97246 AJ245011 AJ245017 AJ245028 AJ245041 AJ245051 AJ245065 AJ245236 U22391 Z49143 Z74665 AF087428 S66098 Z70650 AJ244929 AF006528 AF022004 AF021983 U00556 AJ245035 Z70617 Z70605 AJ245052 AJ245046 AF087424 AF174054 S67110 U21257 U21267 U21268 Z35492 U71103 AF021991 L23518 Z70644 AJ245036 Z49141 AF089001 Z74695 Z46304 AF021957 AF021990 AF022005 AF062527 AF021947 Z70604 Z70610 AF062104 Z49135 X64235 Z46341 Z46305 Z46307 Z49136 AJ244996 Z46342 AJ244931 AJ244935 AJ244937 AJ244938 L12192 AJ244939 AJ244940 AJ244941 Z46308 AJ244962 AF062234 AJ244973 AJ244984 AJ244985 AF174088 AJ279519 AJ279521 AJ279526 AJ245009 AJ279531 AJ245008 AJ244994 AJ244991 AJ244990 AJ244988 AJ244987 X87440 AJ245238 Z70625 Z70626 Z70641 Z70643 AJ244975 Z70616 Z70637 AJ244982 AJ244967 AJ239377 AJ245057 AF021948 AF107239 AJ245040 L34163 AF062231 Z70627 AF062113 AF006527 AF174041 AJ279537 Z70642 U00497 Z70639 AJ245054 AJ244960 AJ279524 AJ244943 AJ249631 AF035041 AJ245039 AJ245050 AF107233 AJ239362 AJ244969 Z46278 Z46290 Z46274 Z46281 AJ239351 L25293 AJ244944 AJ244951 Z46280 Z46270 AJ245043 Z46276 AF107241 Z46271 Z46277 AJ245034 Z46273 AJ244992 Z46282 Z70638 Z46275 AJ244972 Z46272 Z46279 Z46269 AF087422 M74469 X64159 AF103243 X64156 AJ244942 Z46316 AJ222547 Z46322 Z46324 Z46326 Z46327 AJ222556 Z46329 Z46330 Z46302 AJ222561 AJ222549 AJ222568 AJ222570 AJ222571 Z49139 AJ222578 AJ222562 AJ222577 Z46323 AJ222576 AJ222566 Z46315 AJ222557 AJ222564 AJ222559 AJ222573 AJ222575 Z46318 AJ222548 Z46319 AJ222552 AJ222550 AJ222567 AJ222558 AJ222563 Z46317 X87438 AJ222555 AJ240581 AF103161 AJ240580 AJ240594 Y17929 AJ240553 AJ240573 AJ240558 AJ240555 Y17927 Y17949 AJ240561 Y17948 Y17933 Y17947 Y17944 Y17928 Y17931 Y17934 AJ240595 Y17943 Y17932 Y17930 AJ240590 AJ240560 Y17945 AJ240556 S79918 AF103278 AW364256 AF103299 AF103122 X75022 AF004937 Z30557 Z30677 Z30573 Z30576 Z30561 Z30674 Z30562 Z30575 AW403129 AJ203192 AW404253 AW237246 A1654630 H61354

Table 46A lists about 714 genes upregulated in esophageal cancer relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 47A lists about 113 genes upregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 48A lists about 162 genes downregulated in esophageal tumors relative to normal esophagus. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

TABLE 46A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenes number
 Unigenes Title: Unigenes gene title
 R1: 90th percentile of esophageal tumor AIs divided by the 70th percentile of normal tissue AIs, where the 15th percentile of the normal tissue AIs was subtracted from both the numerator and denominator.

Pkey	ExAccn	UnigenelD	Unigenes Title	R1
413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	31.57
411243	AB038886	Hs.69319	CA11	26.06
422168	AA586894	Hs.112408	S100 calcium-binding protein A7 (psorias)	25.65
401781			Target Exon	23.23
424098	AF077374	Hs.139322	small proline-rich protein 3	21.35
425211	M18667	Hs.1867	progastricsin (pepsinogen C)	20.37
417366	BE185289	Hs.1076	small proline-rich protein 18 (cornifin)	20.33
401780			NM_005557:Homo sapiens keratin 16 (foca)	18.94
421948	L42583	Hs.334309	keratin 6A	18.13
400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin)	18.01
429538	BE182592	Hs.11261	small proline-rich protein 2A	17.31
400666			NM_002425:Homo sapiens matrix metallopro	17.28
418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial)	16.96

	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	16.35
	408522	AI541214	Hs.46320	Small proline-rich protein SPRK [human,	16.22
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	15.64
	421582	AI910275		trefol factor 1 (breast cancer, estrogen	14.86
5	425679	X05997	Hs.159177	lipase, gastric	14.53
	421773	W69233	Hs.112457	ESTs	14.26
	433091	Y12642	Hs.3185	lymphocyte antigen 6 complex, locus D	14.26
	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	13.93
10	444325	AW152618	Hs.16757	ESTs	13.24
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	13.19
	420783	AI659838	Hs.99923	lectin, galactoside-binding, soluble, 7	11.98
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.99
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	10.77
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	10.31
15	446292	AF081497	Hs.279682	Rh type C glycoprotein	9.69
	421978	AJ243662	Hs.110196	NICE-1 protein	9.68
	448811	AI590371	Hs.199460	ESTs	9.38
	453331	AI240665		ESTs	9.37
20	423634	AW959908	Hs.1690	heparin-binding growth factor binding pr	9.28
	413719	BE439580	Hs.75498	small inducible cytokine subfamily A (Cy	9.18
	406587	M31126		matrix metalloproteinase 11 (stromelysin	9.13
	454034	NM_000691	Hs.575	aldehyde dehydrogenase 3 family, member	9.04
	450701	H39960	Hs.288467	hypothetical protein XP_098151	8.77
25	418585	Z36830	Hs.87268	annexin A8	8.76
	421110	AJ250717	Hs.1355	cathepsin E	8.42
	407788	BE514982	Hs.38991	S100 calcium-binding protein A2	8.42
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	8.38
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	8.18
	427666	AI791495	Hs.180142	calmodulin-like skin protein (CLSP)	8.11
30	450375	AA009647		a disintegrin and metalloproteinase doma	8.03
	401785			NM_002275*-Homo sapiens keratin 15 (KRT1	7.97
	445891	AW391342	Hs.199460	DPCR1 protein	7.95
	437053	AU077018	Hs.3235	keratin 4	7.93
35	423271	W47225	Hs.126256	interleukin 1, beta	7.80
	409757	NM_001898	Hs.123114	cystatin SN	7.74
	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	7.64
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.58
	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	7.55
40	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	7.26
	448045	AJ297436	Hs.20166	prostate stem cell antigen	7.14
	408243	Y00787	Hs.624	interleukin 8	7.13
	429359	W00482	Hs.2399	matrix metalloproteinase 14 (membrane-in	7.08
	437191	NM_006846	Hs.331555	serine protease inhibitor, Kazal type, 5	7.04
45	407366	AF026942	Hs.17518	gb-Homo sapiens c1g33 mRNA, partial sequ	7.04
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.98
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	6.89
	414774	X02419	Hs.77274	plasminogen activator, urokinase	6.85
	439926	AW014875	Hs.137007	ESTs	6.84
50	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.82
	429259	AA420450	Hs.292911	Plakophilin	6.77
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	6.71
	424834	AK001432	Hs.153408	Homo sapiens cDNA FLJ10570 fis, clone NT	6.67
	429228	AI553633	Hs.326447	ESTs	6.61
55	426312	AF026939	Hs.181874	interferon-induced protein with tetrati	6.60
	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	6.58
	441362	BE614410	Hs.23044	RAO51 (S. cerevisiae) homolog (E coli Re	6.55
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	6.54
	446989	AK001898	Hs.16740	hypothetical protein FLJ11036	6.53
60	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	6.51
	422166	W72424	Hs.112405	S100 calcium-binding protein A9 (calgran	6.49
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	6.48
	428471	X57348	Hs.184510	stratitin	6.46
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	6.45
65	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.44
	401747			Homo sapiens keratin 17 (KRT17)	6.42
	421508	NM_004833	Hs.105115	absent in melanoma 2	6.42
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	6.42
	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	6.41
70	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	6.38
	422596	AF063611	Hs.118633	2'-5'-oligoadenylate synthetase-like	6.38
	409601	AF237621	Hs.80828	keratin 1 (epidermolytic hyperkeratosis)	6.36
	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	6.35
	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	6.33
75	425415	M13903	Hs.157091	involucrin	6.32
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.30
	415989	AI267700		ESTs	6.23
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.21
	449228	AJ403107	Hs.148590	protein related with psoriasis	6.21
80	436749	AA584890	Hs.5302	lectin, galactoside-binding, soluble, 4	6.18
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	6.06
	418663	AK001100	Hs.41690	desmocollin 3	6.04
	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.98
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	5.96

5	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	5.93
	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	5.92
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	5.92
	424620	AA101043	Hs.151254	kallikrein 7 (chymolytic, stratum com	5.84
	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	5.76
10	400665			NM_002425:Homo sapiens matrix metallopro	5.75
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.72
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	5.72
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	5.71
	422765	AW409701	Hs.1578	baculoviral IAP repeat-containing 5 (sur	5.70
15	439606	W79123	Hs.58561	G protein-coupled receptor 87	5.70
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ101195 fis, clone HE	5.68
	433447	U29195	Hs.3281	neuronal pentraxin II	5.67
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	5.64
	408000	L11690	Hs.198689	bulbous pemphigoid antigen 1 (230/240kD)	5.62
20	413219	AA878200	Hs.118727	Homo sapiens cDNA FLJ13692 fis, clone PL	5.60
	428450	NM_014791	Hs.184339	KIAA0175 gene product	5.53
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.50
	416250	AA581386	Hs.73452	hypothetical protein MGC10791	5.48
	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	5.47
25	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	5.44
	439223	AW238299	Hs.250618	UL16 binding protein 2	5.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	5.42
	402994			NM_002453*:Homo sapiens myxovirus (influ	5.40
	447333	BE090580	Hs.70704	hypothetical protein dJ61688.3	5.40
30	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	5.36
	454241	BE144666		gb:CM2-HT0176-041099-017-c02 HT0176 Homo	5.33
	408716	AI567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	5.32
	449722	BE280074	Hs.23960	cyclin B1	5.31
	428434	AW363590	Hs.65551	Homo sapiens, Similar to DNA segment, Ch	5.30
35	426283	NM_003937	Hs.169139	kynureninase (L-kynurenine hydrolase)	5.29
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	5.29
	417720	AA205625	Hs.208067	ESTs	5.29
	424008	R02740	Hs.137555	putative chemokine receptor, GTP-binding	5.28
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	5.27
40	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	5.26
	430280	AA361258	Hs.237868	interleukin 7 receptor	5.25
	422627	BE335857	Hs.118787	transforming growth factor, beta-induced	5.24
	402075			ENSP00000251056*:Plasma membrane calcium	5.24
	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	5.24
45	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	5.22
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	5.22
	418558	AW082266	Hs.86131	Fas (TNFRSF6)-associated via death domain	5.21
	422440	NM_004812	Hs.116724	aldo-keto reductase family 1, member B10	5.20
	428188	M98447	Hs.22	transglutaminase 1 (K polypeptide epider	5.20
50	406663	U24683	Hs.293441	immunoglobulin heavy constant mu	5.19
	409178	BE393948	Hs.50915	kallikrein 5	5.15
	443426	AF098158	Hs.9329	chromosome 20 open reading frame 1	5.14
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	5.10
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	5.09
55	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	5.09
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	5.08
	411274	NM_002776	Hs.69423	kallikrein 10	5.07
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	5.03
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	5.03
60	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	5.02
	412755	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	5.02
	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	5.02
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	5.00
	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	5.00
65	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.97
	405770			NM_002362:Homo sapiens melanoma antigen,	4.96
	444783	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act	4.94
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	4.94
	426866	U02330	Hs.172816	neuregulin 1	4.93
70	423017	AW178761	Hs.227948	serine (or cysteine) proteinase inhibitor	4.92
	455601	AI368680	Hs.816	SRV (sex determining region Y)-box 2	4.91
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.90
	427786	BE407863	Hs.256871	ESTs	4.87
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	4.86
75	444371	BE540274	Hs.239	forkhead box M1	4.86
	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	4.85
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	4.84
	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	4.83
	409402	AF208234	Hs.695	cystatin B (stealin B)	4.81
80	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.79
	401994			Target Exon	4.77
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	4.74
	421574	AJ000152	Hs.105924	defensin, beta 2	4.69
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.69
	422109	S73265	Hs.1473	gastrin-releasing peptide	4.68
	439453	BE264974	Hs.6566	thyroid hormone receptor interactor 13	4.68
	407944	R34008	Hs.239727	desmocollin 2	4.67

5	411296	BE207307	Hs.10114	growth suppressor 1	4.65
	433364	AI075407	Hs.296083	ESTs, Moderately similar to I54374 gene	4.65
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothel	4.61
	421335	X99977	Hs.103505	ARS component B	4.60
	422515	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.59
	453779	N35187	Hs.43398	28kD interferon responsive protein	4.59
	423575	C18863	Hs.163443	periostin (OSF-2os)	4.59
	417308	H60720	Hs.81892	KIAA0101 gene product	4.58
10	428651	AF196478	Hs.188401	annexin A10	4.58
	424354	NM_014314	Hs.145612	RNA helicase	4.58
	404996			Target Exon	4.56
	404240			NM_018950:Homo sapiens major histocompat	4.56
	453095	AW295660	Hs.252756	ESTs	4.55
15	410407	X66839	Hs.63287	carbonic anhydrase IX	4.55
	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	4.55
	450685	L15533	Hs.423	pancreatitis-associated protein	4.54
	425483	AF231022	Hs.158159	FAT tumor suppressor (Drosophila) homolo	4.53
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.52
20	408380	AF123050	Hs.44532	diubiquitin	4.47
	443859	NM_013409	Hs.9914	folistatin	4.46
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	4.44
	412140	AA219631	Hs.73625	RAB6 Interacting, kinesin-like (rabklins	4.44
	421777	BE562088	Hs.108196	HSPC037 protein	4.44
25	408908	BE296227	Hs.250822	serine/threonine kinase 15	4.43
	408122	AI432652	Hs.42824	hypothetical protein FLJ10718	4.42
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	4.42
	400419	AF084545		Target	4.42
	452571	W31518	Hs.34665	ESTs	4.41
30	430044	AA464510	Hs.152812	ESTs	4.41
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	4.39
	448111	AA053486	Hs.20315	interferon-induced protein with tetratri	4.39
	443347	AI052543	Hs.133244	melanoma-derived leucine zipper, extra-n	4.39
	453884	AA355925	Hs.36232	KIAA0186 gene product	4.38
35	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	4.37
	417900	BE250127	Hs.82906	CDC20 (cell division cycle 20, S. cerevi	4.37
	424046	AF027866	Hs.138202	serine (or cysteine) proteinase inhibito	4.37
	427983	M17706	Hs.2233	colony stimulating factor 3 (granulocyte	4.36
	448357	N20169	Hs.108923	RAB38, member RAS oncogene family	4.36
40	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	4.34
	439999	AA115811	Hs.6838	ras homolog gene family, member E	4.34
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	4.34
	409703	NM_006187	Hs.56009	2'-5'-oligoadenylate synthetase 3 (100 k	4.32
	402447			C1000201:gi 204416 gb AA02627.1 (L0519	4.31
45	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	4.28
	432731	R31178	Hs.287820	fibronectin 1	4.27
	422397	AJ223366	Hs.116051	Homo sapiens cDNA: FLJ22495 fis, clone H	4.27
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	4.25
	425580	L11144	Hs.1907	galanin	4.25
50	421506	BE302796	Hs.105097	thymidine kinase 1, soluble	4.23
	409433	AA074382	Hs.135255	ESTs	4.23
	430630	AW269920	Hs.2621	cystatin A (stefin A)	4.22
	447343	AA256641	Hs.236894	ESTs, Highly similar to S02392 alpha-2-m	4.21
	407047	X65965		gb:H.sapiens SOD-2 gene for manganese su	4.20
55	432375	BE536069	Hs.2962	S100 calcium-binding protein P	4.20
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.19
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	4.19
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	4.18
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	4.17
60	410286	AI739159	Hs.61898	DKFZP586N2124 protein	4.16
	448844	AI581519	Hs.177164	ESTs	4.16
	432680	T47364	Hs.278613	interferon, alpha-inducible protein 27	4.16
	417559	AA204688	Hs.62954	ESTs	4.16
	402992			Target Exon	4.15
65	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytostatin)	4.14
	422100	AI096988	Hs.111554	ADP-ribosylation factor-like 7	4.13
	409512	AW979187	Hs.293591	melanoma differentiation associated prot	4.12
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.11
	407137	T97307		gb:ye53h05.s1 Scores fetal liver spleen	4.10
70	411263	BE297802	Hs.69360	kinesin-like 6 (mitotic centromere-assoc	4.10
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.10
	423905	AW579980	Hs.135150	lung type-I cell membrane-associated gly	4.09
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.08
	417933	X02308	Hs.82962	thymidylate synthetase	4.08
75	418689	AI360883	Hs.274448	hypothetical protein FLJ11029	4.06
	417678	X06560	Hs.82396	2'-5'-oligoadenylate synthetase 1 (40-46	4.06
	451541	BE279383	Hs.26557	plakophilin 3	4.06
	433848	AF095719	Hs.93764	carboxypeptidase A4	4.06
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.04
80	429599	AA808106	Hs.123664	ESTs	4.03
	450823	T81223	Hs.22011	complement-c1q tumor necrosis factor-rel	4.02
	423787	AJ295745	Hs.235204	nuclear pore complex protein	4.00
	431250	BE264649	Hs.251377	taxol resistance associated gene 3	4.00
	416091	AF295370	Hs.283082	defensin, beta 3	3.97

	427557	NM_002659	Hs.179657	plasminogen activator, urokinase recepto	3.97
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.97
	402408			NM_030920*:Homo sapiens hypothetical pro	3.97
5	424927	AW973666	Hs.153850	hypothetical protein C321D2.4	3.95
	414907	X90725	Hs.77597	polo (Drosophila)-like kinase	3.95
	452888	AW955454	Hs.30942	ephrin-B2	3.95
	456525	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.95
	450983	AA305384	Hs.25740	ERO1 (S. cerevisiae)-like	3.94
10	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	3.94
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.94
	422094	AF129535	Hs.272027	F-box only protein 5	3.94
	414945	BE076358	Hs.77657	lymphocyte antigen 6 complex, locus E	3.93
	404286			C6001909:gi704441 dbj BAA18909.1 (D298	3.93
	423961	D13666	Hs.136348	periostin (OSF-2os)	3.92
15	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	3.91
	447377	X77343	Hs.334334	transcription factor AP-2 alpha	3.91
	435066	BE261750	Hs.4747	dyskeratosis congenita 1, dyskerin	3.91
	446998	N99013	Hs.16762	Homo sapiens mRNA: cDNA DKFZp56482082 (f	3.91
20	421904	BE143533	Hs.109309	hypothetical protein FLJ20035	3.90
	441553	AA281219	Hs.121296	ESTs	3.90
	428093	AW594506	Hs.104830	ESTs	3.90
	441020	W79283	Hs.35962	ESTs	3.89
	447078	AW885727	Hs.9914	ESTs	3.89
25	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	3.89
	417621	AV654694	Hs.82316	Interferon-induced, hepatitis C-associat	3.87
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	3.87
	426059	BE292842	Hs.166120	interferon regulatory factor 7	3.86
	419833	AA251131	Hs.220697	ESTs	3.85
30	451807	W52854	Hs.27099	hypothetical protein FLJ23293 similar to	3.85
	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	3.83
	452203	X57522		transporter 1, ATP-binding cassette, sub	3.83
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	3.83
	414809	AA434699	Hs.77356	transferrin receptor (p90, CD71)	3.83
35	442599	AF078037	Hs.324051	RelA-associated inhibitor	3.82
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.82
	449539	W80363	Hs.58446	ESTs	3.82
	419079	AW014836	Hs.18844	ESTs	3.81
	410434	AF051152	Hs.63668	toll-like receptor 2	3.81
40	408660	AA525775		ESTs, Moderately similar to PC4259 ferri	3.80
	409142	AL136877	Hs.50758	SMC4 (structural maintenance of chromoso	3.80
	435099	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.80
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.79
	425761	AI015709	Hs.172089	Homo sapiens mRNA: cDNA DKFZp58612022 (f	3.79
45	444665	BE613126	Hs.47783	B aggressive lymphoma gene	3.78
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.78
	414561	AI064813	Hs.195155	Homo sapiens amino acid transport system	3.78
	411789	AF245505	Hs.72157	Adican	3.77
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	3.77
50	449378	AW664026	Hs.59892	ESTs	3.76
	449961	AW265634	Hs.133100	ESTs	3.76
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.75
	407242	M18728		gb:Human nonspecific crossreacting antib	3.75
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	3.75
55	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	3.75
	422675	BE018517	Hs.119140	eukaryotic translation initiation factor	3.74
	422699	BE410590	Hs.119257	ems1 sequence (mammary tumor and squamou	3.74
	441954	AI744935	Hs.8047	Fanconi anemia, complementation group G	3.74
	410290	AA402307	Hs.322844	hypothetical protein DKFZp564A176	3.73
60	422648	D86983	Hs.118893	Melanoma associated gene	3.72
	428953	AA306610	Hs.348183	tumor necrosis factor receptor superfam	3.71
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito	3.71
	428728	NM_016625	Hs.191381	hypothetical protein	3.71
	400245			Eos Control	3.71
65	442432	BE093589	Hs.38178	hypothetical protein FLJ23468	3.70
	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	3.70
	424840	D79987	Hs.153479	extra spindle poles, S. cerevisiae, homo	3.70
	440659	AF134160	Hs.7327	claudin 1	3.69
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	3.67
70	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	3.67
	425081	X74794	Hs.154443	minichromosome maintenance deficient (S.	3.66
	409432	D49372	Hs.54460	small inducible cytokine subfamily A (Cy	3.65
	428291	AA534009	Hs.183487	interferon stimulated gene (20kD)	3.63
	414883	AA926960		CDC28 protein kinase 1	3.63
75	428398	AI249368	Hs.98558	ESTs	3.63
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	3.63
	408482	NM_000676	Hs.45743	adenosine A2b receptor	3.63
	404287			C6001909:gi704441 dbj BAA18909.1 (D299	3.63
	431941	AK000106	Hs.272227	Homo sapiens cDNA FLJ20099 fis, clone CO	3.61
80	414110	BE251752		gb:601112444F1 NIH_MGC_16 Homo sapiens c	3.61
	427857	AL133017	Hs.2210	hypothetical protein FLJ22865	3.61
	419968	X04430	Hs.93913	interleukin 6 (interferon, beta 2)	3.61
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	3.60
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	3.60

	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	3.60
	430994	AA490346	Hs.40530	Homo sapiens, clone MGC:17624, mRNA, com	3.60
	456534	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	3.59
	437340	AL353935	Hs.135917	hypothetical protein DKFZp761D1823	3.59
5	435793	AB037734	Hs.4993	KIAA1313 protein	3.59
	437016	AU076916	Hs.5398	guanine monophosphate synthetase	3.59
	420247	AA256930	Hs.44680	hypothetical protein FLJ20979	3.58
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	3.57
	422282	AF019225	Hs.114309	apolipoprotein L	3.57
10	424635	AA420687	Hs.115455	Homo sapiens cDNA FLJ14259 fis, clone PL	3.57
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.57
	408015	AW136771	Hs.244349	epidermal differentiation complex protel	3.56
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transforimi	3.56
	449039	AI962602	Hs.74284	hypothetical protein MGC2714	3.56
15	446269	AW263155	Hs.14559	hypothetical protein FLJ10540	3.55
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	3.55
	428977	AK001404	Hs.194698	cyclin B2	3.55
	402995			NM_002453*:Homo sapiens myxovirus (influ	3.55
	416065	BE267931	Hs.78996	proliferating cell nuclear antigen	3.54
20	432917	NM_014125	Hs.241517	PRO0327 protein	3.54
	439750	AL359053	Hs.57664	Homo sapiens mRNA full length insert cDN	3.53
	445411	AL137255	Hs.12646	hypothetical protein FLJ22693	3.52
	438113	AI467908	Hs.8882	ESTs	3.52
	414420	AA043424	Hs.76095	immediate early response 3	3.51
25	419682	H13139	Hs.92282	paired-like homeodomain transcription fa	3.50
	447208	BE315291	Hs.237971	hypothetical protein MGC5627	3.50
	432543	AA552690	Hs.152423	Homo sapiens cDNA: FLJ21274 fis, clone C	3.49
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	3.49
30	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	3.49
	429249	X81479	Hs.2375	egl-like module containing, mucin-like,	3.48
	413900	AW409747	Hs.75612	stress-induced-phosphoprotein 1 (Hsp70/H	3.48
	424242	AA337476	Hs.347408	hypothetical protein MGC13102	3.48
	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	3.47
35	446480	NM_014578	Hs.15114	ras homolog gene family, member	3.46
	414825	X06370	Hs.77432	epidermal growth factor receptor (avian	3.46
	428855	BE544095	Hs.164960	BarH-like homeobox 1	3.46
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.46
	450506	NM_004460		fibroblast activation protein, alpha	3.46
40	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	3.45
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.45
	405545			Target Exon	3.45
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	3.44
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.44
45	417944	AU077196	Hs.82985	collagen, type V, alpha 2	3.44
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	3.44
	431228	AB006746	Hs.198282	phospholipid scramblase 1	3.44
	422363	T55979	Hs.115474	replication factor C (activator 1) 3 (38	3.43
	440502	AI824113	Hs.78281	regulator of G-protein signalling 12	3.43
50	448741	BE614567	Hs.19574	hypothetical protein MGC5469	3.43
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.43
	406646	M33630	Hs.308026	major histocompatibility complex, class	3.42
	413281	AA861271	Hs.222024	transcription factor BMAL2	3.42
	449101	AA205847	Hs.23016	G protein-coupled receptor	3.42
55	430890	X54232	Hs.2699	glypican 1	3.41
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	3.41
	412429	AV660262	Hs.75765	GRO2 oncogene	3.41
	443211	AI128388	Hs.143655	ESTs	3.41
	422209	AF005210	Hs.113222	chemokine (C-C motif) receptor 8	3.40
60	428303	AW974476	Hs.183601	regulator of G-protein signalling 16	3.39
	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	3.39
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	3.39
	422101	AW404176	Hs.111611	ribosomal protein L27	3.39
	457670	AF119666	Hs.23449	Insulin receptor tyrosine kinase substra	3.38
65	437033	AW248354	Hs.5409	RNA polymerase I subunit	3.37
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	3.37
	417059	AL037672	Hs.81071	extracellular matrix protein 1	3.37
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	3.36
	414812	X72755	Hs.77367	monokine induced by gamma interferon	3.36
70	436748	BE159107	Hs.159263	collagen, type VI, alpha 2	3.36
	401797			Target Exon	3.36
	428309	M97815	Hs.183650	cellular retinoic acid-binding protein 2	3.35
	421563	NM_006433	Hs.105806	granulysin	3.35
	402294			Target Exon	3.34
75	414024	AA134712	Hs.22410	gb:zm79g08.r1 Stratagene neuroepithelium	3.34
	401961			NM_021626:Homo sapiens serine carboxypep	3.33
	418462	BE001596	Hs.85266	Integrin, beta 4	3.33
	418867	D31771	Hs.89404	msh (Drosophila) homeo box homolog 2	3.33
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.33
80	412420	AL035668	Hs.73853	bone morphogenetic protein 2	3.33
	404440			NM_021048:Homo sapiens melanoma antigen,	3.33
	432398	AA307808	Hs.2979	trefoil factor 2 (spasmolytic protein 1)	3.33
	421677	H64092	Hs.38282	ESTs	3.33
	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	3.32

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	3.32
	417197	AW994561	Hs.151777	eukaryotic translation initiation factor	3.32
	429669	BE185499	Hs.2471	KIAA0020 gene product	3.32
	409636	AA305729	Hs.18272	amino acid transporter system A1	3.32
5	429415	NM_002593	Hs.202097	procollagen C-endopeptidase enhancer	3.32
	405386			Target Exon	3.32
	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	3.31
	448275	BE514434	Hs.20830	kinesin-like 2	3.31
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.31
10	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	3.31
	431830	Y16645	Hs.271387	small inducible cytokine subfamily A (Cy	3.31
	422575	AK000546	Hs.118552	hypothetical protein FLJ20539	3.31
	404171			NM_000636*Homo sapiens superoxide dismu	3.31
	418464	R87580	Hs.144531	gb:ym89h07.r1 Soares adult brain N2b4HB5	3.31
15	425666	AW162943	Hs.250618	UL16 binding protein 2	3.31
	410226	A1831958	Hs.61053	hypothetical protein	3.30
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.30
	443247	BE614387	Hs.333893	c-Myc target JPO1	3.30
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	3.30
20	428336	AA503115	Hs.183752	microseminoprotein, beta-	3.29
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.29
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	3.28
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.28
	405778			NM_005361:Homo sapiens melanoma antigen,	3.28
25	419488	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3	3.27
	421150	A913562	Hs.189902	ESTs	3.27
	406400			kallikrein 8 (neuropsin/ovasin) (KLK8)	3.27
	455813	BE141577		gb:QV2-HT0083-071299-018-a11 HT0083 Homo	3.27
30	426064	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3	3.27
	458814	A1489857	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.27
	458791	BE615453	Hs.346509	dedicator of cyto-kinesis 1	3.27
	418551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	3.26
	429002	AW248439	Hs.2340	junction plakoglobin	3.26
35	450000	A1952797	Hs.10888	hypothetical protein FLJ21709	3.25
	407777	AA161071	Hs.71465	squalene epoxidase	3.25
	419485	AA489023	Hs.99807	ESTs, Weakly similar to unnamed protein	3.25
	426437	BE076537	Hs.169895	ubiquitin-conjugating enzyme E2L 6	3.24
	415701	NM_003878	Hs.78619	gamma-glutamyl hydrolase (conjugase, fol	3.24
40	412617	AL037159	Hs.74619	proteasome (prosome, macropain) 26S subu	3.24
	447519	U46258	Hs.339665	ESTs	3.24
	412561	NM_002286	Hs.74011	lymphocyte-activation gene 3	3.24
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.24
	423198	M81933	Hs.1634	cell division cycle 25A	3.23
45	415091	AL044872	Hs.77910	3-hydroxy-3-methylglutaryl-Coenzyme A sy	3.23
	441085	AW136551	Hs.181245	Homo sapiens cDNA FLJ12532 fis, clone NT	3.22
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.22
	408901	AK001330	Hs.48855	hypothetical protein FLJ10468	3.22
	425849	AJ000512	Hs.295323	serum/glucocorticoid regulated kinase	3.22
50	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.22
	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	3.21
	409197	N54706	Hs.303025	chromosome 11 open reading frame 24	3.21
	412641	M16660	Hs.74335	heat shock 90kD protein 1, beta	3.21
	413436	AF238083	Hs.68061	sphingosine kinase 1	3.21
55	408636	BE294925	Hs.46680	CGI-12 protein	3.21
	412115	AK001763	Hs.73239	hypothetical protein FLJ10901	3.21
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.21
	411573	AB029000	Hs.70823	KIAA1077 protein	3.20
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.19
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homoto	3.19
	435014	BE560898	Hs.10026	mitochondrial ribosomal protein L17	3.18
	401176			Target Exon	3.18
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	3.17
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.16
65	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	3.16
	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	3.16
	452012	AA307703	Hs.279766	kinesin family member 4A	3.16
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	3.15
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	3.15
70	433020	A1375726	Hs.279918	hypothetical protein	3.14
	437915	A1637993	Hs.202312	Homo sapiens clone N11 NTera2D1 teratoca	3.14
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.14
	420005	AW271106	Hs.133294	ESTs	3.14
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.13
75	412270	AC005262	Hs.73797	guanine nucleotide binding protein (G pr	3.13
	421975	AW961017	Hs.6459	hypothetical protein FLJ11856	3.13
	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	3.12
	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.11
	431722	AF161528	Hs.268049	hypothetical protein	3.11
80	427239	BE270447	Hs.174070	ubiquitin carrier protein	3.11
	413385	M34455	Hs.840	indoleamine-pyrrrole 2,3 dioxygenase	3.10
	439780	AL109688		gb:Homo sapiens mRNA full length insert	3.10
	422885	BE244068	Hs.121544	interleukin 12 receptor, beta 1	3.10
	418090	U57059	Hs.83429	tumor necrosis factor (ligand) superfam	3.10

	439755	AW748482	Hs.77873	B7 homolog 3	3.10
	404170			NM_000636*:Homo sapiens superoxide dismu	3.09
	417370	T28651	Hs.82030	tryptophanyl-tRNA synthetase	3.09
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	3.09
5	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	3.08
	421155	H87879	Hs.102267	lysyl oxidase	3.08
	441224	AU076964	Hs.7753	calumenin	3.08
	424326	NM_014479	Hs.145296	disintegrin protease	3.08
10	429413	NM_014058	Hs.201877	DESC1 protein	3.08
	436251	BE515065	Hs.295585	nucleolar protein (KKE/D repeat)	3.08
	446510	H58305	Hs.15165	retinoic acid induced 14	3.08
	442620	C00138	Hs.8535	Homo sapiens mRNA for KIAA1668 protein,	3.07
	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	3.07
	426682	AV660038	Hs.2056	UDP glycosyltransferase 1 family, polype	3.07
15	448853	NM_012204	Hs.22302	general transcription factor IIIC, polyp	3.07
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	3.07
	408915	NM_016651	Hs.48950	heptacellular carcinoma novel gene-3 pro	3.06
	435505	AF200492	Hs.211238	interleukin-1 homolog 1	3.06
	412577	Z22958	Hs.74076	CD163 antigen	3.06
20	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	3.06
	416084	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kin	3.05
	430393	BE185030	Hs.241305	estrogen-responsive B box protein	3.05
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	3.04
25	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	3.04
	444726	NM_005147	Hs.84981	interferon regulatory factor 6	3.04
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	3.04
	437741	BE561610	Hs.5809	putative transmembrane protein; homolog	3.04
	442643	U82756	Hs.3991	PRP4/STK/WD splicing factor	3.04
30	429358	AB037825	Hs.200317	KIAA1404 protein	3.03
	410068	AI633888	Hs.58435	FYN-binding protein (FYB-120/130)	3.03
	426746	J03626	Hs.2057	uridine monophosphate synthetase (orotid	3.03
	409154	U72882	Hs.50842	interferon-induced protein 35	3.02
	442173	N76101	Hs.8127	KIAA0144 gene product	3.02
35	447400	AK000322	Hs.18457	hypothetical protein FLJ20315	3.01
	450962	BE535647	Hs.25723	Sjogren's syndrome/scleroderma autoantig	3.01
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	3.01
	411387	AW842339	Hs.130815	hypothetical protein FLJ21870	3.01
	438662	AA223599	Hs.6351	cleavage and polyadenylation specific fa	3.01
40	459107	AA811881	Hs.28505	ubiquitin-conjugating enzyme E2H (homolo	3.00
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	3.00
	416110	Z42262	Hs.322844	hypothetical protein DKFZp564A176	3.00
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	3.00
	448569	BE382657	Hs.21486	signal transducer and activator of trans	3.00
45	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.00
	400200			NM_002788*:Homo sapiens proteasome (pro	3.00
	403330			Target Exon	2.99
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.99
	403416	AI744626		KIAA0564 protein	2.97
50	403438			NM_031419*:Homo sapiens molecule possess	2.96
	447942	F12628	Hs.155470	hypothetical protein MGC16040	2.96
	427722	AK000123	Hs.180479	hypothetical protein FLJ20116	2.95
	414806	D14694	Hs.77329	phosphatidylserine synthase 1	2.94
	440086	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom	2.94
55	429547	AW009166	Hs.99376	ESTs	2.93
	419121	AA374372	Hs.89626	parathyroid hormone-like hormone	2.90
	431890	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	2.89
	417259	AW903838	Hs.81800	chondroitin sulfate proteoglycan 2 (vers	2.89
	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.86
60	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	2.86
	423425	AA375756	Hs.14449	KIAA1609 protein	2.86
	412851	AI826502	Hs.106149	ESTs	2.86
	400664			NM_002425:Homo sapiens matrix metallopro	2.86
	454140	AB040888	Hs.41793	hypothetical protein FLJ10474	2.85
65	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.85
	421116	T19132	Hs.101850	retinol-binding protein 1, cellular	2.84
	432343	NM_002960	Hs.2961	S100 calcium-binding protein A3	2.83
	423767	H18283	Hs.132753	F-box only protein 2	2.82
	413476	U25849	Hs.75393	acid phosphatase 1, soluble	2.82
70	441801	AW242799	Hs.86366	ESTs	2.80
	441565	AW953575	Hs.303125	p53-induced protein PIGPC1	2.80
	416539	Y07909	Hs.79368	epithelial membrane protein 1	2.79
	428959	AF100779	Hs.194680	WNT1 inducible signaling pathway protein	2.79
	422947	AA306782	Hs.122552	G-2 and S-phase expressed 1	2.75
75	417849	AW291587	Hs.82733	nidogen 2	2.74
	450434	AA166950	Hs.195870	hypothetical protein FLJ14991	2.73
	430466	AF052573	Hs.241517	polymerase (DNA directed), theta	2.72
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564A01278	2.71
	424874	AA347951	Hs.326413	Homo sapiens cDNA FLJ20812 fis, clone AD	2.71
80	453633	AA357001	Hs.34045	hypothetical protein FLJ20764	2.71
	447854	AW138454	Hs.11594	ESTs	2.71
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.70
	412636	NM_004415		desmoplakin (DPI, DPII)	2.69
	420576	AA297634	Hs.54925	KIAA1858 protein	2.68

5	442932	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	2.68
	425071	NM_013989	Hs.154424	deiodinase, lodothyronine, type II	2.68
	410491	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence	2.66
	428698	AA852773	Hs.334838	KIAA1866 protein	2.64
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	2.64
10	447347	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro	2.64
	429505	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	2.63
	406137			NM_000179:Homo sapiens mutS (E. coli) h	2.63
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.62
	443054	AI745185	Hs.8939	yes-associated protein 65 kDa	2.59
15	452620	AA436504	Hs.119286	ESTs	2.59
	420552	AK000492	Hs.98806	hypothetical protein	2.59
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	2.56
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.56
	448454	NM_005879	Hs.21254	TRAF interacting protein	2.55
20	425776	U25128	Hs.159499	parathyroid hormone receptor 2	2.55
	436238	AK002163	Hs.301724	hypothetical protein FLJ11301	2.54
	440676	NM_004987	Hs.112378	LIM and senescent cell antigen-like doma	2.54
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.54
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.53
25	407804	AF228603	Hs.39957	pleckstrin 2 (mouse) homolog	2.53
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	2.51
	411908	L27943	Hs.72924	cytidine deaminase	2.49
	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	2.48
	430024	AI808780	Hs.227730	integrin, alpha 6	2.47
30	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	2.46
	425345	AIU077297	Hs.155894	protein tyrosine phosphatase, non-recept	2.45
	423881	AK001720	Hs.134403	hypothetical protein FLJ10858	2.45
	407853	AA336797	Hs.40499	dickkopf (Xenopus laevis) homolog 1	2.45
	457819	AA057484	Hs.35406	ESTs, Highly similar to unnamed protein	2.44
35	408296	AL117452	Hs.44155	DKFZP586G1517 protein	2.42
	413048	M93221	Hs.75182	mannose receptor, C type 1	2.40
	403851			C5002154*:g17299015[gb]AA54217.1[AE0	2.39
	433745	AF075320	Hs.28980	hypothetical protein FLJ14540	2.37
	423903	M57765	Hs.1721	interleukin 11	2.37
40	427700	AA262294	Hs.180383	dual specificity phosphatase 6	2.36
	419373	NM_003244	Hs.90077	TG-interacting factor (TALE family homeo	2.32
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	2.31
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	2.31
	406974	M57293		gb:human parathyroid hormone-related pep	2.31
45	401924			ENSP00000246632*:CDNA FLJ20261 fis, clon	2.30
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	2.29
	420923	AF097021	Hs.273321	differentially expressed in hematopoieti	2.29
	436608	AA628980		down syndrome critical region protein DS	2.28
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	2.27
50	434398	AA121098	Hs.3838	serum-inducible kinase	2.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	2.26
	418030	BE207573	Hs.83321	neuromedin B	2.25
	404927			Target Exon	2.25
	438549	BE386801	Hs.21858	trinucleotide repeat containing 3	2.24
55	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	2.23
	411388	X72925	Hs.69752	desmocollin 1	2.21
	445757	AW449065	Hs.13264	KIAA0856 protein	2.18
	405069			NM_006212*:Homo sapiens 6-phosphofructo-	2.17
	414035	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito	2.16
60	443168	AI038653	Hs.50500	ESTs	2.15
	444301	AK000136	Hs.10760	asporin (LRR class 1)	2.13
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	2.11
	426471	M22440	Hs.170009	transforming growth factor, alpha	2.10
	445019	AI205540	Hs.281295	ESTs	2.08
65	402021			NM_031891:Homo sapiens cadherin 20, type	2.07
	431866	NM_012098	Hs.8025	angiopoietin-like 2	2.05
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	2.04
	409571	AA504249	Hs.187585	ESTs	2.03
	450831	R37974	Hs.25255	ESTs	1.99
70	408353	BE439838	Hs.44298	mitochondrial ribosomal protein S17	1.99
	445960	AI268399	Hs.140489	ESTs, Weakly similar to LIN1_HUMAN LINE-	1.98
	448356	AL120837	Hs.20993	high-glucose-regulated protein 8	1.97
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	1.91
	426850	BE247670	Hs.172765	MAP/microtubule affinity-regulating kina	1.90
75	427335	AA448542	Hs.251677	G antigen 7B	1.90
	450649	NM_001429	Hs.25272	E1A binding protein p300	1.88
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	1.88
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	1.88
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	1.86
80	433226	AW503733	Hs.9414	KIAA1488 protein	1.86
	413129	AF292100	Hs.104613	RP42 homolog	1.85
	432606	NM_002104	Hs.3056	granzyme K (serine protease, granzyme 3;	1.85
	446620	AA128808	Hs.179902	transporter-like protein	1.81
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	1.79
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	1.78
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	1.77
	423482	BE280172	Hs.129228	galactokinase 2	1.77

5	433201	AF130988	Hs.58346	ectodysplasin 1, anhidrotic receptor	1.76
	419125	AA642452	Hs.130881	B-cell CLL/lymphoma 11A (zinc finger pro	1.75
	425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	1.74
	405102			C15001220*gi 4469558 gb AAD21311.1 (AF	1.74
	433201	AB040896	Hs.21104	KIAA1463 protein	1.73
	420798	W93774	Hs.99936	keratin 10 (epidermolytic hyperkeratosis	1.65
	437860	AA333063	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	1.62
	414961	U27266	Hs.927	myosin-binding protein H	1.61
10	428405	Y00762	Hs.2266	cholinergic receptor, nicotinic, alpha p	1.61
	422170	AI791949	Hs.112432	anti-Mullerian hormone	1.61
	431846	BE019924	Hs.271580	uroplakin 1B	1.58
	404468			C3000442*gi 11120696 ref NP_068518.1 c	1.57
	405779			NM_005367:Homo sapiens melanoma antigen,	1.55
15	441129	AA074904	Hs.296420	ESTs, Weakly similar to T18651 hypotheti	1.55
	427244	AA402400	Hs.178045	ESTs	1.52
	411411	AA345241	Hs.55950	ESTs, Weakly similar to KIAA1330 protein	1.52
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	1.51
	418367	AA326035	Hs.59236	hypothetical protein DKFZp434L0718	1.51
20	40340	AW895503	Hs.125276	ESTs	1.48
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	1.47
	424750	D29956	Hs.152818	ubiquitin specific protease 8	1.46
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	1.44
	406374			C16001364*gi 11067373 ref NP_067689.1 C	1.43
25	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	1.40
	404405			Target Exon	1.39
	401258			NM_030932*:Homo sapiens diaphanous (Dros	1.38
	433323	AA805132	Hs.159142	ESTs	1.36
	427441	AA412605	Hs.343879	SPANX family, member C	1.33
30	444707	AI188613	Hs.41690	desmocollin 3	1.31
	409103	AF251237	Hs.112208	XAGE-1 protein	1.27
	451106	BE382701	Hs.25960	N-MYC oncogene	1.27
	434804	AA649530	Hs.348148	gb:ms44f05.s1 NC1_CGAP_Alv1 Homo sapiens	1.23
	430586	NM_001942	Hs.2633	desmoglein 1	1.21
35	429325	AW088739	Hs.243770	ESTs	1.19
	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	1.03
	418827	BE327311	Hs.47166	HT021	1.01
	404104			C6001378*gi 1171748 sp P46530 NOTC_BRAR	1.00

TABLE 46B

Key: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

45	Pkey	CAT Number	Accession
	413808	2905_1	AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841726 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374260 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354662 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI638062 AI282258 AI580678 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888882 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI40394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 AW868723 BE937150 AA955002 AW863338 BE841767
	421582	13358_1	X00474 NM_003225 X52003 M12075 BI765761 AW950155 AI571948 BI760569 AA308400 AA568312 BI761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50595 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909584 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035
75	406687	0_0	M31126
	450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H58605 BE157601 AA113758
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
80	426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM458657 AU128438 BE384458 AL353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
	454241	685806_1	BE184942 BE184946 AW238414 BE144666

452203	2630_1	BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 B1823519 B1770023 AL554969 B1489905 A1304693 AW259547 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 A1569694 AW073296 A1361433 AA564644 AA487429 BE858232 AA838610 A1539114 A1719375 A1829129 BG057675 A1423422 AU158860 BE300555 AW170777 AA586956 AL571789 AL556850 AL576404 AL582800 B1256544 BF342301 BG875994 AA054458 AA353161 A1940434 BE816522 AL577636 A1479650 AW150377 AU154395 AW951271 A1032220 A1819778 A1346733 AW771150 AW512525 A1249904 AA279809 A1352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 B1819184 AV660190 AL556475 A1620020 AW089888 AW079179 Z21518 AA687601 F04651 A1783951 T57198 A1433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 A1266514 A1538823 A1475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 A1682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 B1560216 B1753586 AW975281 AA664986 AA525775 AA056342 A1538978 X79449 BC017853 AL121035 BF196384 AW119044 A1028023 AW451110 A1971911 AW015069 A1079170 A1376367 A1264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AL567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 A1074589 A1523475 BE890249 AW406263 BE074258 AV729485 BF809610 BG058619 AA677244 BE179838 AA622264 A1460106 AA740411 A1099168 A1078223 A1682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F09669 AW844043 U10439 B1711870 AW245957 A1158567 AA679305 AA679316 W72510 A1346029 BG059762 AW251062 AA132373 A1925621 A1860230 A1340172 AW192891 A107980 A1094937 A1042115 A1200901 BE328452 AA644678 AA551209 BE351065 AA970761 N88609 AW002028 AA160826 A1422774 AW873114 AW073597 AW664483 A1218710 AW020550 AW190607 A1984545 A1871921 A1333970 A1452887 A1818335 A398655 A1554424 A1274187 BE465703 AW512940 AW241366 A1923954 AA576649 AW168294 AA813181 AA912168 A1049738 AW514073 AA548255 A1569630 BE710031 AA244182 A1341697 AA563904 A1537990 AW517908 AW172943 Z39498 A1750294 AW150414 A1253293 BE825720 T31860 AW150775 D0310 A1150892 AU133933 BE781148 A1038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW866705 BE093482 BG990396 A1499917 AA054452 H05484 A1826502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 B1021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 B1919250 B1253018 AW130996 BE074249 BE895428 B1034862 BE083277 BF952166 AF274943 BG494894 A1719075 AA908783 A1935150 A1422691 AA910644 AA583187 BM272167 A1828996 AA527373 AW972459 A1831360 AA772418 A1033892 A1010926 AU154749 A1459432 A1423513 A1094597 AA740817 A1991988 A1090262 A1312104 B1256707 AA459522 AA416871 A1075239 A1339996 AA701623 A1139549 A1336880 AA633648 A1989380 A1362835 AA399239 A1146955 BF514270 N92892 A1348243 A1277887 AA459292 A1494230 BF507531 A1492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 A149682 A1457100 AW589407 AW300758 BE220715 BE220658 BE569091 BM009647 BF900351 A1537692 A1203723 A1857576 AA584410 AW371667 BM172363 BE253764 BE250764 BE255757 BE251752 BE251925 U09278 NM_004460 U76833 AF007822 AL550894 BG203919 AL575714 A1478772 AW022667 AW613820 A1435793 A1051768 A1200109 AA436611 BG208151 A1446661 BG215551 BM449645 AW630055 BG620125 AL550932 AW471133 AU136648 BE925603 BF828688 BE141577 BE141585 BE141587 AL109688 R23655 R26578 BC005265 BG176720 AW006027 BM352064 AW026316 A1635822 A1880584 A1693769 A1092211 B1492387 A1400449 AW166297 BF939910 AA232282 AW021432 A1338893 AA494308 AA854899 A1436795 AW069256 AA682373 A1092748 AA993184 A1260777 A1081758 A1240686 B161863 A1378423 AA465237 A1376096 AA035579 A1087306 AA448162 AA129977 A1090903 A1080686 A1288939 N33004 A1801240 AW021546 A1370773 A1086064 AA669528 A1250053 A1870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 A1582295 A1417525 A1563975 A1093566 A1077743 A1290741 AW073417 BE875418 BM264076 BG876884 A1580535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 A1908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 M77830 NM_004415 AF139055 BG681115 BG740377 B1712964 BG006656 AA128470 B1438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 B1039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 B58704 AA852212 AW366566 B1090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 B1036305 BG990973 B1040954 BF919911 AU140155 A1951766 A1434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 B1039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082516 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE668470 BE931048 BF999889 BF368816 BE184924 BE159846 BE714632 BE184948 BG986845 AA131128 AA098991 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE596084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927275 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE719915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 A1190590 A1554403 A1392926 AU158477 B1467252 AU159919 A1760816 BF082516 A1439101 AA451923 A1340326 A1590975 B1791553 A1700963 A142882 AA039975 AA946936 AA644381 BM314884 AA702424 A1417612 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026864 A1830049 AW780435 A1078449 A1819984 A1858282 B1468588 A1860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207 A1205263 BF082491 AW021347 A1568096 BE939862 AA088865 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 A1910434 BF082513 A1494069 A1270027 A1635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 B1762796 BG287391 AW798780 BE780445 BE926470 AW799118 BF087996 BE002273 AW879451 A1571075 BE067786 AW721320 A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1686869 A1568892 A1915596 AW105614 A1887258 A1538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713858 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 A1905927 BF992780 AW858312 BG954443 B1770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE969209 BE969210 B1089483 BE005273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 B1040941 AA337270 AW384371 AW847442 B1058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 A1284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 B1013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 A1498487 BC015981 A1301615 AA628980 A126803 BF184719
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TABLE 46C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401781	7249190	Minus	83215-83435,83531-83656,83740-83901,8423

5	401760	7249190	Minus	28397-28617,28920-29045,29135-29296,2941
	400666	8118496	Plus	17982-18115,20297-20456
	401785	7249190	Minus	165776-165996,166189-166314,166408-16656
	401747	9789672	Minus	118596-118816,119119-119244,119609-11976
	400665	8118496	Plus	16879-17023
	402994	2996643	Minus	4727-4969
	402075	8117407	Plus	121907-122035,122804-122921,124019-12416
	405770	2735037	Plus	61057-62075
10	401994	4153858	Minus	42904-43124,43211-43336,44607-44763,4519
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	404240	5002624	Minus	116132-116407,116653-116922
	402447	9796540	Plus	47605-47729,51696-51821,52070-52257,5330
	402992	7767907	Minus	42137-42515
	402408	9796239	Minus	110326-110491
15	404286	2326514	Plus	51086-51301
	405387	6587915	Minus	3769-3833,5708-5895
	404287	2326514	Plus	53134-53281
	402995	2996643	Minus	5962-6216
20	405545	1054740	Plus	118677-118807,119091-119296,121628-12182
	401797	6730720	Plus	6973-7118
	402294	2282012	Minus	2575-3000
	401961	4581193	Minus	124054-124209
	404440	7528051	Plus	80430-81581
25	405386	6579238	Minus	40959-41297
	404171	9930793	Plus	173667-173783,176876-177055
	405778	7280331	Plus	18748-19757
	406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077
	401176	9438469	Minus	20475-20734
30	404170	9930793	Plus	168836-169248

TABLE 47A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Maximum of esophageal tumor AIs divided by the 98th percentile of the normal esophagus AIs

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
45	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin)	31.70
	411243	AB039886	Hs.69319	CA11	30.12
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial)	18.46
	444325	AW152618	Hs.16757	ESTs	18.22
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothetical	17.52
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	16.28
50	400666			NM_002425:Homo sapiens matrix metallopro	15.59
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	15.22
	425679	X06997	Hs.159177	lipase, gastric	14.60
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase)	13.14
	431723	AW058350	Hs.16762	Homo sapiens mRNA; cDNA DKFZp564B2062 (f	12.60
55	446519	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.00
	453331	AI240665		ESTs	11.20
	431620	AA126109	Hs.264981	2'-5'-oligoadenylate synthetase 2 (69-71	10.77
	408380	AF123050	Hs.44532	diubiquitin	10.32
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.32
60	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	10.22
	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	10.18
	408243	Y00787	Hs.624	interleukin 8	9.80
	414359	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	9.75
	450375	AA009647		a disintegrin and metalloproteinase doma	9.12
65	407366	AF026942	Hs.17518	gb:Homo sapiens clg33 mRNA, partial sequ	8.88
	433447	U29195	Hs.3281	neuronal pentraxin II	8.64
	421508	NM_004833	Hs.105115	absent in melanoma 2	8.46
	452862	AW378065	Hs.8687	ESTs	8.34
	432828	AB042326	Hs.287402	chondroitin 4-sulfotransferase	7.92
70	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fs, clone PL	7.86
	409757	NM_001898	Hs.123114	cystatin SN	7.62
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	7.60
	413670	AB000115	Hs.75470	hypothetical protein, expressed in osteo	7.58
	452410	AL133619		Homo sapiens mRNA; cDNA DKFZp434E2321 (f	7.46
75	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	7.44
	406687	M31126		matrix metalloproteinase 11 (stromelysin	7.24
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.18
	439343	AF086161	Hs.114611	hypothetical protein FLJ11808	7.13
80	429228	AI553633	Hs.326447	ESTs	7.04
	421110	AJ250717	Hs.1355	cathepsin E	6.98
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	6.88
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	6.88
	406673	M34996	Hs.198253	major histocompatibility complex, class	6.72
	421582	AI910275		trefoil factor 1 (breast cancer, estroge	6.52

5	447164	AF026941	Hs.17518	Homo sapiens cig5 mRNA, partial sequence	6.40
	409403	AA668224	Hs.6634	Homo sapiens cDNA: FLJ22547 fis, clone H	6.32
	439926	AW014875	Hs.137007	ESTs	6.32
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.12
	411296	BE207307	Hs.10114	growth suppressor 1	6.03
	426312	AF026939	Hs.181874	interferon-induced protein with tetratri	5.86
	413441	A1929374	Hs.75367	Sro-like-adaptor	5.86
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	5.81
10	417715	AW969587	Hs.86366	ESTs	5.76
	413808	J00287		Homo sapiens mRNA for caldesmon, 3' UTR	5.63
	400665			NM_002425:Homo sapiens matrix metallopro	5.60
	424408	A1754813	Hs.146428	collagen, type V, alpha 1	5.53
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	5.44
	444527	NM_005408	Hs.11383	small inducible cytokine subfamily A (Cy	5.42
15	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	5.40
	416768	AA363733	Hs.1032	regenerating islet-derived 1 alpha (panc	5.38
	430413	AW842182	Hs.241392	small inducible cytokine A5 (RANTES)	5.08
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	5.08
20	422530	AW972300	Hs.118110	bone marrow stromal cell antigen 2	5.04
	413278	BE563085	Hs.833	interferon-stimulated protein, 15 kDa	4.92
	436856	A1469355	Hs.127310	ESTs	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.60
	421362	AK000050	Hs.103653	hypothetical protein FLJ20043	4.53
25	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	4.48
	404240			NM_018950:Homo sapiens major histocompat	4.36
	435523	T62849	Hs.11090	membrane-spanning 4-domains, subfamily A	4.34
	437763	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1	4.29
	425139	AW630488	Hs.25338	protease, serine, 23	4.24
30	415989	A1267700		ESTs	4.20
	408202	AA227710	Hs.43658	DKFZP586L151 protein	4.11
	450701	H39960	Hs.288467	hypothetical protein XP_098151	4.06
	423271	W47225	Hs.126256	interleukin 1, beta	4.02
	414774	X02419	Hs.77274	plasminogen activator, urokinase	3.96
35	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	3.90
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.86
	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	3.86
	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	3.76
	408122	A1432652	Hs.42824	hypothetical protein FLJ10718	3.49
40	408049	AW076098	Hs.345588	desmoplakin (DPI, DPII)	3.44
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	3.37
	435370	A1964074	Hs.225838	ESTs	3.29
	443378	AW392550	Hs.9280	proteasome (prosome, macropain) subunit,	3.19
	443071	AL080021	Hs.8986	complement component 1, q subcomponent,	3.18
45	409154	U72882	Hs.50842	interferon-induced protein 35	3.13
	445417	AK001058	Hs.12680	Homo sapiens cDNA FLJ10196 fis, clone HE	3.12
	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.00
	406646	M33600	Hs.308026	major histocompatibility complex, class	2.76
	402992			Target Exon	2.57
50	452304	AA025386	Hs.61311	ESTs, Weakly similar to S10590 cysteine	2.54
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	2.52
	413945	NM_000591	Hs.75627	CD14 antigen	2.51
	423225	AA852604	Hs.125359	Thy-1 cell surface antigen	2.50
	443883	AA114212	Hs.9930	serine (or cysteine) proteinase inhibitor	2.48
55	415149	X12451	Hs.78056	calhepsin L	2.47
	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	2.46
	410422	AL042014	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	2.45
	413936	AF113676	Hs.297681	serine (or cysteine) proteinase inhibitor	2.45
	409202	AA236881	Hs.51043	hexosaminidase B (beta polypeptide)	2.39
60	422562	A1962060	Hs.118397	AE-binding protein 1	2.35
	443639	BE269042	Hs.9661	proteasome (prosome, macropain) subunit,	2.28
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	2.19
	412471	M63193	Hs.73946	endothelial cell growth factor 1 (platelet	2.19
	449717	AB040935	Hs.23954	cerebral cell adhesion molecule	2.03
65	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.03
	428981	BE313077	Hs.93135	ESTs, Weakly similar to ALU2_HUMAN ALU S	1.83
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	1.79
	406778	H06273	Hs.101651	Homo sapiens mRNA; cDNA DKFZp434C107 (fr	1.70
	408716	A1567839	Hs.151714	Homo sapiens mRNA for KIAA1769 protein,	1.69
70	412773	H15785	Hs.74573	similar to vaccinia virus HindIII K4L OR	1.66
	414024	AA134712	Hs.22410	gbczm79g08.r1 Stratagene neuroepithelium	1.65
	426530	U24578	Hs.276625	complement component 4A	1.58
	414945	BE076358	Hs.77667	lymphocyte antigen 6 complex, locus E	1.52

75

TABLE 47B

Key: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

80

Key	CAT Number	Accession
453331	16559_1	BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993

			H01642 BF510304 AA626915 AA746952 AI161014 AA099554 BG572534 AI803329 AI809932 AI808765 AA411449 AI378760 AA976929 AI378620 AA909684 R75632 AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 BG001590 BF107035 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758 5 450375 16559_3 452410 59661_1 AL133619 AI435410 AA622747 AW272464 AI215594 AI673758 AI476447 AI804128 AI581345 AI026826 AI300820 AW513621 AA256162 AI559724 AI493388 AA614641 AI125754 AI214351 AI567080 AI200813 AI476629 AI685732 AA602400 AA730140 AI565082 AI269603 AI807095 AA905453 AA505909 AI204595 AI582930 AI686077 AA757863 AA730154 AA654048 BI831663 AI734138 AI734130 AI732734 AW043563 AI741241 AI732741 BF111446 BE677727 AA437369 AA426284 AA433997 AA425820 10 406687 0_0 421582 13358_1 M31126 X00474 NM_003225 X52003 M12075 B1765761 AW950155 AI571948 B1760569 AA308400 AA568312 B1761955 AA507595 AA614579 AA614409 BF747698 BM142326 AA307578 AI925552 AA578674 AA582084 AW009769 AA514776 AA588034 BG271505 AA858276 BM142503 AW050700 AI307407 AI202532 AA524242 AI909772 AI970839 BG236516 AW750216 AA587613 AI909749 AI909751 AI910083 AA614539 R55292 AA507418 AI570199 AI888812 AW867550 AI921557 AW469096 AI925581 AI679986 AW473623 BE841640 BF061525 AI445703 AI925072 AW863188 15 AW863076 BE841731 AW863167 BE841390 BE841365 BF374078 BE841760 BE841694 BE841769 AA335110 BE841692 BF374073 AA335204 BF374079 BE841713 AA335167 BE841584 AW868103 BE841645 BE841765 AI076336 AW867433 BF373831 BE841758 AW868911 AW863155 AW868847 BE841651 AA335145 BE841670 BF374260 BF374088 BE841661 BE841728 BI335729 BE841739 BE841663 AW863104 AA335201 AA335143 BF906965 AW867493 BE841505 BF374250 BE841766 BF373837 AW863191 BE841705 AW863154 AW868673 AW867311 AA335896 BE841753 AW863407 BE937102 BF374252 BF374247 BF374255 BE841785 AW029590 AW131278 AI801021 AW058240 AW058400 AW029230 20 AW029432 AW130609 AW029128 AW130469 AI570155 AI620272 AW029259 AI801389 AI888662 AI926902 AI801799 AI610344 AI452852 AW131174 AI581069 AI225028 AI446689 AI923321 AI439430 AI801502 AI679707 AW028944 AI933684 AI801724 AI537779 AI354652 AI470250 AI536872 AI891151 AW868019 AW006034 AI702599 AA335192 AA335165 AA335189 AI933725 AW044393 AI888797 BE841677 BE841681 AA335141 AW008176 AA335223 AI888837 AW868622 AI803901 AW005718 AI538062 AI282258 AI580578 AI445803 AI445394 AI868168 AA335144 AI926349 AA335210 AA334919 AA335163 AA335216 AI678342 BF374135 AI932922 AA335214 AA335109 AI570325 AI452619 AI926109 25 AI453488 AI678606 AW869289 AW869211 BE841580 AI679368 AI888682 AI926170 BF508305 AW869315 AA334926 BE841712 AW026584 AA335200 BE841764 AV730339 AW474979 AI286344 AI446430 AI537612 AA335166 AW868051 AI679133 AI949520 BE841652 AI949532 BE937113 BE841789 BE841643 AW130556 BE841761 AW868716 AW868698 BE841669 BE937108 AA335158 AA335153 AA335159 AW867404 AW868692 BE841742 AW868711 AW867546 BE841699 AA335198 AA335146 AW868150 BE841660 T99129 BE841740 BE841714 AA335154 AW868815 BF373812 BE841657 BE841780 AI440394 AA335215 AA335202 AA335162 AA335160 AI801656 AI678499 BF374019 AW130236 30 AI826057 AI572459 AI932773 AA335197 AI611752 AA335224 AI452592 AA335147 AA335149 AA334928 AA335114 AA335111 AI567048 AW029395 AI570326 BF373838 BE841691 BE841776 AW863485 BF374093 AW130376 BE841732 AI446393 AI446781 AW867547 AW029012 AA335227 AW869307 AW869350 AW868709 AW869407 AW005017 AI679252 AI925523 AW151553 AW863109 AI445917 AI799620 AI921607 AW008153 AI520957 AI610620 AI679828 AI868151 AI537839 AI679547 T28354 AI282567 AA335207 R83655 BF906963 AW131160 AI925626 AW029396 AW028445 AW008410 AW152586 AW008476 AI801040 AI453669 AI621200 AA334925 BF374069 BF374075 N53208 BF374246 35 AW868723 BE937150 AA955002 AW863338 BE841767 415989 10194_1 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236
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TABLE 47C

Pkey:	Unique number corresponding to an Eos probeset		
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.		
Strand:	Indicates DNA strand from which exons were predicted.		
NI_position:	Indicates nucleotide positions of predicted exons.		
Pkey	Ref	Strand	NI_position
400666	8118496	Plus	17982-18115,20297-20456
400665	8118496	Plus	16879-17023
404240	5002624	Minus	116132-116407,116653-116922
402992	7767907	Minus	42137-42515

TABLE 48A:

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	90th percentile of normal esophagus AIs divided by the 90th percentile of esophageal tumor AIs

Pkey	ExAccn	UnigeneID	Unigene Title	R1
407245	X90588	Hs.172004	titin	37.43
426752	X69490	Hs.172004	titin	30.23
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	23.69
407013	U35637		gb:Human nebulin mRNA, partial cds	17.09
400440	X83957	Hs.83870	nebulin	15.56
406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	14.21
428087	AA100573	Hs.182421	troponin C2, fast	13.03
417070	Z19077	Hs.172004	titin	13.02
406707	S73840	Hs.931	myosin, heavy polypeptide 2, skeletal mu	12.61
405001	U58196		interleukin enhancer binding factor 1	12.53
418391	NM_003281	Hs.84673	troponin I, skeletal, slow	12.46
418205	L21715	Hs.83760	troponin I, skeletal, fast	12.40
422633	X56832	Hs.118804	enolase 3, (beta, muscle)	12.21
400499			C10001858.gi[6679124]ref[NP_032759.1] ne	11.99
418390	AF133820	Hs.84665	titin immunoglobulin domain protein (myo	10.53
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	10.21
417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	10.14
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	10.13
408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	10.00
416373	AA195845	Hs.73680	ESTs, Weakly similar to S12658 cysteine-	9.65
415672	N53097	Hs.193579	ESTs	9.57
409096	AA194412	Hs.50550	sarcomeric muscle protein	9.48

	431360	NM_000427	Hs.251680	loricrin	9.42
	416982	J05401	Hs.80691	creatine kinase, mitochondrial 2 (sarc	9.20
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	9.15
5	422069	AJ010063	Hs.343603	titin-cap (telethonin)	8.96
	409028	AB014513	Hs.49998	Z-band alternatively spliced PDZ-motif	8.64
	437205	AW975934	Hs.283382	ESTs, Weakly similar to I38344 titin, ca	8.48
	421296	NM_002666	Hs.103253	perlepin	8.47
	412129	M21984	Hs.73454	troponin T3, skeletal, fast	8.39
10	434352	AF129505	Hs.86492	small muscle protein, X-linked	8.28
	418026	BE379727	Hs.83213	fatty acid binding protein 4, adipocyte	7.93
	408591	AF015224	Hs.46452	mammaglobin 1	7.88
	435124	AA725362	Hs.120456	ESTs	7.76
	430581	AW969675	Hs.291232	ESTs	7.70
15	454229	AW957744	Hs.278469	lacrimal proline rich protein	7.68
	424734	AI217685	Hs.96844	ESTs	7.59
	428221	U96781	Hs.183075	ATPase, Ca transporting, cardiac muscle,	7.57
	431204	F28841	Hs.250760	cytochrome c oxidase subunit VIa polypep	7.41
	443727	Z25389	Hs.18459	ESTs	7.21
20	408753	AI337192	Hs.47438	SH3 domain binding glutamic acid-rich pr	7.04
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	6.98
	424485	AI685069	Hs.272556	peptidylarginine deiminase type 1	6.93
	403805			Target Exon	6.87
	429997	NM_006789	Hs.227457	apolipoprotein B mRNA editing enzyme, ca	6.72
25	418532	F00797	Hs.85844	neurotrophic tyrosine kinase, receptor,	6.70
	419711	C02621	Hs.159282	ESTs	6.70
	422640	M37984	Hs.118845	troponin C, slow	6.68
	433839	F35430	Hs.146070	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.55
	406703	X13100	Hs.173084	myosin, heavy polypeptide 3, skeletal mu	6.34
30	451621	AI879148	Hs.26770	fatty acid binding protein 7, brain	6.27
	446962	AI351421	Hs.279709	muscle specific ring finger protein 1	6.20
	411102	AA401295	Hs.23926	triadin	6.17
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.15
	454059	NM_003154	Hs.37048	statherin	5.95
35	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	5.85
	434360	AW015415	Hs.127780	ESTs	5.57
	420813	X51501	Hs.99949	prolactin-induced protein	5.52
	417376	AA253314	Hs.154103	LM protein (similar to rat protein kina	5.46
	424688	AA216287	Hs.1815	myosin, light polypeptide 3, alkali; ven	5.42
40	446523	NM_003063	Hs.334629	sarcolipin	5.41
	402270			Target Exon	5.25
	437846	AA773866	Hs.244569	esophagus cancer-related gene-2	5.24
	424982	U94777		phosphorylase, glycogen; muscle (McArdle	5.17
	414657	AA424074	Hs.76780	protein phosphatase 1, regulatory (inhib	5.14
45	410621	AA194329	Hs.172004	titin	5.10
	429134	AA448953	Hs.99004	ESTs	5.06
	436519	AJ278124	Hs.238756	myozenin	5.04
	447023	AA356764	Hs.17109	integral membrane protein 2A	5.03
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	5.02
50	426451	AI908165	Hs.169946	GATA-binding protein 3 (T-cell receptor	5.00
	433635	AI074502	Hs.134292	hypothetical protein MGC12921	4.98
	429892	NM_003803	Hs.2504	myomesin 1 (skelemin) (185kD)	4.96
	411021	F00055	Hs.172004	titin	4.95
	416349	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	4.93
55	424897	D63216	Hs.153684	frizzled-related protein	4.92
	406741	AA058357	Hs.74466	carcinoembryonic antigen-related cell ad	4.92
	428824	W23624	Hs.173059	ESTs	4.78
	418692	AK000268	Hs.87383	hypothetical protein	4.74
	448406	AW772298	Hs.21103	Homo sapiens mRNA; cDNA DKFZp564B076 (fr	4.73
60	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.66
	424049	AB014524	Hs.138360	KIAA0624 protein	4.65
	439609	AW971945	Hs.293236	ESTs	4.65
	433122	AB019391	Hs.58049	ESTs	4.62
	415447	Z97171	Hs.78454	myocilin, trabecular meshwork inducible	4.59
65	415655	W05433		ESTs	4.59
	442376	W95588	Hs.129982	Homo sapiens cDNA FLJ12228 fis, clone MA	4.58
	452308	AI167560	Hs.61297	ESTs	4.57
	418072	F35210	Hs.86507	Human DNA sequence from clone RP3-353C17	4.56
	429413	NM_014058	Hs.201877	DESC1 protein	4.53
70	423725	AJ403108	Hs.132127	hypothetical protein LOC57822	4.53
	438704	AI435060	Hs.32825	ESTs	4.50
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine;g	4.49
	430699	AW969847	Hs.292718	ESTs, Weakly similar to RET2_HUMAN RETIN	4.48
	419050	NM_000036	Hs.89570	adenosine monophosphate deaminase 1 (iso	4.46
75	422313	AF045941	Hs.115166	scellin	4.43
	417045	F01180	Hs.332030	Homo sapiens ORF1	4.41
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	4.39
	435101	AI743156	Hs.131064	ESTs	4.37
	432408	N39127		ESTs, Weakly similar to A46010 X-linked	4.35
80	439705	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	4.35
	429930	AI580809	Hs.99569	ESTs	4.30
	429624	AA458648	Hs.99476	ESTs, Weakly similar to 1313184B alpha1	4.26
	429454	AL039940	Hs.202949	KIAA1102 protein	4.20
	411000	N40449	Hs.201619	ESTs, Weakly similar to S38383 SEB4B pro	4.11

5	429852	AB010445	Hs.225948	small inducible cytokine subfamily A (Cy	3.99
	428560	AI243209	Hs.98669	ESTs, Weakly similar to B47411 ADPribosy	3.95
	438328	AI492261	Hs.32450	ESTs	3.84
	451917	AW391351	Hs.50820	Homo sapiens unknown mRNA	3.84
	453876	AW021748	Hs.110406	ESTs, Weakly similar to I38022 hypotheti	3.83
	414807	AI738616	Hs.77348	hydroxyprostaglandin dehydrogenase 15-(N	3.82
	430171	AF086289	Hs.234766	skin-specific protein	3.80
	422287	F16365	Hs.114346	cytochrome c oxidase subunit VIIa polype	3.75
10	446082	AI274139	Hs.156452	ESTs	3.74
	449003	X76342	Hs.389	alcohol dehydrogenase 7 (class IV), mu o	3.70
	431205	AA194560	Hs.250763	tropomodulin 4 (muscle)	3.68
	443265	AI916207	Hs.9167	SH3 domain binding glutamic acid-rich pr	3.68
	424747	AA346241	Hs.231887	EST	3.67
15	410223	S73775	Hs.60708	calsequestrin 1 (fast-twitch, skeletal m	3.63
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	3.62
	453817	AW755253	Hs.61920	ESTs	3.57
	416431	AW384459	Hs.172004	titin	3.52
	425971	AF135024	Hs.165296	kallikrein 13	3.49
20	412452	AA215731	Hs.79265	suppression of tumorigenicity 5	3.48
	421512	AB007923	Hs.265848	myomegalin	3.41
	413922	AI535895	Hs.221024	ESTs	3.37
	419648	T73661	Hs.91877	thyroid hormone responsive SPOT14 (rat)	3.36
	418067	AI127958	Hs.83393	cystatin E/M	3.32
25	426666	AL080190	Hs.189242	Homo sapiens mRNA; cDNA DKFZp434A202 (fr	3.29
	451681	Z28564	Hs.255950	ESTs, Weakly similar to AA64_HUMAN 64 KD	3.26
	420197	AW139647	Hs.88134	ESTs, Weakly similar to A57291 cytokine	3.23
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	3.21
30	404270			NM_006061:Homo sapiens specific granule	3.21
	409169	F00991	Hs.50889	(clone PVHLC2-24) myosin light chain 2	3.17
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	3.13
	452023	AB032999	Hs.27566	KIAA1173 protein	3.08
	417713	D42047	Hs.82432	KIAA0089 protein	2.99
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	2.97
35	450300	AL041440	Hs.58210	ESTs, Highly similar to ITH4_HUMAN INTER	2.97
	451814	AA847992	Hs.137003	ESTs	2.83
	452360	AI742082	Hs.98539	ESTs	2.67
	431938	AA938471	Hs.54431	specific granule protein (28 kDa); cyste	2.57
	408104	AW972927	Hs.293968	ESTs	2.57
40	444329	W73753	Hs.209637	hypothetical protein FLJ12921	2.54
	439652	W67826	Hs.55412	ESTs, Weakly similar to K1CJ_HUMAN KERAT	2.50
	432191	AA043193	Hs.273186	hypothetical protein, clone Telethon(lta	2.33
	425855	AF135025	Hs.159679	kallikrein 12	2.32
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	2.28
45	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.25
	411388	X72925	Hs.69752	desmocollin 1	2.25
	425721	AC002115	Hs.159309	uropod 1A	2.12
	430520	NM_016190	Hs.242057	chromosome 1 open reading frame 10	2.10
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	2.02
50	417405	W28657	Hs.5307	ESTs	2.01
	434560	R13052	Hs.3964	Homo sapiens clone 24877 mRNA sequence	1.95
	417074	Z49878	Hs.81131	guanidinoacetate N-methyltransferase	1.79
	430513	AJ012008	Hs.241586	G6C protein	1.68
	454478	AW805749	Hs.318885	superoxide dismutase 2, mitochondrial	1.68
55	416559	AI039195	Hs.128060	ESTs	1.66
	447205	BE617015	Hs.11006	ESTs, Moderately similar to T17372 plasmin	1.64
	415780	U75898	Hs.78846	heat shock 27kD protein 2	1.55
	409702	AI752244		eukaryotic translation elongation factor	1.50

60

TABLE 48B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

65

Pkey CAT Number Accession

70

407013 2073_7 U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376
424982 25362_1 AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967
F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311
F32380 F25216 F19679 F18658 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940
F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W08091 F16457 F24094
F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012
415555 15499_1 AJ276240 N70563 F37502 F29200 F27903 F18577 F19683 F20867 Z28857 F30994 F31752 F17375 F15601 F17543 F17411
432408 2061_18 AV724258 AA247153 BF736219 BF513744 AW058048 AI082691 AA865520 N39127 AV724549 F20776 AA249747 AW970392 AA535433 F36964
F33894
409702 38388_1 AK056951 AK026458 BI439120 BM021106 F30243 BM055214 BM054962 BM069667 F37401 AA563621 AI752243 AI720773 AI933014 F18964
F35317 F35258 F27772 H39537 AW445222 F19408 H28557 F30608 F31797 F30980 BF837737 BF837688 AL551046 BI758668 BI765038 BI837440
BE392882 BI438801 AI093511 AI752244 AI784111 BG490221 BF338840 BF338974 BG896472 AL576843 AW966769 F25388 F37436 H28558
AI025548 AA782333 F30929 F36002 F21229 AI720539 AA719449 F21231 F18924 AA626886 F30774 F27704 F31411 F31127 F33381 F36153
F31793 F31138 F31966 F33901 AA298244 BI757347 AI810201 AI692843 F29441 H51409 F21804 AW973249 F18440 F17572 F32499 AA327152
AA534140 AI188088 F18893 F23362 AA010888 F18143 Z28500 H27651 AI720790 F22425 H13178 H28577 F21098 F37777 F21466 F16598
F23420 AL574723 R75610 F34035 F17845 F18560 F25902 R79117 F35534 F15713 AI612800 F16563 F15645 F33609 F29995 BG939623 F17385
F17384 F18660 F17922 F15523 AI093253 F18359 F31452 F00232 AI583430 BM021353 AA284108 H27650 H29935 BE708208 AA010737 H51451

Z19399 A1678418 A1952535 F17265 F17826 F37939 F35639 F17367 W75962 R70189 Z28755 R72106 AA335915 R75700 R79116 W72887
A1581552 R71403 F23388 C03913 B1756149 B1116109 BF790727 AL553994 R82966 W47487 AA456066 AW984608 BE708220 BG490537 W47419

5 TABLE 48C
Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of
10 Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
405001	6015406	Minus	104646-104819
400499	9796071	Minus	148495-148806
15 403805	8140491	Minus	51483-51742,53429-53511
402270	3108020	Plus	117656-117822
404270	9828129	Minus	3649-3750,4161-4306,5962-6049,6849-6965

Table 49A. 1562 genes upregulated in lung cancer relative to normal body tissues

25 Table 49A shows 1562 genes upregulated in lung cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Certain predicted protein domains are noted.

35 Pkey: Unique Eos probeset identifier number
ExAccon: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 90th percentile of lung tumor AIs divided by the 50th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from the numerator and denominator.

40 Pkey; ExAccon; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

421502; AF111856; Hs.105039; solute carrier family 34 (sodium phosphate), member 2; Ribosomal_L20_Na_Pi_cotrans; TM=Y; 24.06
439335; AA742697; Hs.62492; ESTs, Weakly similar to B39056 proline-rich protein 15 - rat [R.norvegicus]; none; SS=M; 21.70
45 406521; X57809; Hs.181125; Immunoglobulin lambda locus; ig_HSP70_Ppx-GppA; TM=M; 19.36
421341; AJ243212; Hs.279611; deleted in malignant brain tumors 1; zona_pellucida_CUB_SRCR; SS=M; 16.99
452304; AA025386; Hs.61311; ESTs, Weakly similar to S10590 cysteine proteinase [H.sapiens]; none; none; 16.67
429259; AA420450; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none; none; 16.50
454034; NM_000691; Hs.575; aldehyde dehydrogenase 3 family, member A1; aldedh; 16.24
50 408000; L11690; Hs.620; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,Fid,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,ALP3; TM=M; 14.75
421798; N74880; Hs.29877; N-acylsphingosine amidohydrolase (acid ceramidase)-like; SAPA,Surfactant_B,none; 14.18
439706; AW872527; Hs.59761; ESTs, Weakly similar to DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 [H.sapiens]; none; none; 13.94
45 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4; TM=Y; SS=M; 13.54
417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; IL1; SS=M; 12.97
444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothetical protein YGL050w - yeast (Saccharomyces cerevisiae) [S.cerevisiae]; Collagen; TM=M; SS=M; 12.92
408243; Y00787; Hs.624; Interleukin 8; IL8,PAS,IL8; TM=M; 12.76
448133; AA723157; Hs.73769; folate receptor 1 (adult); Folate_rec,MIP; TM=M; SS=M; 12.50
60 414809; A434699; Hs.77356; transferrin receptor (p90, CD71); PA; TM=Y; 12.12
436553; AW407157; Hs.181125; Immunoglobulin lambda locus; ig_HSP70_Ppx-GppA; TM=M; 12.00
418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none; none; 11.99
419593; AA133749; Hs.301350; FXD domain-containing ion transport regulator 3; ATP1G1_PLM_MAT8; TM=Y; SS=M; 11.88
417866; AW067903; Hs.82772; collagen, type XI, alpha 1; Collagen,COLFI,TSPN,laminin_G,CorA; SS=M; 11.38
65 414998; NM_002543; Hs.77729; oxidised low density lipoprotein (lectin-like) receptor 1; lectin_c; TM=Y; SS=M; 11.21
428970; BE276891; Hs.194691; retinoic acid induced 3; 7tm_3; TM=Y; SS=M; 11.08
418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member B2; aldedh; TM=M; SS=M; 11.01
425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolv,HATPase_c; SS=M; 10.69
418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (metanoma, p16, Inhibits CDK4); ank; 10.65
70 439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_La,PKD,MHC_J; TM=M; SS=Y; 10.52
441835; AB036432; Hs.184; advanced glycosylation end product-specific receptor; homeobox_Acyltransferase,notch,EGF,ank,Acyltransferase; 10.47
451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ABC_tran,SRP54; TM=Y; SS=M; 10.33
443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none; TM=M; 10.21
452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig_Rhbd_glycop; TM=Y; SS=M; 10.14
417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); PTN_MK; TM=M; SS=Y; 10.13
75 433091; Y12642; Hs.3185; lymphocyte antigen 6 complex, locus D; UPAR_LY6,loxin,Activin_recq; TM=M; SS=Y; 10.12
454098; W27853; Hs.292911; ESTs, Highly similar to S60712 band-6-protein [H.sapiens]; none; none; 10.05
414812; X72755; Hs.77367; monokine induced by gamma interferon; IL8; TM=M; SS=Y; 9.98
430832; A1073913; Hs.100686; ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]; none; none; 9.79
422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; none,pkinase,fn3,jg; 9.60
80 414987; AA524394; Hs.294022; hypothetical protein FLJ14550; SH2; TM=M; 9.54
439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA_ABC_tran,CosE; TM=M; 9.52
430260; AA361258; Hs.237868; interleukin 7 receptor; fn3,none; 9.48

- 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); Kunitz_BPTI,fn3,vwa,Collagen,beta-lactamase;TM=M;SS=M; 9.44
- 418882; NM_004996; Hs.89433; ATP-binding cassette, sub-family C (CFTR/MRP), member 1; ABC_membrane,ABC_tran;TM=Y;SS=M; 9.32
- 435472; AW972330; Hs.283022; triggering receptor expressed on myeloid cells 1; Ig;TM=M;SS=M; 9.26
- 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-macroglobulin receptor precursor [H.sapiens]; none,none; 9.18
- 419508; AW997938; Hs.90788; ATP-binding cassette, sub-family C (CFTR/MRP), member 3; ABC_tran,ABC_membrane;TM=Y;SS=M; 9.06
- 441384; AA447849; Hs.288660; Homo sapiens cDNA: FLJ22182 fis, clone HRC00953; 7tm_3,none; 8.98
- 446292; AF081497; Hs.279682; Rh type C glycoprotein; Ammonium_transp,FecCD;TM=Y;SS=M; 8.74
- 436972; AA284679; Hs.25640; claudin 3; PMP22_Claudin;TM=Y;SS=M; 8.71
- 421817; AF146074; Hs.108660; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; Fascidin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 8.71
- 423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; vwa,CACHE;TM=M; 8.66
- 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1;TM=Y;SS=M; 8.63
- 438091; AW373062; ; nuclear receptor subfamily 1, group 1, member 3; hormone_rec,zf-C4,none; 8.60
- 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; TK;TM=M; 8.57
- 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; ubiquitin;SS=M; 8.56
- 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase;SS=M; 8.52
- 414774; X02419; Hs.77274; plasminogen activator, urokinase; kringe,trypsin,plasmin,thrombin;SS=M; 8.49
- 430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 8.42
- 413011; AW068115; Hs.821; biglycan; LRR,LRRNT;SS=M; 8.40
- 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; GILT;TM=M;SS=Y; 8.39
- 411089; AA456454; ; cell division cycle 2-like 1 (PITSLRE proteins); none,none; 8.37
- 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); BIR;TM=M; 8.34
- 453922; AF053305; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; none,SS=M; 8.25
- 449019; AI949095; Hs.67776; ESTs, Weakly similar to T22341 hypothetical protein F4788.5 - Caenorhabditis elegans [C.elegans]; none,none; 8.24
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; hydrolase;TM=M; 8.22
- 416819; U77735; Hs.80205; p1m-2 oncogene; pkinase;SS=M; 8.19
- 451541; BE279383; Hs.26557; plakophilin 3; Armadillo_seg;TM=M; 8.16
- 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; ABC_tran,M,SMC_N,SMC_C,DUF164,none; 8.16
- 429002; AW248439; Hs.2340; junction plakoglobin; Armadillo_seg;TM=M; 8.14
- 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.14
- 421757; Z20897; Hs.296259; paraoxonase 3; Arylesterase;SS=Y; 8.10
- 414821; MG3835; Hs.77424; Fc fragment of IgG, high affinity Ia receptor for (CD64); Ig;TM=Y;SS=M; 8.03
- 439285; AL133918; ; hypothetical protein FLJ20093; Ig,pkinase,LRR,LRRNT,LRRCT,none; 7.97
- 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B; Sema,PSI,Integrin_B;TM=Y; 7.86
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2; pkinase;TM=M; 7.85
- 424779; AL046851; Hs.153053; CD37 antigen; transmembrane4;TM=Y;SS=M; 7.85
- 409340; BE174629; Hs.321130; hypothetical protein MGC2771; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,Bola,RUN;TM=M; 7.84
- 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); SH3,TPR;TM=M; 7.73
- 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Ig;TM=Y;SS=M; 7.72
- 430378; Z29572; Hs.2556; tumor necrosis factor receptor superfamily, member 17; IL2;SS=M; 7.71
- 451253; H48299; Hs.26126; claudin 10; PMP22_Claudin,Peptidase_M1,K_tetra;TM=Y;SS=M; 7.70
- 435575; AF213457; Hs.44234; triggering receptor expressed on myeloid cells 2; Ig;TM=Y;SS=M; 7.70
- 427747; AW411425; Hs.180655; serine/threonine kinase 12; pkinase;TM=M; 7.70
- 426251; M24283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; Ig,ICAM_N;TM=M;SS=M; 7.67
- 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExtB;TM=Y;SS=M; 7.64
- 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; SAM_PNT,none; 7.54
- 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding protein; 7tm_1;TM=Y;SS=M; 7.52
- 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); Y_phosphatase,DSPC;TM=M; 7.46
- 421071; AI311238; Hs.104476; ESTs, Weakly similar to CGHUIE collagen alpha 1(XI) chain precursor [H.sapiens]; none;TM=Y;SS=M; 7.40
- 421481; AW391972; Hs.104696; KIAA1324 protein; none;TM=M;SS=M; 7.39
- 439089; W06391; ; nuclear receptor subfamily 1, group 1, member 3; hormone_rec,zf-C4,none; 7.38
- 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; aa_permeases,pyridoxal_deC,bromodomain,PHD,MBD,AT_hook,DDT,PI3_P14_kinase,FAT,FATC,Bola,RUN;TM=M; 7.36
- 448988; Y09763; Hs.22785; gamma-aminobutyric acid (GABA) A receptor, epsilon; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 7.36
- 416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; none;TM=M; 7.31
- 418506; AA084248; Hs.85339; G protein-coupled receptor 39; none,none; 7.25
- 441553; AA281219; Hs.121296; ESTs; none,FG-GAP,Integrin_A; 7.25
- 422311; AF073515; Hs.114948; cytokine receptor-like factor 1; fn3;TM=M; 7.21
- 415817; U88967; Hs.78967; protein tyrosine phosphatase, receptor-type, Z polypeptide 1; fn3,Y_phosphatase,carb_anhydrase;TM=Y;SS=M; 7.20
- 438746; AI885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; transferrin,Guanylate_kin,PDZ,SH3; 7.20
- 412723; AA648459; Hs.335951; hypothetical protein AF301222; none;TM=M; 7.14
- 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 7.14
- 428582; BE336699; Hs.185055; BENE protein; none;TM=Y;SS=M; 7.12
- 418462; BE001596; Hs.85266; Integrin, beta 4; fn3,Integrin_B,Cab-beta,EGF;TM=M;SS=M; 7.08
- 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 7.02
- 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M; 7.00
- 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; Ig,Isodh,Ribosomal_L6,F-box;TM=Y;SS=M; 6.98
- 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; Furin-like,pkinase,Recep_L_domain,YLP,none; 6.97
- 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M; 6.96
- 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; ITAM;TM=Y;SS=M; 6.93
- 428479; U00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; pkinase,ICE_p10,ICE_p20;TM=M;SS=M; 6.93
- 421532; AW138207; Hs.146170; hypothetical protein FLJ22969; Armadillo_seg,HEAT;TM=M; 6.91
- 451035; AU076785; Hs.430; plasmin 1 (I isoform); ehfand,CH,Adaplin_N;SS=M; 6.86
- 432407; AA221036; ; gbzr03112r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEV M P10272 POL POLYPROTEIN ; mRNA sequence; DEAD,helicase_C_rnm,Ndr,Cys_knot,TIL,vwa,vwd,IQ,RILa,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp_1,Ribosomal_S21,rnp;TM=M; 6.84
- 442599; AF078037; Hs.324051; RelA-associated inhibitor; SH3,ank;TM=M; 6.77
- 448243; AW369771; Hs.52620; integrin, beta 8; Integrin_B,none; 6.76
- 427557; NM_002659; Hs.179557; plasminogen activator, urokinase receptor; UPAR_LY6,ET,PLA2_inh;SS=M; 6.75
- 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; SRCR,Lysyl_oxidase;TM=M;SS=M; 6.74
- 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; sugar_tr;TM=Y;SS=M; 6.73

- 430397; A1924533; Hs.105607; bicarbonate transporter related protein 1; HCO3_cotransp;TM=Y;; 6.71
 449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; 7tm_1;TM=Y;SS=M; 6.71
 431630; NM_002204; Hs.255829; integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor); FG-GAP,Rhadd_glycop,Integrin_A;TM=Y;SS=M; 6.70
 410434; AF051152; Hs.63668; toll-like receptor 2; LRR,LRRC,TIR;TM=M;SS=M; 6.69
 424925; NM_002432; Hs.153837; myeloid cell nuclear differentiation antigen; PAAD_DAPIN,HIN; 6.69
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor); vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 6.65
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 6.64
 430770; AA765694; Hs.123296; ESTs; none,none; 6.63
 412270; AC005262; Hs.73797; guanine nucleotide binding protein (G protein), alpha 15 (Gq class); G-alpha,arf;TM=M; 6.59
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005735; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricin_B_lectin; 6.59
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPC;TM=M; 6.59
 413048; M93221; Hs.75182; mannose receptor, C type 1; fn2Jectin_c,Ricin_B_lectin,Xlink;TM=Y;SS=M; 6.58
 429345; R11141; Hs.199695; hypothetical protein; K_tetra,SAM; 6.58
 416110; Z42262; Hs.322844; hypothetical protein DKFZp564A176; Sama,PSI,TIG,Integrin_B;TM=Y;SS=M; 6.58
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; Metaalophos;TM=M;SS=M; 6.57
 426746; J03826; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); Pribosyltran,OMPdecase;TM=M; 6.57
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA. transcript (F8A), mRNA;; pkinase,Fibrillarin,none; 6.56
 456373; BE247706; Hs.89751; membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide); none;TM=Y;; 6.53
 444006; BE395085; Hs.10085; type I transmembrane protein Fn14; Idl_recep_a,PKD,MHC,J;TM=M;SS=Y; 6.53
 411027; AF072099; Hs.87846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; inositol_P,lg;TM=M; 6.52
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;TM=Y;SS=M; 6.52
 432920; U97689; Hs.3128; polymerase (RNA) II (DNA directed) polypeptide H; none;TM=M; 6.48
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII KAL ORF; PLDC;TM=M; 6.48
 409208; Y00093; Hs.51077; integrin, alpha X (antigen CD11C (p150), alpha polypeptide); vwa,FG-GAP,Integrin_A,vwa,Integrin_A,FG-GAP; 6.43
 424441; X14850; Hs.147097; H2A histone family, member X; histone,C8FD_NFYB_HMF; 6.43
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; ig;TM=Y;SS=M; 6.41
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fs, clone PLACE2000103; HLH,death,TNFR_c6,Acyl-CoA_hydro; 6.41
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese,DSPC,Y_phosphatase,Ribosomal_S3_N;TM=M; 6.39
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; FBPass;TM=M; 6.37
 424273; W40460; Hs.144442; phospholipase A2, group X; phospholipase;TM=M;SS=Y; 6.37
 428385; AF112213; Hs.184062; putative Rab5-interacting protein; SH2,SH3;SS=M; 6.36
 432636; AA340864; Hs.278562; claudin 7; PMP22_Claudin;TM=Y;SS=M; 6.34
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc,Rhodanese,none; 6.34
 451734; NM_006176; Hs.26944; neurogranin (protein kinase C substrate, RC3); IQ,7tm_1;TM=M; 6.34
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; none;TM=M;SS=Y; 6.34
 401027; ; Target Exon; none,none; 6.26
 418299; AA279530; Hs.83968; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin_B,EGF,PSI;TM=Y;SS=M; 6.22
 429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); SH2;SS=M; 6.21
 408113; T82427; Hs.194101; Homo sapiens cDNA: FLJ20869 fs, clone ADKA02377; 7tm_3,none; 6.20
 408771; AW732573; Hs.47584; potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3; ethand,ion_trans,K_tetra,none; 6.19
 456534; X91195; Hs.100623; phospholipase C, beta 3, neighbor pseudogene; LIM,PDZ,pkinase;SS=M; 6.18
 408482; NM_000676; Hs.45743; adenosine A2b receptor; 7tm_1;TM=Y;SS=M; 6.17
 426427; M86699; Hs.169840; TTK protein kinase; pkinase;; 6.17
 445019; AJ205540; Hs.281295; ESTs; none,none; 6.16
 438552; AJ245820; Hs.6314; type I transmembrane receptor (seizure-related protein); none,none; 6.15
 414907; X90725; Hs.77597; polo (Drosophila)-like kinase; Ribosomal_L37ae,pkinase,POLO_box,IRNA-synt_1b,dynamin,dynamin_2,GED,bZIP,M; 6.14
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; PI3_P4_kinase,FAT,FATC;TM=M; 6.13
 417421; AL138201; Hs.82120; nuclear receptor subfamily 4, group A, member 2; hormone_rec,zf-C4;SS=M; 6.13
 425776; U25128; Hs.159499; parathyroid hormone receptor 2; 7tm_2,HRM;TM=Y;SS=M; 6.12
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz-Frizzled,7tm_2,TM=Y;SS=M; 6.12
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M; 6.12
 421445; AA913059; Hs.104433; Homo sapiens, clone IMAGE:4054868, mRNA; ion_trans,K_tetra,asp; 6.11
 444143; AW747996; Hs.160999; ESTs, Moderately similar to A56194 thromboxane A-2 receptor, endothelial [H.sapiens]; Bcl-2,none; 6.10
 423887; AL080207; Hs.134585; DKFZP434G232 protein; ABC_tran;TM=Y; 6.10
 409638; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y;; 6.09
 411020; NM_006770; Hs.67726; macrophage receptor with collagenous structure; SRCR,Collagen;TM=Y;SS=M; 6.09
 425354; U62027; Hs.155935; complement component 3a receptor 1; 7tm_1;TM=Y;SS=M; 6.08
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); PAF-AH_1b,Lipase_GDSL;TM=M; 6.07
 421753; BE314828; Hs.107911; ATP-binding cassette, sub-family B (MDR/TAP), member 6; ABC_tran,ABC_membrane;TM=Y;SS=M; 6.07
 406908; Z25437; ; gb,H.sapiens protein-tyrosine kinase gene, complete CDS.; none,none; 6.07
 425849; AJ000512; Hs.296323; serum/glucocorticoid regulated kinase; pkinase,pkinase_C;TM=M;SS=M; 6.06
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; C1q,Collagen;SS=M; 6.05
 414883; AA926960; ; CDC28 protein kinase 1; CKS; 6.05
 414166; AW88894; Hs.75789; N-myc downstream regulated; DEAD,helicase_C_rrm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,R1la,abhydrolase,TGF-beta,DUF139,TPR,DSPC,tsp_1,Ribosomal_S21.rvp;TM=M; 6.03
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin,fn2;TM=Y;SS=M; 6.03
 448782; AL050295; Hs.22039; KIAA0758 protein; 7tm_2,lg,GPS,SEA;TM=Y; 6.03
 449101; AA205847; Hs.23016; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 6.01
 445462; AA378776; Hs.286649; hypothetical protein MGC3077; none;; 6.00
 424381; AA285249; Hs.146329; protein kinase Chk2; pkinase,FHA,DnaJ;TM=M; 6.00
 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; pkinase;TM=M; 5.99
 439310; AF086120; Hs.102793; ESTs; casein_kappa,pkinase,lg,none; 5.97
 414972; BE263782; Hs.77695; KIAA0008 gene product; GKAP;TM=M; 5.97
 425976; C75094; Hs.334514; NG22 protein; voltage_CLC;TM=Y;SS=M; 5.94
 444946; AW139205; Hs.156457; hypothetical protein FLJ22408; abhydrolase,abhydrolase_2;TM=Y;SS=M; 5.93
 411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin;TM=M; 5.93
 421462; AF016495; Hs.104624; aquaporin 9; MIP;TM=Y;SS=M; 5.92
 426761; AI015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586i2022 (from clone DKFZp586i2022); none;TM=Y;SS=M; 5.92
 407792; AI077715; Hs.39384; putative secreted ligand homologous to fixt1; none;TM=M;SS=Y; 5.91
 428771; AB028992; Hs.193143; KIAA1069 protein; C2,P1-PLC-Y,P1-PLC-X;TM=M; 5.91
 438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; ig,MHC_II_alpha,none; 5.91

- 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN;NA;NA; 5.90
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; Peptidase_M49,EGF,Ig,Neuregulin;TM=M; 5.90
 408790; AW580227; Hs.47860; neurotrophic tyrosine kinase, receptor, type 2; Ig,pkinase,LRR,LRRNT,LRRCT;TM=Y;SS=M; 5.89
 413186; AU077141; Hs.75231; solute carrier family 16 (monocarboxylic acid transporters), member 1; sugar_tr;TM=Y;SS=M; 5.89
 430696; AA531276; Hs.59509; ESTs; pkinase,PP2C;none; 5.88
 422609; Z46023; Hs.118721; sialidase 1 (lysosomal sialidase); BNR,SH2,SH3,pkinase;TM=Y;SS=M; 5.88
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; none;TM=M;SS=Y; 5.88
 429619; AL120751; Hs.211568; eukaryotic translation initiation factor 4 gamma, 1; none;none; 5.86
 437429; H79981; Hs.5613; Homo sapiens mRNA; cDNA DKFZp564E2222 (from clone DKFZp564E2222); SH2,SH3,BTB; 5.86
 436576; A1458213; Hs.77542; ESTs; 7tm_1,DnaJ; 5.85
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, calcium-dependent); C2,PLA2_B;TM=M; 5.85
 419981; AA897581; Hs.128773; ESTs; pkinase,DAG_PE-bind,pkinase_C,OPR;none; 5.83
 428953; AA306610; Hs.348183; tumor necrosis factor receptor superfamily, member 6b, decoy; 60s_ribosomal,Ribosomal_L10,TNFR_c6,DEAD; 5.83
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; PSS;TM=Y;SS=M; 5.82
 451320; AW118072; diacylglycerol kinase, zeta (104kD); none;TM=M; 5.82
 400991; ; Target Exon; Armadillo_seg,lectin_c;none; 5.81
 456906; AF117646; Hs.156637; Cas-BR-M (murine) ectropic retroviral transforming sequence c; zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3;TM=M; 5.81
 434263; N34895; Hs.44648; ESTs; Ig;none; 5.81
 428293; BE250944; Hs.183556; solute carrier family 1 (neutral amino acid transporter), member 5; eIF6,SDF;TM=M; 5.78
 421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; p450;TM=Y;SS=M; 5.78
 449539; W80363; Hs.58446; ESTs; pkinase,Furin-like,Recep_L_domain;none; 5.77
 409012; AL117435; Hs.49725; DKFZP434I216 protein; PH,RhoGEF;TM=M;SS=M; 5.77
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); MIF,sugar_tr;none; 5.75
 409533; AW969543; Hs.21291; mitogen-activated protein kinase kinase kinase 13; Peptidase_C48;none; 5.73
 457001; J03258; Hs.2062; vitamin D (1,25-dihydroxyvitamin D3) receptor; hormone_rec,zf-C4,Metallothio_5;TM=M; 5.73
 416084; L16991; Hs.79006; deoxythymidylate kinase (thymidylate kinase); none;none; 5.72
 448569; BE32657; Hs.21486; signal transducer and activator of transcription 1, 91kD; SH2,STAT,STAT_bind,STAT_prot;TM=M; 5.72
 452295; BE379936; Hs.28866; programmed cell death 10; serpin;none; 5.72
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; NUDIX;TM=M;SS=M; 5.72
 448733; NM_005629; Hs.187958; solute carrier family 6 (neurotransmitter transporter, creatine), member 8; SNF;TM=Y; 5.71
 417015; M83772; Hs.80876; flavin containing monooxygenase 3; FMO-like,pyr_redox;TM=Y;SS=M; 5.69
 453323; AF034102; Hs.32951; solute carrier family 29 (nucleoside transporters), member 2; Nucleoside_tran;TM=Y;SS=M; 5.69
 410290; AA402307; Hs.322844; hypothetical protein DKFZp564A176; Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 5.69
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 46kD; rrm,hormone_rec,zf-C4,sugar_tr; 5.69
 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; none;TM=Y;SS=M; 5.66
 447250; AB78909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; PP2C;TM=M; 5.65
 438113; A1467908; Hs.8882; ESTs; 7tm_1;none; 5.65
 421391; AW304350; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; Ig;none; 5.64
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; Sm,pkinase; 5.64
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA. VERSION NM_000178.1 GI; MutS_C,PWWP,MutS_N;TM=M; 5.63
 421917; AB028943; Hs.109445; KIAA1020 protein; BTB,zf-C2H2,PI3_P14_kinase,PI3K;TM=M; 5.62
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; PABP,rrm,pkinase,14-3-3; 5.62
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; SH3,PH,RhoGEF;TM=M; 5.61
 446872; X97058; Hs.16362; pyrimidinergic receptor P2Y, G-protein coupled, 6; 7tm_1;TM=Y;SS=M; 5.59
 433662; W07162; Hs.150826; CATX-8 protein; ras,ABC_tran,arf;TM=M;SS=M; 5.59
 449029; N28989; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; aa-permeases;TM=Y;SS=M; 5.58
 431238; AV656840; Hs.285115; Interleukin 13 receptor, alpha 1; fn3;TM=Y;SS=M; 5.57
 430508; A1015435; Hs.104637; ESTs; SDF;TM=Y;SS=M; 5.56
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; 7tm_1;TM=Y;SS=M; 5.55
 421677; H64092; Hs.38282; ESTs; A1pp,Armadillo_seg,IBB; 5.54
 429083; Y08397; Hs.227817; BCL2-related protein A1; Bcl-2;TM=M; 5.54
 429563; BE619413; Hs.2437; eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD); hexapep,W2,hormone2,DUF29;TM=M; 5.52
 412817; AL037159; Hs.74519; proteasome (prosome, macropain) 26S subunit, non-ATPase, 2; PC_rep;TM=M; 5.51
 452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; pkinase;TM=M; 5.51
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (from clone DKFZp547C136); ABC_tran,GTP_EFTU,ABC_membrane;none; 5.50
 423778; Y09267; Hs.132821; flavin containing monooxygenase 2; FMO-like,pyr_redox;TM=Y;SS=M; 5.48
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); SH3,PX;TM=M; 5.48
 434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fls, clone HEMBB1001304; Nucleoside_tra2;none; 5.48
 426691; NM_006201; Hs.171834; PCTAIRE protein kinase 1; pkinase;TM=M; 5.48
 453905; NM_002314; Hs.36568; LIM domain kinase 1; pkinase,LIM,PDZ,zf-PARP;TM=M; 5.48
 412939; AW411491; Hs.75059; eukaryotic translation elongation factor 1 gamma; none;none; 5.44
 430486; BE062109; Hs.241551; chloride channel, calcium activated, family member 2; none;TM=Y;SS=M; 5.43
 430066; A1929659; Hs.237825; signal recognition particle 72kD; TPR,AIRC,SAICAR_synt; 5.40
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; kinesin,fn3,Y_phosphatase;TM=M; 5.40
 411825; AK000334; Hs.72289; hypothetical protein FLJ20327; SNF,Zip;TM=Y; 5.36
 400205; ; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA.(APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; DUF173;SS=M; 5.35
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 5.34
 407786; AA687538; Hs.38972; tetraspan 1; transmembrane4;TM=Y;SS=M; 5.34
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent), methenyltetrahydrofolate cyclohydrolase; myb_DNA-binding,THF_DHG_CYH,THF_DHG_CYH_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M; 5.32
 400210; ; Eos Control; Adap_comp_sub,Clat_adaptor_s;TM=M; 5.32
 414825; X06370; Hs.77432; epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog); Furin-like,pkinase,Recep_L_domain;TM=M;SS=M; 5.31
 414035; Y00630; Hs.75716; serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2; serpin;SS=M; 5.30
 416000; R82342; Hs.79856; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; none,sugar_tr; 5.30
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK,CoaE; 5.29
 424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; SH2,SH3,pkinase;TM=M; 5.29
 450298; AL041949; Hs.24758; hepatocyte growth factor-regulated tyrosine kinase substrate; none;none; 5.29
 456672; AK002016; Hs.114727; Homo sapiens, clone MGC:16327, mRNA, complete cds; none,PK,PK_C,myosin_head,RhoGAP; 5.28
 410068; A163388; Hs.68435; FYN-binding protein (FYN-120130); SH3;TM=M; 5.28
 456629; AW891965; Hs.279789; histone deacetylase 3; HSP90,HATPase_c,zf-C2H2,PHD;none; 5.27
 417218; AA005247; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); pkinase,Sema,PSI,TIG,integrin_B;TM=Y;SS=M; 5.26
 444051; N48373; Hs.10247; activated leucocyte cell adhesion molecule; none;none; 5.26

- 404083; ; C6002159; gi|528027|pir|JAS3593 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor ty; none;SS=M; 5.26
 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; mito_carr;TM=M; 5.26
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; SH2,SH3,kinase;TM=M; 5.26
 427732; NM_002980; Hs.2199; secretin receptor; 7tm_2,HRM;TM=M;SS=M; 5.25
 5 425921; NM_007231; Hs.162211; solute carrier family 6 (neurotransmitter transporter), member 14; SNF;TM=Y;SS=M; 5.25
 448030; N30714; Hs.325960; membrane-spanning 4-domains, subfamily A, member 4A; none;TM=Y;SS=M; 5.24
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; WD40,fn3,Ig;TM=M; 5.23
 446620; AA128808; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 5.23
 422616; BE300330; Hs.118725; selenophosphate synthetase 2; AIRS,AIRS_C;TM=M; 5.23
 10 447131; NM_004585; Hs.17466; retinoic acid receptor responder (tazarotene induced) 3; none;TM=Y; 5.21
 446272; BE268912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; SH3,HS1_rep;TM=M; 5.20
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2;TM=M; 5.19
 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; Troponin,Exo_endo_phos,IQ;TM=M; 5.19
 446635; AC002563; Hs.15767; citron (rho-interacting, serine/threonine kinase 21); CNH,DAG_PE-bind,PH,Involucrin,M;TM=M; 5.19
 15 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C,none; 5.19
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, subfamily J, member 15; IRK;TM=Y; 5.19
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; Ribosomal_S14,ank,kinase,death,none; 5.18
 442200; AW590572; Hs.235768; ESTs; none,none; 5.18
 446566; H95741; Hs.17914; membrane-spanning 4-domains, subfamily A, member 6A; none;TM=Y;SS=M; 5.18
 20 452690; A1536070; Hs.15085; ESTs; pou,homeobox,lign_chan,ANF_receptor; 5.18
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); Ion_trans,SPRY,RYDR,ITPR,RyR,MIR;TM=Y; 5.17
 431441; U1961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 5.16
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 5.16
 25 407601; AC002300; Hs.37129; sodium channel, nonvoltage-gated 1, beta (Liddle syndrome); ASC;TM=Y;SS=M; 5.15
 429500; X78565; Hs.289114; hexabrachion (tenascin C, cytotoxin); EGF,fn3,fibrinogen_C,toxin_2,Keratin_B2;TM=M;SS=Y; 5.15
 411984; NM_005419; Hs.72988; signal transducer and activator of transcription 2, 113kD; SH2,STAT,STAT_bind,STAT_prot;TM=M; 5.15
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 5.14
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; kinase,PBD;TM=M; 5.14
 30 453102; NM_007197; Hs.31664; frizzled (Drosophila) homolog 10; Fz,Frizzled,7tm_2;TM=Y;SS=M; 5.14
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; SRP14,TNFR_c6;SS=M; 5.14
 430563; AA481269; ; ATP-binding cassette, sub-family C (CFTR/MRP), member 5; ABC_tran,GTP_EFTU,ABC_membrane,none; 5.13
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; sugar_tr;TM=Y; 5.12
 35 431183; NM_006855; Hs.250896; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3; ER_lumen_recept;TM=M;SS=M; 5.12
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarotene induced) 1; none,none; 5.11
 418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase 1; kinase,CNH;TM=M; 5.11
 409524; AW402151; Hs.54673; tumor necrosis factor (ligand) superfamily, member 13; TNF;TM=Y;SS=M; 5.11
 436856; A1469355; Hs.127310; ESTs; pkinase,rm;TM=M; 5.09
 411296; BE207307; Hs.10114; growth suppressor 1; 2OG-Fell_Oxy;TM=M;SS=M; 5.09
 40 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; rm;TM=M; 5.09
 404440; ; NM_021048; Homo sapiens melanoma antigen, family A, 10 (MAGEA10), mRNA. VERSION NM_021049.1 GI; MAGE;TM=M; 5.08
 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.08
 422100; A096988; Hs.111554; ADP-ribosylation factor-like 7; arf,ras;TM=M; 5.07
 452222; AW806287; Hs.21432; SEX gene; Sema,TIG,PSI,GDI; 5.07
 45 430300; U08085; Hs.238648; oncostatin M receptor; fn3;TM=Y;SS=M; 5.07
 408369; R38438; Hs.182575; solute carrier family 15 (H?? transporter), member 2; PTR2;TM=Y; 5.07
 422112; BE540240; Hs.111783; Lsm1 protein; Sm,BAG;SS=M; 5.06
 449961; AW265634; Hs.133100; ESTs; kinase,Furin-like,Recep_L_domain,none; 5.06
 430024; A1808780; Hs.227730; Integrin, alpha 6; Integrin_A,FG-GAP;TM=Y;SS=M; 5.06
 50 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; HSP90,HATPase_c;TM=M; 5.05
 437608; AA761605; Hs.292308; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase,RIO1,none; 5.05
 400296; AA305627; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y; 5.04
 446232; A1281848; Hs.194691; retinoic acid induced 3; 7tm_3,none; 5.04
 425262; D87119; Hs.155418; GS3955 protein; kinase;SS=M; 5.04
 55 414703; BE243877; Hs.76941; ATPase, Na? transporting, beta 3 polypeptide; Na_K-ATPase;TM=Y;SS=M; 5.03
 434808; AF155108; Hs.256150; Homo sapiens, Similar to RIKEN cDNA 2810027O19 gene, clone MGC:14827, mRNA, complete cds; none;TM=M; 5.03
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member 21; death,TNFR_c6;TM=Y;SS=M; 5.03
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; none,none; 5.03
 60 448913; AA194422; Hs.22564; myosin VI; rm,zf-RanBP,kinase,GST_C,EtS,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_N,bZIP,zf-C2H2,PHD,BTB,TFIIS,AT_hook,SAM;TM=M; 5.02
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 5.02
 427618; NM_000760; Hs.2175; colony stimulating factor 3 receptor (granulocyte); fn3;TM=M;SS=M; 5.02
 417666; A1345001; Hs.82380; menage a trois 1 (CAK assembly factor); zf-C3HC4;TM=M; 5.02
 65 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); CDK5_activator,none; 5.01
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; ras,arf,TK;SS=M; 5.01
 426285; U20620; Hs.343581; karyopherin alpha 1 (importin alpha 5); Armadillo_seg,IBB;TM=M; 5.01
 421233; AA209534; Hs.284243; tetraspan NET-6 protein; transmembrane4;TM=Y;SS=M; 5.01
 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; SH2,STAT,STAT_bind,STAT_prot,none; 5.00
 70 425345; A1077297; Hs.155894; protein tyrosine phosphatase, non-receptor type 1; Y_phosphatase,DSF;TM=M;SS=M; 5.00
 446946; A1878932; Hs.317; topoisomerase (DNA) I; Topoisomerase_I,Topoisomerase_I_N,RnaAD,Hanta_nucleocap;TM=M; 4.99
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); TPR,PDZ,VW,Guanylate_kin;TM=M; 4.98
 412116; AW402166; Hs.784; Epstein-Barr virus induced gene 2 (lymphocyte-specific G protein-coupled receptor); 7tm_1;TM=Y;SS=M; 4.98
 400792; AA635062; ; Homo sapiens mRNA: cDNA DKFZp434O0515 (from clone DKFZp434O0515); zf-C3HC4,CARD,BIR;TM=M; 4.98
 75 417018; M16038; Hs.80887; v-yes-1 Yamaguchi sarcoma viral related oncogene homolog; SH2,SH3,kinase;TM=M; 4.98
 427247; AW504221; Hs.174103; Integrin, alpha L (antigen CD11a (p180), lymphocyte function-associated antigen 1; alpha polypeptide); vwa,integrin_A,FG-GAP;TM=Y;SS=M; 4.98
 442080; AW444761; Hs.44565; ESTs; ank; 4.97
 454042; H22570; ; hypothetical protein FLJ20093; ig,kinase,LRR,LRRNT,LRRCT,none; 4.97
 452688; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; 7tm_1;TM=Y;SS=M; 4.96
 80 416276; U41060; Hs.79136; LIV-1 protein, estrogen regulated; Peptidase_C4,Osteopontin,Zip;TM=Y;SS=M; 4.96
 408847; AW290997; Hs.30348; ESTs; kinase,Ig,none; 4.96
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; ig,kinase;TM=Y;SS=M; 4.95
 450737; AW007152; Hs.203330; ESTs; trypsin,Idl_recept_a,none; 4.95
 443354; AW970672; Hs.9247; protein kinase, AMP-activated, alpha 1 catalytic subunit; pkinase,RIO1;TM=M; 4.94

- 414135; NM_004419; Hs.1218; dual specificity phosphatase 5; Rhodanese, DSPc, Y_phosphatase; TM=M; 4.94
- 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys, ig, FAD_Synth, kh, lkh_C, pkinase; SS=M; 4.94
- 434206; AW136973; Hs.180479; ESTs, Weakly similar to S69890 mlogen inducible gene mtg-2 [H.sapiens]; PH; TM=M; 4.93
- 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); 7tm_1, 7tm_2; TM=Y; SS=M; 4.93
- 5 408716; AI567839; Hs.151714; Homo sapiens mRNA for KIAA1769 protein, partial cds; UvrD-helicase, RNB, Runt; TM=M; 4.93
- 426437; BE076537; Hs.169895; ubiquitin-conjugating enzyme E2L 6; Armadillo_seg, UQ_con, none; 4.92
- 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kinase 4 mRNA, 3' untranslated region, partial sequence; Els, SAM_PNT; TM=M; 4.92
- 414570; Y00285; Hs.76473; insulin-like growth factor 2 receptor; fn2, CIMR; TM=M; SS=M; 4.92
- 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; ig; TM=Y; SS=M; 4.92
- 10 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; DEAD, helicase_C, CARD; TM=M; 4.91
- 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); ig, ITAM, Zn_cus; TM=Y; SS=M; 4.91
- 404289; ; NM_002944; Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; fn3, pkinase, DUF139; TM=Y; SS=M; 4.90
- 428141; D50402; Hs.182611; solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1; Nramp; TM=Y; 4.90
- 15 407853; AA335797; Hs.40499; dickkopf (Xenopus laevis) homolog 1; none; TM=M; SS=Y; 4.89
- 432179; X75208; Hs.2913; EphB3; EPH_lbd, fn3, pkinase, SAM; TM=Y; SS=M; 4.89
- 401083; ; NM_016582; Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 GI; PTR2; TM=Y; SS=M; 4.89
- 402211; AA811738; ; KIAA0430 gene product; ion_trans, K_tetra; TM=Y; 4.88
- 421541; NM_003942; Hs.105584; ribosomal protein S6 kinase, 90kD, polypeptide 4; pkinase, pkinase_C; TM=M; 4.87
- 431810; X67155; Hs.270845; kinesin-like 5 (mitotic kinesin-like protein 1); kinesin; TM=M; 4.86
- 20 425295; AA431366; Hs.37251; ESTs; pkinase, none; 4.86
- 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; DNA_ligase; 4.86
- 419168; AI336132; Hs.33718; Homo sapiens cDNA FLJ12641 fis, clone NT2RM4001953; none, none; 4.86
- 442875; BE623003; Hs.23625; Homo sapiens clone TCCCTA00142 mRNA sequence; K_tetra, DUF51; none; 4.86
- 25 425455; L18964; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; 4.86
- 410293; AK000047; Hs.61960; hypothetical protein; K_tetra; TM=M; 4.86
- 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; C1q, Collagen; SS=M; 4.85
- 445903; AI347487; Hs.132781; class I cytokine receptor; fn3; TM=Y; 4.85
- 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a ligand); 7tm_1; TM=Y; SS=M; 4.85
- 30 428820; AA436187; Hs.172631; Integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); vwa, Integrin_A, FG-GAP; TM=Y; SS=M; 4.84
- 445143; U29171; Hs.75852; casein kinase 1, delta; zf-C3HC4, Filamin, zf-B_box, NHL, pkinase, zf-MIZ; TM=M; 4.82
- 427157; U51166; Hs.173824; thymine-DNA glycosylase; UDG; TM=M; 4.81
- 427857; AL133017; Hs.2210; hypothetical protein FLJ22865; myosin_head, IQ, zf-MYND; TM=M; SS=M; 4.81
- 35 422233; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); aldedh, aakinese; TM=M; 4.81
- 414280; BE410769; Hs.75873; zyxin; LIM, ig, pkinase; TM=M; SS=M; 4.81
- 424570; AA343306; Hs.133511; ESTs; SH3, ank, none; 4.80
- 451144; AW956103; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c, none; 4.80
- 402705; AA214618; ; activator of S phase kinase; AhpC-TSA; TM=M; SS=M; 4.80
- 410024; AW191024; Hs.55016; hypothetical protein FLJ21935; SH3; TM=M; 4.80
- 40 419972; AL041465; Hs.182982; golgin-67; none, none; 4.80
- 427127; AW802282; Hs.22265; pyruvate dehydrogenase phosphatase; PP2C; none; 4.80
- 413476; U25849; Hs.75393; acid phosphatase 1, soluble; LMWP; TM=M; SS=M; 4.80
- 415801; R24219; Hs.278443; Fc fragment of IgG, low affinity IIb, receptor for (CD32); ig; TM=Y; 4.79
- 402233; ; NM_030760; Homo sapiens endothelial differentiation, sphingolipid G-protein-coupled receptor, 8 (EDG8), mRNA; 7tm_1; TM=Y; SS=M; 4.79
- 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; NusG; SS=M; 4.79
- 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; ptkB; TM=M; 4.79
- 405370; ; NM_005569; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA; pkinase, LIM, PDZ; SS=M; 4.79
- 416498; U33632; Hs.79351; potassium channel, subfamily K, member 1 (TWIK-1); ion_trans; TM=Y; SS=M; 4.78
- 429921; AA526911; Hs.82772; collagen, type XI, alpha 1; Collagen, COL1, TSPN, laminin_G, CorA; SS=M; 4.78
- 50 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase; TM=M; 4.78
- 433133; AB027249; Hs.104741; PDZ-binding kinase; T-cell originated protein kinase; pkinase; TM=M; 4.78
- 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); none; TM=M; SS=Y; 4.78
- 417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; ig, abhydrolase; 4.78
- 55 450334; AF035959; Hs.24879; phosphatidic acid phosphatase type 2C; PAP2; TM=Y; SS=M; 4.78
- 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase; SS=M; 4.77
- 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (from clone DKFZp586P2321); none; NA; NA; 4.77
- 446196; AI744888; Hs.149470; ESTs; zf-C3HC4, Sulfate_transp, STAS; 4.77
- 429305; AF095727; Hs.287832; myelin protein zero-like 1; ig, transmembrane4; TM=Y; SS=M; 4.77
- 426812; AF105365; Hs.172613; solute carrier family 12 (potassium/chloride transporters), member 7; none; TM=Y; 4.77
- 60 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); Armadillo_seg, IBB, DEAD, helicase_C, Sec63, DDT, PHD, bromodomain; TM=M; 4.77
- 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; DSPc; TM=M; 4.77
- 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702; GDI, 7tm_1, none; 4.76
- 447207; AA442233; Hs.17731; hypothetical protein FLJ12892; none; TM=M; 4.76
- 65 400846; ; ; sortilin-related receptor, L (DLR class) A repeats-containing (SORL1); EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.76
- 452355; N54926; Hs.29202; G protein-coupled receptor 34; 7tm_1, OATP_C; TM=Y; 4.75
- 406809; AF000574; Hs.22405; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2; ig, Gemini_mov; TM=M; SS=M; 4.75
- 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; MAGE; TM=M; 4.75
- 444042; NM_004915; Hs.10237; ATP-binding cassette, sub-family G (WHITE), member 1; ABC_tran, PRK, GBP; TM=Y; 4.74
- 70 410408; AI989703; Hs.1466; glycerol kinase; FGGY, FGGY_C; TM=M; 4.73
- 411653; AF070578; Hs.71168; Homo sapiens clone 24674 mRNA sequence; none; NA; NA; 4.73
- 437667; BE616412; Hs.286218; junctional adhesion molecule 1; none, HLH; 4.73
- 417781; BE279380; Hs.82563; KIAA0153 protein; TTL_Acyl_transf; 4.73
- 453966; BE148734; Hs.63325; transmembrane protease, serine 4; trypsin, ldl_recept_a, none; 4.73
- 75 412228; AW503785; Hs.73792; complement component (3d/Epsin Barr virus) receptor 2; sushi; TM=Y; SS=M; 4.73
- 418255; AW135405; Hs.37251; ESTs; pkinase, none; 4.73
- 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; SDF; TM=Y; SS=M; 4.73
- 406906; Z25424; ; gb: H.sapiens protein-serine/threonine kinase gene, complete CDS; none, none; 4.73
- 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; Metallophos; TM=M; 4.72
- 80 424909; S78187; Hs.153752; cell division cycle 25B; Rhodanese; SS=M; 4.72
- 422599; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; NDK, PH, Oxysterol_BP; SS=M; 4.71
- 426136; AW957239; ; gb: EST369309 MAGE resequences, MAGD Homo sapiens cDNA, mRNA sequence; PP2C; none; 4.71
- 446203; Z47553; Hs.14286; flavin containing monooxygenase 5; FMO-like, pyr_redox; TM=Y; SS=M; 4.71
- 451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase, DAG_PE-bind, pkinase_C, OPR; none; 4.71

- 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran,ABC_membrane;TM=Y;; 4.70
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; Idh,Idh_C,SH3,pkinase,UBA;TM=M;; 4.70
 427206; NM_004586; Hs.173965; ribosomal protein S6 kinase, 90kD, polypeptide 3; none;none; 4.70
 421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; EGF,F5_F8_type_C,laminin_G,Sulfate_transp,STAS,7tm_3,xan_ur_permease;TM=Y;SS=M; 4.70
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); UQ_con;TM=M; 4.70
 405484; ; C3002124; gi12737280[rel]XP_006682.2] keratin 18 [Homo sapiens]]6633; none;SS=M; 4.70
 401345; M83738; ; protein tyrosine phosphatase, non-receptor type 9; none;TM=M; 4.70
 416602; NM_008159; Hs.79389; nel (chicken)-like 2; EGF,vwc,TSPN;SS=Y; 4.69
 412507; L36645; Hs.73964; EphA4; fn3,pkinase,SAM,EPH_1bd;TM=Y;SS=M; 4.69
 437897; AA770561; Hs.146170; hypothetical protein FLJ22969; zI-DHHC;none; 4.69
 432886; BE159028; Hs.279704; chromatin accessibility complex 1; none;TM=M; 4.69
 400843; ; NM_003105; Homo sapiens sortilin-related receptor, L (DLR class) A repeats-containing (SORL1), mRNA; EGF,fn3,Idl_recept_a,Idl_recept_b,granulin,BNR;TM=Y;SS=M; 4.68
 433409; AI278802; Hs.25661; ESTs; pkinase,pkinase; 4.68
 413869; NM_000878; Hs.75596; interleukin 2 receptor, beta; none;TM=Y;SS=M; 4.68
 430259; BE550182; Hs.127826; RalGEF-like protein 3, mouse homolog; fn3,RA,RasGEF;TM=M;SS=M; 4.68
 425761; AW664214; Hs.196729; ESTs; SH3,Ribosomal_S3Ae; 4.68
 431941; AK000108; Hs.272227; Homo sapiens cDNA FLJ20099 fis, clone COL04544; pkinase,Furin-like,Recep_L_domain;none; 4.68
 419493; AF001212; Hs.90744; proteasome (prosome, macropain) 26S subunit, non-ATPase, 11; CDK5_activator,PCI;none; 4.67
 425968; NM_001761; Hs.1973; cyclin F; cyclin_F-box,cyclin_C;TM=M; 4.67
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 4.67
 453476; AI640500; Hs.24633; SAM domain, SH3 domain and nuclear localisation signals, 1; SH3,SAM;SS=M; 4.67
 412926; AI879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; MARCKS;SS=M; 4.67
 424635; AA420887; Hs.115455; Homo sapiens cDNA FLJ14259 fis, clone PLACE1001076; pkinase,Furin-like,Recep_L_domain;none; 4.66
 446051; BE048061; Hs.37054; ephrin-A3; Ephrin,A_deamin,dsm,z-alpha; 4.66
 436729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 4.66
 408204; AA450501; Hs.43666; protein tyrosine phosphatase type IVA, member 3; Y_phosphatase;TM=M; 4.66
 435542; AA687376; ; ESTs; SH3,Ig,pkinase,PH,spectrin,RhoGEF;none; 4.66
 429682; NM_006306; Hs.211602; SMC1 (structural maintenance of chromosomes 1, yeast)-like 1; ABC_tran,SMC_N,SMC_C,KID;TM=M; 4.66
 417497; AW402482; Hs.82212; CD53 antigen; transmembrane4;TM=Y;SS=M; 4.66
 418735; T18979; Hs.87908; Snf2-related CBP activator protein; helicase_CAT_hook,SNF2_N;TM=M; 4.65
 415117; AF120499; Hs.78016; polynucleotide kinase 3'-phosphatase; Viral_helicase1;TM=M; 4.65
 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; SH2,PH,RA;SS=M; 4.65
 426108; AA622037; Hs.166468; programmed cell death 5; DUF122;TM=M; 4.64
 429263; AA019004; Hs.198396; ATP-binding cassette, sub-family A (ABC1), member 4; ABC_tran,SRP54;TM=Y;SS=M; 4.64
 431886; L77964; Hs.271980; mitogen-activated protein kinase 6; pkinase;TM=M; 4.63
 435049; AL122067; Hs.4746; hypothetical protein FLJ21324; none;TM=M; 4.63
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor); TIMP,pkinase,DAG_PE-bind,RBD; 4.63
 413436; AF238083; Hs.68061; sphingosine kinase 1; DAGK;TM=M; 4.63
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; ehband,Idl_recept_a;SS=M; 4.62
 442590; AI002686; Hs.130313; ESTs; none,Y_phosphatase,Band_41,connexin; 4.62
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium binding domain; ehband;SS=M; 4.62
 423740; Y07701; Hs.293007; aminopeptidase puromycin sensitive; Peptidase_M1,Armadillo_seg; 4.61
 429300; AB011108; Hs.198891; serine/threonine-protein kinase PRP4 homolog; pkinase;TM=M; 4.60
 447232; AW499834; Hs.327; interleukin 10 receptor, alpha; none;TM=M;SS=M; 4.60
 412942; AL120344; Hs.75074; mitogen-activated protein kinase-activated protein kinase 2; pkinase;TM=M; 4.60
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; DSPc; 4.59
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); EGF,lectin_c,sushi;TM=M;SS=M; 4.59
 411125; AA151647; Hs.68877; cytochrome b-245, alpha polypeptide; none;TM=Y;SS=M; 4.59
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; SH3,PH,WW,RhoGAP;SS=M; 4.58
 447312; AW434345; Hs.35908; activating transcription factor 1; rm,zf-RanBP,pkinase,GST_C,Ets,SAM_PNT,ABC2_membrane,myosin_head,IQ,Myosin_bZIP,zf-C2H2,PHD,BTB,TFILS,AT_hook,SAM;TM=M; 4.58
 435254; AW194689; Hs.30778; ESTs; pkinase,Bacterial_PQQ;none; 4.58
 426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone HRC08741; Esterase,enolase,Peptidase_S9;TM=M; 4.58
 421685; AF189723; Hs.106778; ATPase, Ca transporting, type 2C, member 1; Cation_ATPase_C,Cation_ATPase_N,E1-E2_ATPase,Hydrolase,XPG_N;TM=Y;; 4.58
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; fn3,Ig,Y_phosphatase,MAM;TM=Y;SS=M; 4.58
 427640; AF058293; Hs.180015; D-dopachrome tautomerase; COX8,SHMT,Mif,GST_C,EF1G_domain,GST_N,S1,Fz,Frizzled,calreticulin,7tm_2,rm,PAP_assoc;TM=Y;SS=M; 4.57
 441085; AW136551; Hs.181245; Homo sapiens cDNA FLJ12532 fis, clone NT2RM4000200; none;none; 4.57
 409581; U66243; Hs.55039; mitogen-activated protein kinase 12; pkinase;SS=M; 4.57
 423184; NM_004428; Hs.1624; ephrin-A1; Ephrin;TM=M;SS=M; 4.56
 443920; AL037764; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 4.56
 422627; BE336857; Hs.118787; transforming growth factor, beta-induced, 68kD; Fasciclin,ABC_tran,ABC_membrane,GTP_EFTU;TM=M;SS=M; 4.56
 418869; AW516555; ; gb:bxq01d05.x1 Scores_NHCCc_cervical_tumor Homo sapiens cDNA clone 3' similar to contains Alu repetitive element ;contains element MER11 repetitive element ;, mRNA sequence; none,RasGAP,WW,IQ; 4.56
 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus receptor; SPX,EXS;TM=Y;; 4.56
 437157; BE048860; Hs.120655; ESTs; IRK;none; 4.55
 422769; AA938905; Hs.120017; olfactory receptor, family 7, subfamily E, member 38 pseudogene; none;none; 4.55
 457918; AL359590; Hs.162604; hypothetical protein DKFZp762M188; PLD;TM=M; 4.55
 434467; BE552368; Hs.231853; Homo sapiens cDNA FLJ13445 fis, clone PLACE1002962; 7tm_1;none; 4.55
 421140; AA298741; Hs.102135; signal sequence receptor, delta (translocon-associated protein delta); none;TM=Y;SS=M; 4.55
 406364; ; Target Exon; hexapep;TM=M; 4.55
 434682; AA827165; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; Ig;none; 4.54
 438939; H21012; Hs.287657; Homo sapiens cDNA: FLJ21291 fis, clone COL01963; F5_F8_type_C,pkinase,Ets;none; 4.54
 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; EF_TS,UBA;; 4.54
 411165; NM_000169; Hs.69089; galactosidase, alpha; Melibiase;SS=M; 4.54
 408956; AK001868; Hs.49344; hypothetical protein FLJ11008; ion_trans;TM=Y;; 4.54
 416847; L43821; Hs.80261; enhancer of filamentation 1 (cas-like docking; Crk-associated substrate related); SH3;TM=M; 4.53
 410226; AI831958; Hs.61053; hypothetical protein; SH3,TPR;TM=M; 4.53
 422753; AI928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); Sm;SS=M; 4.52
 418355; L42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase;TM=Y;; 4.52
 400261; ; Eos Control; Ig,MHC_IL_beta;TM=Y;SS=M; 4.52
 444633; AF117113; Hs.286218; junctional adhesion molecule 1; Ig;TM=Y;SS=M; 4.52
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo sapiens cDNA, mRNA sequence; Sec7,PH,ANF_receptor,Iig_chan,WD40,IRK; 4.52

- 400303; AA242758; Hs.79136; LIV-1 protein, estrogen regulated; none:none; 4.51
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase,DAG_PE-bind,pkinase_C,OPR;TM=M; 4.51
 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin;TM=M; 4.51
 457906; AW975939; Hs.153290; Homo sapiens cDNA FLJ14318 fis, clone PLACE3000402; none,pkinase; 4.51
 5 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 4.51
 429690; AW956329; Hs.23721; ESTs; none,sugar_tr,Ribosomal_S25; 4.50
 424618; L29472; Hs.1802; major histocompatibility complex, class II, DO beta; ig,MHC_II_beta;TM=Y;SS=M; 4.50
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 4.50
 405490; ; NM_031414;Homo sapiens serine/threonine kinase 31 (STK31), transcript variant 1, mRNA; pkinase,TUDOR;TM=M; 4.50
 10 424494; U78575; Hs.149255; phosphatidylinositol-4-phosphate 5-kinase, type I, alpha; PIP5K;SS=M; 4.50
 441031; A110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen_C,G-alpha,arf;TM=M;SS=M; 4.50
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22_Claudin,none; 4.50
 410423; AW402432; Hs.63469; protein tyrosine phosphatase, non-receptor type 6; SH2_Y_phosphatase,DSPc;TM=M; 4.50
 429556; AW139399; Hs.98988; ESTs; none;TM=M; 4.50
 15 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none;TM=Y; 4.49
 425209; A1049761; Hs.155140; casein kinase 2, alpha 1 polypeptide; pkinase,ABC1;TM=M; 4.49
 425695; NM_005401; Hs.159238; protein tyrosine phosphatase, non-receptor type 14; Y_phosphatase,Band_41,DSPc;TM=M; 4.49
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 4.49
 20 412970; AB026436; Hs.177534; dual specificity phosphatase 10; Rhodanese,DSPc;SS=M; 4.48
 400755; AA635062; ; Homo sapiens mRNA; cDNA DKFZp43400515 (from clone DKFZp43400515); zf-C3HC4,CARD,BIR;TM=M; 4.48
 425566; AW162943; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_1;TM=M;SS=Y; 4.48
 410151; X15723; Hs.59242; paired basic amino acid cleaving enzyme (furin, membrane associated receptor protein); Peptidase_S8,P;TM=Y;SS=M; 4.48
 423536; L22075; Hs.1666; guanine nucleotide binding protein (G protein), alpha 13; UCR_hinge,G-alpha,arf;TM=M; 4.48
 25 424711; NM_005795; Hs.152175; calcitonin receptor-like; 7tm_2,HRM;TM=Y;SS=M; 4.48
 427878; C05766; Hs.181022; CGI-07 protein; none,zf-C2H2; 4.48
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 4.48
 422605; H16646; Hs.118666; hypothetical protein PP591; PAPS_reduct,MuCF_biosynth; 4.47
 410583; AW770280; Hs.36258; ESTs, Moderately similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]; SH3,PDZ,Guanylate_kin,none; 4.47
 30 434419; AL040606; Hs.296939; dual specificity phosphatase 7; DSPc;TM=M; 4.47
 410032; BE065985; gb:RC3-BT0319-120200-014-a09 BT0319 Homo sapiens cDNA, mRNA sequence; abhydrolase_2,none; 4.46
 423078; M35198; Hs.123125; Integrin, beta 6; Integrin_B,EGF_pp-binding;TM=Y;SS=M; 4.46
 400263; ; Fos Control; GTP_EFTU,EGF_C,GTP_EFTU_D2,serpin;TM=M; 4.46
 441406; Z45957; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M; 4.45
 35 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; none;TM=M; 4.45
 413227; M79082; ; ESTs; none:none; 4.45
 441321; H17182; Hs.7771; B-cell associated protein; Band_7;TM=M; 4.45
 457194; H20669; Hs.35406; ESTs, Highly similar to unnamed protein product [H.sapiens]; none,pkinase,PBD; 4.45
 414745; AA160511; Hs.5326; amino acid system N transporter 2; porcupine; none:none; 4.45
 40 404276; ; NM_002944;Homo sapiens v-ros avian UR2 sarcoma virus oncogene homolog 1 (ROS1), mRNA; fn3,pkinase,DUF139;TM=Y;SS=M; 4.45
 426966; A1493134; ; sclerostin; DAN;TM=M;SS=M; 4.45
 408873; AL046017; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none:none; 4.44
 426486; BE178285; Hs.170056; Homo sapiens mRNA; cDNA DKFZp586B0220 (from clone DKFZp586B0220); pkinase,none; 4.44
 432798; AA565309; Hs.194015; ESTs; Integrin_B,Sema,PSI,TIG,none; 4.44
 439568; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; Frizzled,Fz,7tm_2,toxin_2;TM=Y;SS=M; 4.44
 45 417886; AA214584; ; ESTs; SPRY,7tm_3,ANF_receptor,none; 4.43
 452098; A1858183; ; gb:u146a12x1 NCL_CGAP_U11 Homo sapiens cDNA clone 3' similar to contains Alu repetitive element, mRNA sequence; SH3,none; 4.43
 426874; N67325; Hs.347487; ESTs; SH3,TonB_boxC,none; 4.43
 422714; AB018335; Hs.119387; KIAA0792 gene product; DUF221;TM=Y;SS=M; 4.42
 410741; Z11695; Hs.324473; mitogen-activated protein kinase 1; pkinase,none; 4.42
 50 432193; AA372264; Hs.273193; hypothetical protein FLJ10708; pkinase;TM=M; 4.41
 409506; NM_006153; Hs.54589; NCK adaptor protein 1; SH2,SH3;TM=M; 4.41
 429390; AB040942; Hs.201500; KIAA1509 protein; none;TM=M; 4.41
 421859; AA356620; Hs.108947; KIAA0050 gene product; ank,PH,ArlGap;SS=M; 4.41
 55 451527; AF022813; Hs.26518; transmembrane 4 superfamily member 7; none,none; 4.41
 421748; NM_014718; Hs.107809; KIAA0726 gene product; cadherin;TM=Y; 4.40
 410416; BE410072; Hs.63304; protein phosphatase methyltransferase-1; none;TM=M; 4.40
 450457; AA387701; Hs.6639; KIAA1624 protein; none;TM=M;SS=M; 4.40
 433029; NM_014322; Hs.279926; opsin 3 (encephalopsin); 7tm_1,Monooxygenase;TM=Y;SS=M; 4.40
 60 408805; H69512; Hs.48269; vaccinia related kinase 1; pkinase;TM=M; 4.40
 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1;TM=Y;SS=M; 4.40
 440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; SPRY,BAG,UPF0001; 4.40
 451154; AA015879; Hs.33536; ESTs; TIMP,none; 4.40
 433895; A1287912; Hs.3628; mitogen-activated protein kinase kinase kinase 4; pkinase,zf-C4,CNH,ERM;TM=M; 4.40
 65 422034; AC006486; Hs.333069; Ets2 repressor factor; Ets;TM=M; 4.39
 444009; A1380792; Hs.135104; ESTs; TNFR_c6,TIL,none; 4.39
 420020; BE295666; Hs.94382; adenosine kinase; pkb;SS=M; 4.39
 416207; NM_014745; Hs.79077; Homo sapiens, clone MGC:2908, mRNA, complete cds; none;TM=Y;SS=M; 4.39
 417655; AA780791; Hs.14014; hypothetical protein FLJ14813; pkinase,pkinase_C;TM=M; 4.39
 70 402915; ; ENSP00000202587; Bicarbonate transporter-related protein BTR1; HCO3_cotransp;TM=Y; 4.39
 453199; A1336266; Hs.32353; mitogen-activated protein kinase kinase kinase 4; pkinase;TM=M; 4.38
 416033; NM_012201; Hs.78979; Golgi apparatus protein 1; cys_rich_FGFR;TM=Y;SS=M; 4.38
 453672; U73531; Hs.34526; G protein-coupled receptor; 7tm_1;TM=Y;SS=M; 4.38
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 [H.sapiens]; GPS,7tm_2;TM=Y; 4.38
 75 420039; NM_004605; Hs.94581; sulfotransferase family, cytosolic, 2B, member 1; Sulfotransfer;SS=M; 4.38
 412834; R77123; Hs.79881; Homo sapiens cDNA: FLJ23006 fis, clone LNG00414; 7tm_1,none; 4.38
 452203; Y57522; ; transporter 1, ATP-binding cassette, sub-family B (MDR/TAP); ABC_tran,ABC_membrane,SRP54,Thymidylate_kin;TM=Y;SS=M; 4.37
 425317; AW205118; Hs.210546; interleukin 21 receptor; none;TM=Y;SS=M; 4.37
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 4.37
 80 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y79AA1001384, highly similar to Homo sapiens very large G-protein coupled receptor-1 (VLGR1) mRNA; none:none; 4.37
 434071; AF116653; Hs.34192; Homo sapiens PRO0823 mRNA, complete cds; none;TM=M; 4.37
 412596; AA161219; Hs.799; diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor); EGF;TM=Y;SS=M; 4.36
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; fn3;SS=M; 4.36

- 432987; A1864771; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none; TM=Y; SS=M; 4.36
- 436943; A4773838; Hs.5353; caspase 10, apoptosis-related cysteine protease; ICE_p10, ICE_p20, DED; TM=M; 4.36
- 457897; A1356125; Hs.345168; ESTs, Weakly similar to HXA2_HUMAN HOMEBOX PROTEIN HOX-A2 [H.sapiens]; homeobox; NA; NA; 4.36
- 406671; A4129547; Hs.285754; met proto-oncogene (hepatocyte growth factor receptor); Sema, pkinase, TIG, PSI; none; 4.36
- 5 413969; X14034; Hs.75648; phospholipase C, gamma 2 (phosphatidylinositol-specific); SH2, SH3, C2, PH, PI-PLC-Y, PI-PLC-X, PDGF; SS=M; 4.35
- 408101; AW968504; Hs.123073; CDC2-related protein kinase 7; none; none; 4.35
- 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); Man-6-P_recep; TM=M; SS=M; 4.35
- 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; aldo_ke_red; none; 4.35
- 10 438937; AW952654; Hs.244624; ESTs; EPH_jbd, pkinase, fn3, SAM; none; 4.35
- 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; none; lectin_c; 4.35
- 436540; BE397032; Hs.14468; hypothetical protein MGC14226; rrm, Tm_1, SNF; TM=M; 4.34
- 435267; N23797; Hs.110114; ESTs; none; Syja_N, Exo_endo_phos; 4.34
- 405616; ; Target Exon; none; SH3, BAR; 4.34
- 15 432141; BE410964; Hs.272736; nuclear receptor binding protein; pkinase; TM=M; 4.33
- 417927; R73095; Hs.24122; ESTs; none; pkinase; 4.33
- 429849; U33053; Hs.2499; protein kinase C-like 1; pkinase, pkinase_C, HR1; TM=M; 4.33
- 425743; BE396495; Hs.159428; BCL2-associated X protein; Bcl-2; TM=Y; 4.33
- 453863; X02544; Hs.572; orosomucoid 1; lipocalin, aldehyd, ubiquitin, IRK; SS=M; 4.33
- 20 400847; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, Jld_recep_La, Jld_recep_Lb, granulin, BNR; TM=Y; SS=M; 4.33
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT, FATC, PI3_P14_kinase; TM=M; 4.33
- 413858; NM_001610; Hs.75589; acid phosphatase 2, lysosomal; acid_phosphat; TM=Y; SS=M; 4.33
- 442539; AL119506; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP, adenylate kinase; 4.33
- 25 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; IMP4; TM=M; 4.32
- 436703; AW880614; Hs.146381; RNA binding motif protein, X chromosome; rrm, SH3, PH, CH, RhoGEF; 4.32
- 414899; AW975433; Hs.36288; ESTs; pkinase, SH2, SH3; none; 4.32
- 444895; A1674383; Hs.22891; solute carrier family 7 (cationic amino acid transporter, y system), member 8; ASC, death, TNFR_c6; 4.31
- 30 415135; AW673559; Hs.78040; KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1; ER_lumen_recept; none; 4.31
- 444070; NM_015367; Hs.10267; MIL1 protein; Bcl-2; TM=Y; 4.31
- 422611; AA158177; Hs.118722; fucosyltransferase 8 (alpha (1,6) fucosyltransferase); SH3, K-box; TM=M; SS=Y; 4.31
- 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; bromodomain; TM=M; 4.30
- 440883; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; sugar_tr; TM=Y; SS=M; 4.30
- 35 414080; AA135257; Hs.47783; B aggressive lymphoma gene; A1pp; TM=M; 4.30
- 415072; BE263687; Hs.77876; Homo sapiens, clone IMAGE:3461982, mRNA, partial cds; Metallophos, Armadillo_seg; TM=M; 4.30
- 442994; AI026718; Hs.16954; ESTs; ank, pkinase, death, Ribosomal_S14; 4.30
- 432328; A1572739; Hs.195471; 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3; PGAM, 6PF2K; TM=M; 4.29
- 439490; AW249197; Hs.100043; ESTs, Weakly similar to A46302 PTB-associated splicing factor, long form [H.sapiens]; none; TM=M; 4.29
- 40 422005; BE265556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (from clone DKFZp761E212); none; Na_H_Exchange; 4.29
- 415214; A1445236; Hs.125124; EphB2; fn3, pkinase, SAM, EPH_jbd; TM=Y; SS=M; 4.29
- 430316; NM_000875; Hs.239176; insulin-like growth factor 1 receptor; fn3, Furin-like, pkinase, Recep_L_domain; TM=M; SS=M; 4.29
- 429099; BE439552; Hs.196177; phosphorylase kinase, gamma 2 (testis); pkinase, Bac_DNA_binding; TM=M; 4.29
- 425843; BE313280; Hs.159627; death associated protein 3; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 4.28
- 437603; AW979259; Hs.293673; ESTs; death; none; 4.28
- 45 439975; AW328081; Hs.6817; inosine triphosphatase (nucleoside triphosphate pyrophosphatase); Ham1p_like; TM=M; 4.28
- 424512; X53002; Hs.149846; Integrin, beta 5; integrin_B, EGF; TM=Y; SS=M; 4.28
- 442980; AA857025; Hs.8878; kinesin-like 1; kinesin, Luteo_ORF3, DUF164; TM=M; 4.28
- 420166; AW732276; Hs.95583; transmembrane 4 superfamily member (tetraspan NET-7); transmembrane4; TM=Y; SS=M; 4.27
- 409582; R27430; Hs.271565; ESTs; none; Neur_chan_LBD, Neur_chan_mem; 4.27
- 50 439096; AA830185; ; ESTs; ras; none; 4.27
- 414561; A1064813; Hs.195155; Homo sapiens amino acid transport system N2 (SN2) mRNA, complete cds; Aa_trans; TM=Y; 4.27
- 411835; U29343; Hs.72550; hyaluronan-mediated motility receptor (RHAMM); bZIP; SS=M; 4.27
- 428781; AF164799; Hs.193384; putative 28 kDa protein; pkinase, DAG_PE-bind, pkinase_C, OPR; SS=M; 4.27
- 55 430603; AA148164; Hs.247280; HBV associated factor; zfc3HC4, zfc-RanBP, pkinase; 4.27
- 415149; X12451; Hs.78056; cathepsin L; Peptidase_C1; SS=M; 4.26
- 444838; AV651680; Hs.208558; ESTs; integrin_A, FG-GAP; none; 4.26
- 402328; ; Target Exon; pkinase; TM=M; 4.26
- 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none; none; 4.26
- 60 420942; H03514; Hs.15589; ESTs; none; pkinase; 4.26
- 453902; BE502341; Hs.3402; ESTs; none; none; 4.26
- 425505; AL036458; ; gb:DKFZp564D2062_r1_564 (synonym: htr2) Homo sapiens cDNA clone DKFZp564D2062_5', mRNA sequence; arf, G-alpha; none; 4.26
- 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor 3A; Neur_chan_LBD, Neur_chan_mem; TM=Y; SS=M; 4.26
- 432269; NM_002447; Hs.2942; macrophage stimulating 1 receptor (c-met-related tyrosine kinase); pkinase, Sema, PSI, TIG, A4_EXTRA; TM=M; SS=M; 4.26
- 65 417007; AF224741; Hs.80768; chloride channel 7; CBS, voltage_CLC; TM=Y; 4.26
- 447960; AW954377; Hs.26412; ring finger protein 26; zfc3HC4; TM=Y; SS=M; 4.26
- 442300; A1765908; Hs.129166; ESTs; none; SS=M; 4.25
- 421856; NM_016447; Hs.108931; MAGUK protein p55T; Protein Associated with Lins 2; SH3, PDZ, Guanylate_kin, L27; TM=M; 4.25
- 452110; T47667; Hs.28005; Homo sapiens cDNA FLJ11309 fis, clone PLACE1010076; pkinase, Activin_recp; none; 4.25
- 70 422451; AA310753; Hs.42491; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; PDZ, SH2, STAT, STAT_bind, STAT_prot; none; 4.25
- 453955; AW579207; Hs.304666; ESTs, Weakly similar to I78855 serine/threonine-specific protein kinase [H.sapiens]; fn3, ig, MAM; none; 4.25
- 457670; AF119666; Hs.23449; insulin receptor tyrosine kinase substrate; SH3; TM=M; 4.25
- 419133; U46116; Hs.89627; protein tyrosine phosphatase, receptor type, G; fn3_Y_phosphatase, carb_anhydrase, DSPc; TM=Y; SS=M; 4.25
- 419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; aa_permeases; TM=Y; SS=M; 4.25
- 75 415198; AW009480; Hs.943; natural killer cell transcript 4; none; TM=M; 4.24
- 416440; A1823912; Hs.79335; Homo sapiens, Similar to SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 1, clone MGC:15280, mRNA, complete cds; SWI; TM=M; 4.24
- 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothetical protein [H.sapiens]; none, spectrin, SH3, PH, CH; 4.24
- 449444; AW818436; Hs.23590; solute carrier family 16 (monocarboxylic acid transporters), member 4; none; TM=Y; SS=M; 4.24
- 80 433848; AF095719; Hs.93764; carboxypeptidase A4; Zn_carbOpept, Propep_M14; SS=M; 4.24
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glucose transporter), member 10; sugar_tr; TM=Y; SS=M; 4.24
- 412681; AW983655; Hs.172004; titin; fn3, ig, SGXXSG, pkinase; TM=M; 4.24
- 424653; AW977534; Hs.151469; calcium/calmodulin-dependent serine protein kinase (MAGUK family); none; none; 4.24
- 421066; AU076725; Hs.101408; branched chain aminotransferase 2, mitochondrial; aminotran_4; 4.23

- 428338; AF147765; Hs.232093; ESTs; fn2,CIMR;TM=M;SS=M; 4.23
 443329; BE262943; Hs.9234; hypothetical protein MGC1936; none;TM=Y;SS=M; 4.23
 432314; AA533447; Hs.312989; ESTs; Xlink;none; 4.23
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none;TM=M; 4.23
 5 454166; AW993356; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 4.23
 442596; AI457102; Hs.347970; Human glucose transporter pseudogene; none;none; 4.23
 442549; AI751601; Hs.8375; TNF receptor-associated factor 4; MATH,zf-TRAF,zf-C3HC4;SS=M; 4.22
 424154; AF026004; Hs.141660; chloride channel 2; voltage_CLC,CBS,EPO_TPO,PC_rep; 4.22
 433419; AI830342; Hs.211272; ESTs; transmembrane4;none; 4.22
 10 421921; H83363; Hs.6820; translocase of inner mitochondrial membrane 10 (yeast) homolog; zf-Tim10_DDP,ethand,CH,spectrin,serpin;TM=M; 4.22
 445633; AI453386; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK;none; 4.22
 424812; AF059252; Hs.153299; DOM-3 (C. elegans) homolog 2; none;TM=M; 4.22
 410668; BE379794; Hs.65403; hypothetical protein; death,TNFR_c6;TM=Y;SS=M; 4.22
 15 416636; N32536; Hs.42645; solute carrier family 16 (monocarboxylic acid transporters), member 6; none;none; 4.22
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3;TM=M; 4.21
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; none;none; 4.21
 400208; ; Eos Control; FCH,RhoGAP,SH3;TM=M; 4.21
 405369; ; NM_005669; Homo sapiens LIM domain kinase 2 (LIMK2), transcript variant 2a, mRNA.; pkinase,LIM,PDZ;SS=M; 4.21
 445350; AF052112; Hs.12540; lysophospholipase I; abhydrolase_2;TM=M; 4.21
 20 441208; AI339704; Hs.150401; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens];
 lon_trans,RYDR,JTPR,MIR;none; 4.21
 427217; AA399272; Hs.144341; ESTs; ANP,GHMP_kinases;none; 4.21
 400845; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA;
 EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 4.21
 25 422667; H25642; ; ESTs; FMO-like,FMO-like; 4.21
 450056; BE047394; Hs.8208; ESTs, Weakly similar to S71512 hypothetical protein T2 - mouse [M.musculus];
 ABC_tran,ABC_membrane,ig,MHC_II_beta,SRP54,proteasome,ABC_membrane,ABC_tran; 4.20
 448950; AF288687; Hs.9275; CGI-152 protein; E1-E2_ATPase,Hydrolase;TM=Y; 4.20
 30 408634; AW407254; Hs.182278; calmodulin 2 (phosphorylase kinase, delta); none;none; 4.20
 422335; AA375957; Hs.6682; solute carrier family 7, (cationic amino acid transporter, y system) member 11; none;none; 4.20
 426754; NM_014264; Hs.172052; serine/threonine kinase 18; pkinase;TM=M; 4.20
 435810; BE349853; Hs.2785; keratin 17; zf-Tim10_DDP,SH2,SH3,pkinase,PH,BTK,Ribosomal_L44; 4.20
 446143; BE245342; Hs.306079; sec61 homolog; NUDIX,secY,E1_dehydrog,transket_pyr;TM=Y;SS=M; 4.20
 426626; AI124572; Hs.323879; inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma; zf-C2H2;TM=M; 4.20
 35 403716; ; Target Exon; Adap_comp_sub,PDZ,DEP,DIX,Dishvelled,hexapep,W2,ABC_tran; 4.19
 415749; BE262529; Hs.78771; phosphoglycerate kinase 1; PGK;none; 4.19
 434599; AB002313; Hs.3989; plexin B2; PSI,Sema,TIG;NA;NA; 4.19
 412600; L28824; Hs.74101; spleen tyrosine kinase; SH2,pkinase; 4.19
 416738; N29218; Hs.40290; ESTs; ABC_tran,ABC_membrane;none; 4.19
 40 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; DEAD,helicase_C,PRK,ALP3;TM=M; 4.19
 431385; BE178536; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; none;none; 4.19
 407305; AA715284; ; gb:mv35f03.r1 NC1_CGAP_Br5 Homo sapiens cDNA clone similar to contains Alu repetitive element, mRNA sequence; pkinase,integrin_B,Sema,PSI,TIG;none;
 4.18
 45 452880; AA029332; Hs.87549; ESTs; none,integrin_B; 4.18
 428245; AF151048; Hs.183180; anaphase promoting complex subunit 11 (yeast APC11 homolog); none;SS=M; 4.18
 421964; X73079; Hs.288579; polymeric immunoglobulin receptor; ig,Cobalamin_bind;TM=M;SS=M; 4.18
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M; 4.18
 421790; AW896201; Hs.22654; sodium channel, voltage-gated, type I, alpha polypeptide; lon_trans,IQ,PEP-utilizers_C;TM=Y; 4.18
 429668; AA626142; Hs.179991; ESTs, Weakly similar to S28942 protein kinase C [H.sapiens]; none;none; 4.18
 50 443068; AI188710; ; ESTs; Endonuclease,pkinase,Activin_rec;none; 4.18
 418827; BE327311; Hs.47166; HT021; none;TM=M; 4.18
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine protease; ICE_p10,ICE_p20,DED;TM=M; 4.18
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3,OPR,PX;TM=M; 4.18
 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; none;none; 4.18
 55 438974; AF089816; Hs.6454; chromosome 19 open reading frame 3; PDZ;SS=M; 4.18
 413407; AJ356293; Hs.75339; inositol polyphosphate phosphatase-like 1; SH2,SAM,Exo_endo_phos;SS=M; 4.18
 424954; NM_000546; Hs.1846; tumor protein p53 (L-Fraumeni syndrome); P53,W404,IRK;TM=M; 4.17
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none;none; 4.17
 431544; AK000770; Hs.299329; Homo sapiens cDNA FLJ20763 fis, clone COL09911; none;none; 4.17
 60 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; CBS,IMPDH_C,IMPDH_N,NPD;TM=M; 4.17
 452012; AA307703; Hs.279766; kinesin family member 4A; kinesin,DNA_topoisolv,K-box;TM=M; 4.17
 425606; U52112; Hs.158331; renin-binding protein; none; 4.16
 416817; AA398045; Hs.104679; ESTs; Furin-like,pkinase,Recep_L_domain,fn3;none; 4.16
 65 402447; ; C1000201:gil204416[gb]AA02627.1] (L05195) fructose transporter [Rattus norvegicus] gil44; none;TM=Y;SS=M; 4.16
 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; Euk_porin;TM=M;SS=M; 4.15
 426395; BE151985; Hs.5722; hypothetical protein FLJ23316; pkinase;none; 4.15
 404140; ; NM_006510; Homo sapiens ret finger protein (RFP), transcript variant alpha, mRNA.; zf-C3HC4,SPRY,zf-B_box;SS=M; 4.15
 432268; BE311856; Hs.274230; 3'-phosphoadenosine 5'-phosphosulfate synthase 2; APS_kinase,ATP-sulfonylase;TM=M; 4.15
 70 405516; ; ENSP00000200457; Thyroid receptor interacting protein 6 (TRIP6) (OPA-interacting protein 1) (Zydn related protein 1) (ZRP-1); LIM;TM=M; 4.15
 448390; AL035414; Hs.21068; hypothetical protein; FGGY_C;TM=M; 4.15
 435732; AF229178; Hs.123136; leucine rich repeat and death domain containing protein; none;none; 4.15
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank,PH,Oxysterol_BP,pkinase;TM=M; 4.15
 411558; AA102870; Hs.70725; gamma-aminobutyric acid (GABA) A receptor, pi; Neur_chan_LBD,Neur_chan_memb;TM=Y;SS=M; 4.14
 75 424339; BE257148; Hs.145416; endoglycan; none;TM=Y;SS=M; 4.14
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog; ig,pkinase;TM=Y;SS=M; 4.14
 440524; R71264; Hs.16798; ESTs; SH3,ig,pkinase,PH,spectrin,RhoGEF;none; 4.14
 436115; AW512033; Hs.102004; ESTs; pkinase;none; 4.14
 447050; NM_016314; Hs.17200; STAM-like protein containing SH3 and ITAM domains 2; SH3,VHS,UIM;SS=M; 4.14
 80 418529; AW005695; Hs.250897; TRK-fused gene; Band_41,ERM,pkinase,LRR,LRRCT,MAM,Nucleoplasmin,Tropomyosin,OPR,filament,bZIP,G-gamma,M,DUF164;TM=M; 4.14
 420727; H75701; Hs.99886; complement component 4-binding protein, beta; sushi;SS=M; 4.14
 433075; NM_002959; ; sortilin 1; Exo_endo_phos,Atrophin-1,BNR,Kelch;TM=M; 4.14
 422783; AA598956; Hs.120439; ethanolamine kinase; Choline_kinase;TM=Y; 4.14
 410726; AI623859; Hs.15936; ESTs; pkinase,pro_isomerase;none; 4.14

- 417903; NM_002342; Hs.1116; lympholoxin beta receptor (TNFR superfamily, member 3); TNFR_c6; TM=M; SS=M; 4.14
- 428307; W27393; Hs.183648; protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1; SAM,SH3,HS1_rep; 4.14
- 442434; AA995787; Hs.129583; ESTs; IRK; none; 4.13
- 438361; AA805666; Hs.146217; Homo sapiens cDNA: FLJ23077 fs, clone LNG05840; pkinase, pkinase_C; none; 4.13
- 445580; AF167572; Hs.12912; skk1 (S. pombe) homolog; none; SS=M; 4.13
- 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehand,kazal,arf,res,7tm_1; TM=M; 4.13
- 400252; ; NM_004651; Homo sapiens ubiquitin specific protease 11 (USP11), mRNA substrate 1 (PTPNS1), mRNA; UCH-1,UCH-2; TM=M; 4.13
- 446641; AL049229; Hs.15787; Homo sapiens mRNA; cDNA DKFZp564O1016 (from clone DKFZp564O1016); none, pkinase, PBD; 4.13
- 400209; ; NM_001666; Homo sapiens Rho GTPase activating protein 4 (ARHGAP4), mRNA. VERSION NM_006083.2 G; FCH, RhoGAP, SH3; TM=M; 4.13
- 429012; AW629596; Hs.194726; BCL2-associated athanogene 4; Sm, BAG; SS=M; 4.13
- 411826; AW947946; Hs.26705; CGI-121 protein; none, DSPc; 4.13
- 423189; M59371; Hs.171595; EphA2; fn3, pkinase, SAME, EPH_ibd; TM=Y; SS=M; 4.12
- 413934; U03056; Hs.75619; hyaluronoglucosaminidase 1; Integrin_B, Glyco_hydro_56; SS=M; 4.12
- 414874; D26351; Hs.77515; inositol 1,4,5-trisphosphate receptor, type 3; Ion_trans, MIR, RYDR, JTPR; TM=Y; 4.12
- 432047; NM_016247; Hs.272380; interphotoreceptor matrix proteoglycan 200; EGF, SEA; TM=Y; SS=M; 4.12
- 451820; AW058357; Hs.199248; ESTs; 7tm_1; TM=Y; SS=M; 4.12
- 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; zf-C2H2, BTB, K_letra, WD40, Syntaxin; 4.12
- 424539; L02911; Hs.150402; Activin A receptor, type I (ACVR1) (ALK-2); pkinase, Activin_rec; TM=M; SS=M; 4.12
- 405110; ; C7000199; g12643950[sp]Q9Y6T7[KDGB_HUMAN DIACYLGLYCEROL KINASE. BETA (DGLYCERIDE KINASE ; none, none; 4.12
- 441026; AW179058; Hs.99858; ribosomal protein L7a; pkinase, LRR, LRRCT, Ribosomal_L7a; none; 4.11
- 434142; A1696513; Hs.108705; protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), beta isoform; HEAT, Vitellagenin_N, HEAT_PBS; SS=M; 4.11
- 450505; NM_004572; Hs.25051; plakophilin 2; Armadillo_seg; TM=M; 4.11
- 459601; AL044470; Hs.270604; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none, SH3, PGAM, UBA; 4.10
- 417300; A1765227; Hs.55610; solute carrier family 30 (zinc transporter), member 1; Cation_efflux; TM=Y; SS=M; 4.10
- 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (from clone DKFZp564N0763); none, spectrin, SH3, PH, CH; 4.10
- 416239; AL038450; Hs.48948; ESTs; E1-E2, ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; none; 4.10
- 429311; AF080157; Hs.198998; conserved helix-loop-helix ubiquitous kinase; pkinase; none; 4.10
- 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); Exo_endo_phos, Atraphin-1, BNR, Kelch; TM=M; 4.10
- 418420; AW604405; Hs.324874; hypothetical protein MGC3079; Phosphodiesterase; TM=Y; 4.10
- 434396; AA632270; Hs.162851; Homo sapiens cDNA FLJ14317 fs, clone PLACE3000401; pkinase; none; 4.10
- 454438; AA224053; Hs.172405; cell division cycle 27; SPRY, 7tm_3, ANF_receptor; 4.10
- 439578; AW263124; Hs.315111; nuclear receptor co-repressor/HDAC3 complex subunit; WD40; TM=M; 4.10
- 451995; A1827431; Hs.224645; ESTs, Weakly similar to IF16_HUMAN GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 [H.sapiens]; none, PAAD, DAPIN, HIN; 4.10
- 420340; NM_000734; Hs.97087; CD32 antigen, zeta polypeptide (T13 complex); ITAM; TM=M; SS=M; 4.10
- 442942; AW167087; Hs.131562; ESTs; pkinase; none; 4.09
- 428187; A1687303; Hs.285529; G protein-coupled receptor 49; 7tm_1; none; 4.09
- 418838; AW385224; Hs.35198; ectonucleotide pyrophosphatase/phosphodiesterase 5 (putative function); Phosphodiesterase; TM=Y; SS=M; 4.09
- 416445; AL043004; Hs.79337; KIAA0135 protein; pkinase, PAS; TM=M; 4.08
- 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2; pkinase; TM=M; 4.08
- 403608; ; C3001199; g17494834[pir]T15308 hypothetical protein B0286.2 - Caenorhabditis elegans; 41; 7tm_1, 7tm_2, GPS, WIF; TM=Y; SS=M; 4.08
- 427177; AB006537; Hs.173880; interleukin 1 receptor accessory protein; Ig, TIR; TM=Y; SS=M; 4.08
- 401241; AB028989; ; mitogen-activated protein kinase 8 interacting protein 3; Cys_knot, TGF-beta, vwa, vwc, vwd, TIL, DUF139; SS=M; 4.07
- 444805; AB007899; Hs.12017; homolog of yeast ubiquitin-protein ligase Rsp5; potential epithelial sodium channel regulator; WW, HECT, RNA_pol_A; none; 4.07
- 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 4.06
- 426006; R49031; Hs.22627; ESTs; pkinase, TBC; 4.06
- 434521; NM_002267; Hs.3886; karyopherin alpha 3 (importin alpha 4); Armadillo_seg, IBB; TM=M; 4.06
- 408761; AA057264; Hs.238936; ESTs, Weakly similar to (define not available 7496841) [C.elegans]; 7tm_1; none; 4.05
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD, DAPIN, HIN; SS=M; 4.05
- 413109; AW389845; Hs.110855; ESTs; PHO4; none; 4.05
- 426457; AW894667; Hs.169965; chimerin (chimaerin) 1; DAG_PE-bind, RhoGAP, SH2; TM=M; 4.05
- 435730; AB020635; Hs.4984; KIAA0828 protein; AdoHcyase, TrkA-N, 2-Hacid_DH_C; TM=M; 4.04
- 429747; AB17507; Hs.2490; caspase 1, apoptosis-related cysteine protease (interleukin 1, beta, convertase); CARD, ICE_p10, ICE_p20; SS=M; 4.04
- 444378; R41339; Hs.12569; ESTs; Ig, pkinase, LRR, LRRNT, LRRCT; none; 4.04
- 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; none; TM=Y; SS=M; 4.04
- 427359; AW020782; Hs.79881; Homo sapiens cDNA: FLJ23006 fs, clone LNG00414; 7tm_1; none; 4.04
- 413095; AA494359; Hs.30715; potassium voltage-gated channel, Isk-related family, member 3; none, START; 4.04
- 418540; AF121597; Hs.90877; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ank, CAP_GLY, 7tm_1; 4.03
- 442007; AA301116; Hs.142838; nucleolar phosphoprotein Nopp34; nm, IRK; SS=M; 4.02
- 448659; AF191838; Hs.21712; TANK-binding kinase 1; pkinase; TM=M; 4.02
- 412935; BE267045; Hs.75064; tubulin-specific chaperone c; none; 4.02
- 414844; AA296874; Hs.77494; deoxyguanosine kinase; dNK; 4.02
- 445817; NM_003642; Hs.13340; histone acetyltransferase 1; none; TM=M; 4.02
- 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interacting); SH3, Jg, pkinase, PH, spectrin, RhoGEF; TM=M; 4.02
- 420676; AJ434780; Hs.4248; vav 2 oncogene; RhoGEF, PH, CH, SH2, SH3, DAG_PE-bind; none; 4.02
- 405102; ; C15001220; g14469558[gb]AAD21311.1 [AF126008] breast cancer nuclear receptor-binding aux; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 4.02
- 439964; AJ732902; Hs.124652; Homo sapiens cDNA FLJ12376 fs, clone MAMMA1002494; pkinase; none; 4.01
- 429680; AL035754; Hs.2474; toll-like receptor 1; LRR, LRRCT, TIR; TM=M; SS=M; 4.01
- 453891; AB037751; Hs.36353; Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 1035904; none; none; 4.01
- 426535; AU077012; Hs.288582; ESTs, Weakly similar to ubiquitous TPR motif, Y isoform [H.sapiens]; Kunitz_BPTI, Kunitz_BPTI, 7tm_2, HRM; 3.99
- 424232; AB015982; Hs.143460; protein kinase C, nu; pkinase, DAG_PE-bind, PH; TM=M; 3.99
- 408308; AL033377; Hs.44197; hypothetical protein DKFZp564D0462; none; none; 3.98
- 449517; AW500106; Hs.23643; serine/threonine protein kinase MASK; pkinase; TM=M; 3.98
- 404185; ; Target Exon; sugar_tr; TM=Y; SS=M; 3.98
- 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; none; TM=M; 3.98
- 429638; A1916662; Hs.211577; kinesin 1 (kinesin receptor); bZIP, Tropomyosin, spectrin, LBP, BPL, CETP, B56, M; TM=Y; SS=M; 3.97
- 417386; AL037228; Hs.82043; D123 gene product; NUDIX, secY, E1, dehydrog, transket_pyr; TM=Y; SS=M; 3.97
- 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; MORN, sugar_tr; TM=Y; SS=M; 3.96
- 417183; B52089; Hs.172717; ESTs; pkinase, LRRCT, Ig, LRR, LRRNT; none; 3.95
- 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; none; TM=M; 3.94
- 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank, pkinase; TM=M; 3.94
- 422610; AF153820; Hs.1547; potassium inwardly-rectifying channel, subfamily J, member 2; IRK; TM=Y; 3.94

- 450746; D82673; Hs.278589; general transcription factor II, ϵ ; none; SH3; PX; 3.94
- 418516; NM_005218; Hs.857011; phosphoinositide-3-kinase, catalytic, alpha polypeptide; PI3_P14_kinase, PI3Ka, PI3K_C2, PI3K_rbd, PI3K_p85B; none; 3.94
- 414217; AI309298; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone LNG09846; none; NA; NA; 3.93
- 416537; T99086; Hs.144904; nuclear receptor co-repressor 1; myb_DNA-binding, RNA_pol_A; none; 3.93
- 5 450747; AI064821; Hs.318535; ESTs, Highly similar to 1818357A EWS gene [H.sapiens]; nm, zf-RanBP, GAS2; 3.93
- 444825; AW167613; ; mitogen-activated protein kinase kinase 8; pkinase; TM=M; 3.93
- 408354; AI382803; Hs.159235; ESTs; none; none; 3.93
- 453945; NM_005171; Hs.36908; activating transcription factor 1; rm, zf-RanBP, pkinase, GST_C, Ets, SAM_PNT, ABC2_membrane, myosin_head, IQ, Myosin_N, bZIP, zf-C2H2, PHD, BTB, TFIIS, AT_hook, SAM; TM=M; 3.93
- 10 428532; AF157326; Hs.184786; TBP-interacting protein; Armadillo_seg, VHS, HEAT; TM=M; 3.92
- 413967; AW204431; Hs.117853; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Armadillo_seg, IBB, PHD, DDT; none; 3.91
- 415906; AI751357; Hs.288741; Homo sapiens cDNA: FLJ22256 fis, clone HRC02860; Ephrin; none; 3.91
- 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none; none; 3.91
- 440255; AI932285; Hs.160569; ESTs; none; pkinase; 3.90
- 15 421077; AK000061; Hs.101590; hypothetical protein; ank, pkinase, death, SPRY, SAP, Ribosomal_L24e, SRP54, dDENN, DENN, uDENN; TM=M; 3.90
- 433211; H11850; Hs.12808; MARK; pkinase, UBA, KA1, SS=M; 3.90
- 433233; AB040927; Hs.301804; KIAA1494 protein; SH3, zf-C3HC4; TM=M; 3.90
- 419609; U46415; Hs.270379; gb:HSU46415 Human pancreatic cancer cell line Patu 89881 Homo sapiens cDNA clone xs476, mRNA sequence; PWWP; none; 3.90
- 433198; AA992841; Hs.27263; KIAA1458 protein; none; none; 3.89
- 20 407721; Y12735; Hs.38018; dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 3; pkinase; TM=M; 3.89
- 427657; AV652249; Hs.180107; polymerase (DNA directed), beta; none; TM=M; 3.89
- 453035; AW581943; Hs.334; Rho guanine nucleotide exchange factor (GEF) 5; none; none; 3.89
- 446329; NM_013272; Hs.14805; solute carrier family 21 (organic anion transporter), member 11; kazal, OATP_N, OATP_C; TM=Y; SS=M; 3.89
- 25 429922; Z97630; Hs.226117; H1 histone family, member 0; linker histone; TM=M; 3.88
- 432074; AA525248; Hs.149723; ESTs; Y_phosphatase; none; 3.88
- 435143; R12375; Hs.194600; ESTs; SH3, Ig, pkinase, PH, spectrin, RhoGEF; none; 3.87
- 423198; M81933; Hs.1634; cell division cycle 25A; Rhodanese; none; 3.87
- 428474; AB023182; Hs.184523; KIAA0965 protein; pkinase; TM=M; 3.87
- 30 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT2RP2002066, highly similar to Rattus norvegicus transmembrane receptor Unc5H2 mRNA; death, ZU5; SS=M; 3.86
- 415457; AW081710; Hs.7369; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; MORN, sugar_tr; TM=Y; SS=M; 3.86
- 447061; D86964; Hs.17211; dedicator of cyto-kinesis 2; SH3; TM=M; 3.86
- 35 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC, PAS; TM=M; 3.86
- 451961; NM_003800; Hs.27345; RNA guanylyltransferase and 5-phosphatase; mRNA_cap_enzyme, DSPC, DNA_ligase, mRNA_cap_C; TM=M; 3.86
- 417874; BE616160; Hs.82829; protein tyrosine phosphatase, non-receptor type 2; Y_phosphatase; TM=Y; 3.86
- 446874; AW968304; Hs.56156; ESTs; none; RGS; 3.85
- 418630; AI351311; Hs.251946; poly(A)-binding protein, cytoplasmic 1-like; pkinase; none; 3.85
- 416140; AI918035; Hs.301198; roundabout (axon guidance receptor, Drosophila) homolog 1; none; none; 3.85
- 40 425474; Z48054; Hs.158084; peroxisome receptor 1; TPR; TM=M; 3.85
- 413073; AL038165; Hs.75187; translocase of outer mitochondrial membrane 20 (yeast) homolog; MAS20, zf-A20, VPS9; TM=M; SS=M; 3.85
- 411770; NM_014278; Hs.71992; heat shock protein (hsp110 family); HSP70; TM=M; 3.84
- 428782; X12830; Hs.193400; interleukin 6 receptor; fn3, ig; TM=Y; SS=M; 3.84
- 45 450684; AA872605; Hs.25333; interleukin 1 receptor, type II; ig; TM=Y; SS=M; 3.84
- 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine protease; CARD, ICE_p10, ICE_p20; SS=M; 3.83
- 440332; AI218517; Hs.188051; ESTs; fn3, pkinase, SAM, EPH_rbd; none; 3.83
- 445803; AV655264; Hs.4283; ESTs; pkinase, RGS, PH, myosin_head, Myosin_tail; 3.83
- 435905; AW997484; Hs.5003; KIAA0456 protein; SH3, RhoGAP, FCH; TM=M; 3.83
- 50 414991; C17898; ; gb:C17898 Human placenta cDNA (TFUJ1wara) Homo sapiens cDNA clone GEN-554E10 5', mRNA sequence; Zip; none; 3.83
- 423067; AA321355; Hs.285401; colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage); fn3; TM=Y; SS=M; 3.82
- 419088; AI538323; Hs.52620; integrin, beta 8; integrin_B; none; 3.82
- 411704; AI499220; Hs.71573; hypothetical protein FLJ10074; pkinase; TM=M; 3.82
- 458346; AW510557; Hs.258016; EST; none; TM=M; 3.82
- 445330; R52656; Hs.21691; ESTs; 7tm_1; none; 3.82
- 55 451452; BE560065; Hs.26433; dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminylphosphotransferase 1 (GlcNAc-1-P transferase); Glycos_transf_4; TM=Y; SS=M; 3.81
- 405545; ; Target Exon; ABC_tran, SRP54, ABC_membrane; TM=Y; SS=M; 3.81
- 448165; NM_005591; Hs.20555; meiotic recombination (S. cerevisiae) 11 homolog B; Metallophos, Ribosomal_L15e; SS=M; 3.81
- 60 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig; TM=Y; SS=M; 3.80
- 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate transporter), member 1; PHO4, UM; TM=M; 3.80
- 421684; BE281591; Hs.106768; hypothetical protein FLJ10511; Armadillo_seg; SS=M; 3.80
- 438581; AW977766; Hs.292133; ESTs, Moderately similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase, RIO1; none; 3.79
- 439199; R40373; Hs.26299; ESTs; ion_trans; none; 3.78
- 65 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; TNFR_c6; TM=Y; SS=M; 3.78
- 417691; AU076610; Hs.82399; low density lipoprotein receptor defect C complementing; none; SS=M; 3.78
- 430355; NM_006219; Hs.239818; phosphoinositide-3-kinase, catalytic, beta polypeptide; PI3_P14_kinase, PI3Ka, PI3K_C2, PI3K_rbd, PI3K_p85B; TM=M; 3.78
- 448119; H38587; Hs.346509; dedicator of cyto-kinesis 1; none; TM=Y; 3.78
- 442013; AA506476; Hs.10600; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG Islands. Contains the NIFS gene for cysteine desulfurase, two genes for novel proteins and the gene for the splicing factor CC1.3 with a second isoform (CC1.; none; none; 3.77
- 70 425481; AW978162; Hs.18571; ESTs; none; Oxysterol_BP; 3.77
- 411411; AA345241; Hs.55950; ESTs, Weakly similar to KIAA1330 protein [H.sapiens]; RNA_pol_A, ig, MHCK_EF2_kinase; SS=M; 3.77
- 426866; U02330; Hs.172816; neuregulin 1; Peptidase_M49, EGF, Ig, Neuregulin; TM=M; 3.77
- 430396; D49742; Hs.241363; hyaluronan-binding protein 2; ank, death, ZU5, EGF, kringle, trypsin, Nebulin, LIM; SS=M; 3.77
- 75 434398; AA121098; Hs.3838; serum-inducible kinase; pkinase, POLO_box; TM=M; 3.77
- 415485; AW272990; Hs.18571; ESTs; none; Oxysterol_BP; 3.76
- 453226; AA641926; Hs.61712; pyruvate dehydrogenase kinase, isoenzyme 1; HATPase_c, none; 3.76
- 418758; AW959311; Hs.172012; hypothetical protein DKFZp434J037; pkinase, RIO1; TM=M; 3.76
- 424842; AA034127; Hs.153487; signal transducing adaptor molecule (SH3 domain and ITAM motif) 1; SH3, VHS, LIM; TM=M; 3.75
- 80 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; 3.75
- 419952; AK000867; Hs.93872; KIAA1682 protein; none; TM=M; 3.75
- 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase, UBA, KA1; TM=M; 3.75
- 431696; AA259068; Hs.267819; protein phosphatase 1, regulatory (inhibitor) subunit 2; none; SS=M; 3.75

- 444184; T87841; Hs.282990; Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1. Contains part of a gene for a novel protein similar to membrane transport proteins, the 5' end of a novel gene, ESTs, STSs, GSSs and three CpG islands; pkinase, RIO1, APH, KOW; TM=M; 3.75
- 405411; ; ENSP00000252213; SODIUM BICARBONATE COTRANSPORTER; none; TM=Y; SS=M; 3.75
- 405602; ; Target Exon; pkinase; SS=M; 3.75
- 429355; AW973253; Hs.292689; ESTs; pkinase, bZIP, Armadillo_seg; none; 3.75
- 430153; AW968126; Hs.336679; ESTs; pkinase; none; 3.74
- 414180; AI863304; Hs.120905; Homo sapiens cDNA FLJ11448 fis, clone HEMBA1001391; PI3_Pi4_kinase, PI3Ka, PI3K_C2, PI3K_rbd, PI3K_p85B; none; 3.74
- 432236; AA531132; ; gb:ncj47h06.s1 NCL_CGAP_P9 Homo sapiens cDNA clone, mRNA sequence; pkinase; none; 3.74
- 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp761G18121 (from clone DKFZp761G18121); complete cds; none, spectrin, SH3, PH, CH; 3.74
- 426485; NM_006207; Hs.170004; platelet-derived growth factor receptor-like; ig; SS=M; 3.74
- 408414; AI114688; Hs.17998; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; fn3, ig; TM=Y; SS=M; 3.73
- 409793; AI825463; Hs.147996; protein kinase, X-linked; pkinase, pkinase_C; TM=M; 3.73
- 412456; T32689; Hs.7859; ESTs; BAG; none; 3.73
- 407894; AJ278313; Hs.41143; phosphoinositide-specific phospholipase C-beta 1; C2, PI-PLC-Y, PI-PLC-X; TM=M; 3.73
- 442229; AI885776; Hs.8164; Multibrey nanism; MATH, DENN, GRAM, zf-B_box, dDENN, uDENN; SS=M; 3.73
- 450151; AI088196; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig, pkinase; none; 3.72
- 408331; NM_007240; Hs.44229; dual specificity phosphatase 12; DSPC; TM=M; 3.72
- 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin, ADF; SS=M; 3.72
- 403391; ; C3001164; gij1730196[sp50573]GAR3_RAT GAMMA-AMINOBUTYRIC-ACID RECEPTOR RHO-3 SUBUNIT PRE; none; TM=Y; 3.72
- 417527; AA203524; ; gb:zx56e10.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone 5', mRNA sequence; SH3; SS=M; 3.71
- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase); pkinase; TM=M; 3.71
- 428180; AI129767; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; G-alpha, arf; TM=M; 3.71
- 422127; AW504286; Hs.112049; SET binding factor 1; dDENN, DENN, GRAM, PH; SS=M; 3.70
- 430570; AI17881; Hs.292464; ESTs; 7tm_2, Fz, Frizzled; none; 3.70
- 452561; AI692181; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; 3.69
- 432336; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm, pkinase; TM=M; 3.69
- 419945; AW290975; Hs.118923; ESTs; SH3, PDZ, Guanylate_kin, transferrin; 3.69
- 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3, PDZ, Guanylate_kin; TM=M; 3.68
- 436534; AA721628; Hs.191958; immunoglobulin superfamily receptor translocation associated 2; ig; TM=Y; SS=M; 3.68
- 407202; NS8172; Hs.109370; ESTs; F5_F8_type_C, pkinase, Ets; none; 3.67
- 420297; AI628272; Hs.88323; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; pkinase, TUDOR; none; 3.67
- 417863; AB000450; Hs.82771; vaccinia related kinase 2; pkinase; TM=M; 3.67
- 425304; AA463844; Hs.31339; fibroblast growth factor 11; FGF, Neur_chan_LBD, Neur_chan_memb; none; 3.67
- 418318; U47732; Hs.84072; transmembrane 4 superfamily member 3; transmembrane4; TM=Y; SS=M; 3.67
- 419511; AA429750; Hs.75113; general transcription factor IIIA; Glypican; none; 3.66
- 424315; AW614850; Hs.193384; putative 28 kDa protein; none; none; 3.66
- 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; pkinase; TM=M; 3.66
- 425838; NM_014071; Hs.159613; nuclear receptor coactivator RAP250; peroxisome proliferator-activated receptor interacting protein; thyroid hormone receptor binding protein; none; TM=M; 3.65
- 446983; AA157484; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlink, TIL; TM=Y; SS=M; 3.65
- 434350; AL042940; Hs.93872; KIAA1682 protein; none; none; 3.65
- 457317; AA683016; Hs.12210; hypothetical protein FLJ13732 similar to tensin; SH2; TM=M; 3.65
- 434416; AA805903; Hs.59498; cell division cycle 2-like 5 (cholinesterase-related cell division controller); pkinase; none; 3.65
- 410174; AA306007; Hs.59461; DKFZP434C245 protein; none, DSPC; 3.65
- 423598; BE247600; Hs.155538; ESTs; 7tm_1; TM=Y; SS=M; 3.65
- 440861; BE244115; Hs.7482; KIAA0682 gene product; rrm, Guanylate_kin; TM=M; 3.64
- 454954; AW993013; Hs.49169; KIAA1634 protein; TPR, PDZ, WW, Guanylate_kin; TM=M; 3.64
- 430250; NM_016929; Hs.283021; chloride intracellular channel 5; none; TM=M; 3.64
- 450587; AI828854; Hs.258538; striatin, calmodulin-binding protein; pkinase, WD40; TM=Y; 3.64
- 424893; AW295112; Hs.153648; Homo sapiens cDNA FLJ13303 fis, clone OVARC1001372, highly similar to Homo sapiens liprin-alpha4 mRNA; SAM; SS=M; 3.64
- 425645; AA361027; ; gb:EST70242 T-cell lymphoma Homo sapiens cDNA 5' end, mRNA sequence; HMG_box, DNA_mis_repair, HATPase_c; none; 3.64
- 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, Integrin_B; SS=M; 3.63
- 451292; AB037718; Hs.26204; KIAA1295 protein; SH3; TM=M; 3.63
- 412314; AA825247; Hs.250899; heat shock factor binding protein 1; 7tm_1; TM=Y; SS=M; 3.63
- 418303; AA215701; Hs.186541; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; eIF5, eIF2B, W2, pkinase, UBA, KA1; 3.63
- 452716; AI914925; Hs.222420; ESTs; SH2, STAT, STAT_bind, STAT_prot; none; 3.63
- 403869; ; NM_004520; Homo sapiens kinesin heavy chain member 2 (KIF2), mRNA member 3 (KCNQ3), mRNA; kinesin; TM=M; 3.63
- 450377; AB033091; Hs.74313; KIAA1265 protein; Zip; TM=M; SS=M; 3.63
- 417793; AW405434; Hs.82575; small nuclear ribonucleoprotein polypeptide B; rrm; TM=M; 3.63
- 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD36; TM=Y; SS=M; 3.63
- 429554; NM_012275; Hs.207224; interleukin 1, delta; IL1; TM=M; 3.63
- 417871; AA521368; Hs.24252; ESTs; IBB, Armadillo_seg; none; 3.62
- 437672; AW748265; Hs.5741; flavohemoglobin b57; heme_1, NAD_binding, lipoxygenase, FAD_binding_6; TM=M; 3.62
- 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; lipoxygenase, PLAT; none; 3.62
- 447217; BE465754; Hs.17778; neuropilin 2; CUB, MAM, F5_F8_type_C; TM=M; SS=M; 3.61
- 407961; AW672939; Hs.41694; origin recognition complex, subunit 2 (yeast homolog)-like; none, pkinase, pro_isomerase; 3.61
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1; SH2, SH3, pkinase; SS=M; 3.61
- 455608; BE011437; ; gb:CM4-BN0220-080500-170-f03 BN0220 Homo sapiens cDNA, mRNA sequence; none, CDK5_activator; 3.61
- 407748; AL079409; Hs.38176; KIAA0606 protein; SCN Circadian Oscillatory Protein (SCOP); PP2C, LRR, PH; TM=M; 3.60
- 421474; U76362; Hs.104637; solute carrier family 1 (glutamate transporter), member 7; SDF; TM=Y; SS=M; 3.60
- 449987; AW079749; Hs.184719; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ABC_tran, ABC_membrane, ion_trans; 3.60
- 403142; ; NM_002706; Homo sapiens protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform (PPM1B), mRNA; PP2C; TM=M; 3.60
- 400844; ; NM_003105; Homo sapiens sortilin-related receptor, (LDLR class) A repeats-containing (SORL1), mRNA; EGF, fn3, Ild_recept_a, Ild_recept_b, granulin, BNR; TM=Y; SS=M; 3.59
- 450152; AI138635; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA sequence; ig, pkinase; none; 3.59
- 429782; NM_005754; Hs.220689; Ras-GTPase-activating protein SH3-domain-binding protein; rrm, NTF2; TM=M; 3.59
- 436469; AK001455; Hs.5198; Down syndrome critical region gene 2; none; SS=M; 3.59
- 437400; AB011542; Hs.5599; EGF-like-domain, multiple 5; TNFR_c6, laminin_EGF; TM=Y; 3.58
- 426797; AW936258; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_B, SH3; 3.58
- 431170; AW971246; Hs.291022; ESTs; LRR, CARD; none; 3.58
- 434542; AA769310; Hs.61260; hypothetical protein FLJ13164; PH, Oxysterol_BP; TM=M; SS=M; 3.58

- 420181; AI380089; Hs.158951; ESTs; none; ig, pkinase, LRR, LRRCT; 3.57
 450572; AJ700863; Hs.202494; Homo sapiens cDNA FLJ13245 fis, clone OVARC1000681; Na_sulph_symp; none; 3.57
 433618; AA602539; Hs.345494; ESTs; G-alpha_A_deaminase; 3.57
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; pkinase; none; 3.57
 418512; AW498974; ; diacylglycerol kinase, zeta (104kD); ras; none; 3.57
 451752; AB032997; Hs.26966; KIAA1171 protein; ATP-synt_C, TBC; TM=Y; SS=M; 3.57
 417129; AI381800; Hs.300684; calcitonin gene-related peptide-receptor component protein; none; none; 3.57
 449474; AA019344; Hs.20555; ubiquitin-activating enzyme E1 (A1S9T and BN75 temperature sensitivity complementing); ThiF, UBACT, pkinase, UCH-2, UCH-1, rm, zf-C2H2, zf-RanBP, G-patch; 3.57
 412124; H43376; Hs.288550; Homo sapiens cDNA: FLJ23156 fis, clone LNG09509; none; none; 3.56
 435021; AA922192; Hs.54709; ESTs; EPH_rbd, pkinase, fn3, SAM; none; 3.56
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit, alpha type, 4; proteasome; TM=M; 3.56
 437387; AI198874; Hs.28847; AD026 protein; none; 7tm_1, WD40; 3.56
 422583; AA410506; Hs.27973; KIAA0874 protein; ank, G-alpha; TM=M; 3.56
 452102; U04343; Hs.27954; CD86 antigen (CD28 antigen ligand 2, B7-2 antigen); none; TM=Y; SS=M; 3.56
 420112; NM_005109; Hs.95220; oxidative-stress responsive 1; pkinase; TM=M; 3.55
 437639; AA827712; Hs.291880; ESTs; SH3; none; 3.55
 457500; NM_002759; Hs.274382; protein kinase, interferon-inducible double stranded RNA dependent; dsrm, pkinase; TM=M; 3.55
 415660; AI909007; Hs.78563; ubiquitin-conjugating enzyme E2G 1 (homologous to C. elegans UBC7); UQ_con; TM=M; 3.55
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase, PBD; TM=M; 3.55
 428727; AF078847; Hs.191356; general transcription factor IIF, polypeptide 2 (44kD subunit); PHO4, LIM; TM=M; 3.55
 411190; AA306342; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HRI; TM=M; 3.55
 408683; R58665; Hs.46847; TRAF and TNF receptor-associated protein; Exo_endo_phos; TM=M; 3.55
 412350; AI659306; Hs.73826; protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte); Y_phosphatase, Band_41, PDZ; TM=M; 3.55
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none; TM=Y; SS=M; 3.55
 427283; AL119796; Hs.174185; ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin); Sulfatase, Somatomedin_B, Phosphodiesterase, Endonuclease; TM=M; SS=Y; 3.55
 414888; AL039185; Hs.77558; thyroid hormone receptor interactor 7; HMG14_17; none; 3.55
 424848; AJ263231; Hs.327090; EST; SH3, PDZ, Guanylate_kin; none; 3.54
 402704; ; ; C1001099; ggi605896[ret]NP_009101.1 testis-specific protein kinase 2 (Homo sapiens) ggi4; none; none; 3.54
 444099; DB7432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; aa_permeases; TM=Y; SS=M; 3.54
 429687; AI675749; Hs.211608; nucleoporin 153kD; zf-RanBP, integrin_B; TM=M; 3.53
 413879; AA132961; Hs.212533; Homo sapiens cDNA: FLJ22572 fis, clone HSI02313; none; none; 3.53
 431045; AW986560; Hs.301957; nudix (nucleoside diphosphate linked moiety X)-type motif 5; NUDIX, secY, E1_dehydrog, transkat_pyr; TM=Y; SS=M; 3.53
 423855; AA331761; Hs.254859; ESTs; none, pkinase, UQ_con, vwa, FG-GAP, integrin_A; 3.53
 440682; AW362152; Hs.27181; nuclear receptor binding factor-2 cyclin, bZIP; TM=M; 3.52
 410686; AI733735; Hs.114905; IRE1, S. cerevisiae, homolog of; pkinase, Bacterial_POQ; TM=M; SS=M; 3.52
 449810; AB006881; Hs.23994; activin A receptor, type IIB; pkinase, Activin_recpt; TM=Y; SS=M; 3.52
 418755; Y14443; Hs.88219; zinc finger protein 200; zf-C2H2, zf-BED; TM=M; 3.52
 448804; AW512213; Hs.342849; ADP-ribosylation factor-like 5; arf, Ca_channel_B, SH3; 3.52
 438507; AA809052; Hs.182018; ESTs; none; none; 3.52
 456559; AI336273; Hs.102548; glucocorticoid receptor DNA binding factor 1; none, PAS; 3.51
 410054; AL120050; Hs.58220; Homo sapiens cDNA: FLJ23005 fis, clone LNG00396, highly similar to AF055023 Homo sapiens clone 24723 mRNA sequence; RasGAP, adenylatekinase; 3.51
 422321; AA906427; Hs.181035; hypothetical protein MGC11296; none; TM=M; 3.51
 445701; AF055581; Hs.13131; lymphocyte adaptor protein; SH2, PH; TM=M; 3.50
 407393; AB038237; ; gb|Homo sapiens mRNA for G protein-coupled receptor C5L2, complete cds.; 7tm_1; TM=Y; SS=M; 3.50
 443303; U67319; Hs.9216; caspase 7, apoptosis-related cysteine protease; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 3.50
 420673; AB008112; Hs.99847; peroxisome biogenesis factor 1; AAA, APS_kinase; TM=M; SS=M; 3.49
 424663; NM_002231; Hs.151544; SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome); SH2; TM=M; 3.49
 429327; AA283981; Hs.199248; prostaglandin E receptor 4 (subtype EP4); 7tm_1; TM=Y; SS=M; 3.49
 400178; ; ; Eos Control; none, Somatomedin_B; 3.49
 439549; AW937885; Hs.137314; ESTs; SH2; none; 3.49
 436345; AA873008; Hs.121572; ESTs; CARD, BIR, zf-C3HC4, CARD, BIR, zf-C3HC4; 3.49
 427658; H61387; Hs.30868; nogo receptor; LRR, LRRNT, LRRCT; SS=M; 3.48
 402833; ; ; C1002508; ggi6891937[emb]CAB65797.1 (AL096770) bA150A6.2 (novel 7 transmembrane receptor; none; none; 3.48
 442363; AI337304; Hs.23120; PIST; fn3, pkinase, PDZ, DUF139; TM=Y; SS=M; 3.48
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; none; TM=M; 3.47
 417971; Y08991; Hs.83050; phospholipid-3-kinase, regulatory subunit 4, p150; pkinase, WD40, HEAT; SS=M; 3.47
 432169; Y00971; Hs.2910; phosphoribosyl pyrophosphate synthetase 2; Pribosyltran; 3.47
 447425; AI963747; Hs.18573; acylphosphatase 1, erythrocyte (common) type; Acylphosphatase; SS=M; 3.47
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2, SH3; TM=M; SS=M; 3.46
 401851; ; ; NM_002401*Homo sapiens mitogen-activated protein kinase kinase kinase 3 (MAP3K3), mRNA; pkinase; SS=M; 3.46
 407877; AW016811; Hs.234478; Homo sapiens cDNA: FLJ22648 fis, clone HSI07329; pkinase, pkinase_C; none; 3.45
 432279; N95104; Hs.274260; ATP-binding cassette, sub-family C (CFTR/MRP), member 6; ABC_tran, ABC_membrane; none; 3.45
 437103; AW139408; Hs.152940; ESTs; Choline_kinase; none; 3.45
 420338; AA825595; Hs.88269; Homo sapiens, clone MGC:17339, mRNA, complete cds; 7tm_1; TM=Y; SS=M; 3.44
 422209; AF005210; Hs.113222; chemokine (C-C motif) receptor 8; 7tm_1, 7tm_2; TM=Y; SS=M; 3.44
 410781; AI375672; Hs.165028; ESTs; pkinase, laminin_N1, laminin_N2, EGF, cyclin, F-box, cyclin_C, serpin, ATP-synt_C; 3.44
 437296; AA350994; Hs.20281; KIAA1700; Rhodanese, DSPc; TM=M; 3.43
 419855; AI935182; Hs.144139; ESTs; zf-C3HC4, UBA, Cbl_N, Cbl_N2, Cbl_N3, zf-C3HC4, UBA, Cbl_N, Cbl_N2, Cbl_N3; 3.43
 433336; AF017986; Hs.31386; secreted frizzled-related protein 2; Fz, NTR; SS=M; 3.43
 428483; AI908539; Hs.184592; KIAA0344 gene product; none; none; 3.43
 445119; AF035121; Hs.12337; kinase insert domain receptor (a type III receptor tyrosine kinase); ig, pkinase; TM=Y; SS=M; 3.42
 454468; AI590319; Hs.19122; eukaryotic translation initiation factor 4E-like 3; none, Neur_chan_LBD, Neur_chan_membr, IF4E; 3.42
 410366; W26187; Hs.3327; Homo sapiens cDNA: FLJ22219 fis, clone HRC01637; pkinase, Guanylate_kin, PDZ, SH3, L27; none; 3.42
 422907; AI879263; Hs.77273; Human glucose transporter pseudogene; none; none; 3.42
 449816; AI701457; Hs.38694; ESTs; SET, BAH, PKPK_C; 3.42
 440074; AA863045; Hs.10669; ESTs; Weakly similar to T00050 hypothetical protein KIAA0400 [H.sapiens]; SH3, ank, tubulin-binding, ArfGap, PH; TM=M; SS=M; 3.42
 425475; W56339; Hs.107057; ESTs; pkinase; none; 3.42
 401242; AB028989; ; mitogen-activated protein kinase 6 interacting protein 3; Cys_knot, TGF-beta, vwa, vwc, vwd, TIL, DUF139; SS=M; 3.41
 429276; AF056085; Hs.198612; G protein-coupled receptor 51; 7tm_3, ANF_receptor, bZIP; TM=Y; 3.41
 445806; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase, type I, 107kD; none; none; 3.41
 410908; AA121686; Hs.10592; ESTs; GTP_EFTU, GTP_EFTU_D3, GTP_EFTU_D2; none; 3.41

- 452960; AK001335; Hs.31137; protein tyrosine phosphatase, receptor type, E; Y_phosphatase:none; 3.40
 447898; AW969638; Hs.112318; 6.2 kd protein; none:none; 3.40
 450402; BE218027; Hs.89969; ESTs; SH3:none; 3.40
 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB:none; 3.40
 5 408546; W49512; Hs.46348; bradykinin receptor B1; 7tm_1;TM=Y;SS=M; 3.40
 410927; T77635; ; gb:yc91h06.r1 Soares infant brain 1N1B Homo sapiens cDNA clone 5', mRNA sequence; none:none; 3.40
 409646; AW161391; Hs.709; deoxycytidine kinase; dNK;SS=M; 3.39
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone COL04162; Sulfate_transp,STAS,HMG_box; 3.39
 449343; A1151418; ; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); none:none; 3.39
 10 450511; R07423; Hs.85092; thyroid hormone receptor interactor 11; Myosin_tail,EGF; 3.39
 414271; AK000275; Hs.75871; protein kinase C binding protein 1; bromodomain,PHD,PWWP,zf-MYND;TM=M; 3.38
 418428; Y12490; Hs.85092; thyroid hormone receptor interactor 11; bZIP,kinesin,GTP_cyclohydrol,M;TM=M; 3.37
 422369; AF005216; Hs.115541; Janus kinase 2 (a protein tyrosine kinase); SH2,pkinase;TM=M; 3.37
 456451; A1761180; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none;TM=M; 3.37
 15 438543; AA810141; Hs.192182; ESTs; SH2,pkinase:none; 3.37
 401943; NM_012434; ; solute carrier family 17 (anion/sugar transporter), member 5; none;TM=M; 3.36
 415276; U88666; Hs.78353; SFRS protein kinase 2; pkinase;TM=M; 3.36
 447881; BE620886; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; pkinase,pkinase; 3.35
 434533; AA639257; Hs.292549; ESTs; SH3,PDZ,Guanylate_kin:none; 3.35
 20 432639; AW973785; ; gb:EST385886 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence; none;JRK; 3.35
 410678; BE540516; Hs.293732; hypothetical protein MGC3195; Armadillo_seg;TM=M;SS=Y; 3.35
 402807; ; ENSP00000235229;SEMB; Integrin_B,Sema,PSI;TM=Y; 3.35
 420189; AW296380; Hs.95821; osteoclast stimulating factor 1; SH3,ank; 3.34
 437389; AL359587; Hs.271586; hypothetical protein DKFZp762M115; secY,E1_dehydrog,transkel_pyr:none; 3.34
 25 453423; NM_002647; Hs.32971; phosphoinositide-3-kinase, class 3; PI3_P14_kinase,PI3Ka,PI3K_C2;TM=M; 3.34
 414270; L20852; Hs.347527; solute carrier family 20 (phosphate transporter), member 2; Enterotoxin_A,PHO4;TM=Y;SS=M; 3.33
 417479; A1057052; ; ESTs, Weakly similar to Z195_HUMAN ZINC FINGER PROTEIN 195 [H.sapiens]; LRR,CARD:none; 3.33
 424946; M64572; Hs.153932; protein tyrosine phosphatase, non-receptor type 3; Band_41,PDZ_Y_phosphatase:none; 3.33
 452681; AF153330; Hs.30246; solute carrier family 19 (thiamine transporter), member 2; Folate_carrier;TM=Y;SS=M; 3.33
 30 426477; AA379464; ; gb:EST92386 Skin tumor I Homo sapiens cDNA 5' end, mRNA sequence; DUF6,MATH,BTB; 3.33
 438283; A1458931; Hs.37282; ESTs; none,transmembrane4; 3.33
 421327; AA837295; Hs.188802; ESTs; none,IMP4_Y_phosphatase; 3.33
 432481; AW451645; Hs.151504; Homo sapiens cDNA FLJ11973 fis, clone HEMBB1001221; laminin_G,Collagen,COLFI,CorA,TSPN:none; 3.33
 452682; AA455193; Hs.9071; progesterone membrane binding protein; homeobox:none; 3.32
 35 428997; AF065391; Hs.194718; zinc finger protein 265; zf-RanBP;TM=M; 3.32
 432211; BE274530; Hs.273333; hypothetical protein FLJ110986; FGGY_C;TM=M; 3.31
 443601; A1078554; Hs.15682; ESTs; ank,pkinase,death,Ribosomal_S14; 3.31
 430597; AF062006; Hs.285529; G protein-coupled receptor 49; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 3.31
 419912; AF249745; Hs.6066; Rho guanine nucleotide exchange factor (GEF) 4; SH3,PH,RhoGEF;TM=M; 3.31
 40 400380; NM_018485; Hs.283079; G protein-coupled receptor C5L2; 7tm_1;TM=Y;SS=M; 3.31
 415983; A1436798; Hs.117078; Homo sapiens cDNA: FLJ23028 fis, clone LNG01852, highly similar to HSU08023 Human cellular proto-oncogene (c-met) mRNA; fn3,jg,pkinase;TM=Y;SS=M; 3.31
 441054; AA913591; Hs.126480; ESTs; none,7tm_1; 3.31
 418342; BE002723; ; leptin receptor; ICE_p20,DED,ICE_p10,ICE_p20,DED; 3.31
 45 446128; AW93779; Hs.113029; ribosomal protein S25; none,7tm_1; 3.31
 425086; AW957571; Hs.12319; Homo sapiens cDNA FLJ12774 fis, clone NT2RP2001663, moderately similar to ENOLASE (EC 4.2.1.11); none,Guanylate_kin,PDZ,SH3; 3.31
 425725; NM_012243; Hs.159322; solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3; DUF6;TM=Y;SS=M; 3.30
 422608; AW160644; Hs.118695; potassium voltage-gated channel, subfamily G, member 1; ion_trans,K_tetra;TM=Y; 3.30
 50 429061; Y14039; Hs.195175; CASP8 and FADD-like apoptosis regulator; ICE_p20,DED;TM=M; 3.30
 433656; AW974941; Hs.292385; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; pkinase,ABC1:none; 3.30
 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic) inhibitor alpha; PKI;SS=M; 3.30
 402603; ; ENSP00000251206; KIAA0778 PROTEIN (FRAGMENT); none;TM=Y; 3.30
 418801; AA228366; Hs.115122; ESTs; Integrin_A,FG-GAP:none; 3.30
 55 400275; ; NM_006513; Homo sapiens seryl-IRNA synthetase (SARS), mRNA (SAM68), mRNA; ; IRNA-syn1_2b,Seryl_IRNA_N;TM=M; 3.29
 440286; U29589; Hs.7138; cholinergic receptor, muscarinic 3; 7tm_1;TM=Y; 3.29
 409101; NM_004297; Hs.50512; guanine nucleotide binding protein (G protein), alpha 14; G-alpha:none; 3.29
 432736; AA788898; Hs.179902; transporter-like protein; none;TM=Y;SS=M; 3.29
 408738; NM_014785; Hs.47313; KIAA0258 gene product; none;TM=M; 3.29
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT2RP3002955; Aa_trans:none; 3.29
 60 405328; ; NM_005391; Homo sapiens pyruvate dehydrogenase kinase, isoenzyme 3 (PDK3), mRNA; HATPase_c;SS=M; 3.28
 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit 6; none:none; 3.28
 408756; AA524743; Hs.44883; ESTs; Armadillo_seg,IBB,DEAD,helicase_C,Sec63,DDT,PHD,bromodomain;TM=M; 3.28
 415474; NM_014252; Hs.78457; solute carrier family 25 (mitochondrial carrier, ornithine transporter) member 15; mito_car;TM=M; 3.28
 417805; U38545; Hs.82587; phosphatidase D1, phosphatidylcholine-specific; PH,PLDc,PX;TM=M; 3.28
 65 410254; BE004131; Hs.318510; Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15; ehfand:none; 3.28
 443968; AA287702; Hs.10031; KIAA0955 protein; CARD;TM=M;SS=M; 3.28
 438899; AF085833; Hs.135624; ESTs; none,PI3_P14_kinase,PI3Ka,PI3K_C2,PI3K_rbd,PI3K_p85B; 3.27
 70 415663; AW286841; Hs.313332; ESTs; UQ_con,Neur_chan_LBD,Neur_chan_memb; 3.27
 414087; W19712; ; gb:cb36d03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 5', mRNA sequence; pkinase:none; 3.27
 442833; AA328153; Hs.88201; ESTs, Weakly similar to A Chain A, Crystal Structure Of The Human Acyl Protein Thioesterase 1 At 1.5 A Resolution [H.sapiens]; abhydrolase_2;TM=M; 3.27
 444754; T83911; Hs.11881; transmembrane 4 superfamily member 4; none;TM=Y;SS=M; 3.26
 75 432579; AF043244; Hs.278439; nucleolar protein 3 (apoptosis repressor with CARD domain); CARD;TM=M; 3.26
 458943; AW249181; Hs.19954; ESTs, Weakly similar to T19873 hypothetical protein C41C4.2 - Caenorhabditis elegans [C.elegans]; none,pkinase,RGS; 3.26
 411974; AW880414; Hs.84264; acidic protein rich in leucines; E1-E2_ATPase,Cation_ATPase_C,Cation_ATPase_N,Hydrolase,asp; 3.26
 437145; AF007216; Hs.5462; solute carrier family 4, sodium bicarbonate cotransporter, member 4; HCO3_cotransp;TM=Y; 3.26
 423387; A1012074; ; vasoactive intestinal peptide receptor 1; 7tm_2,HRM,CSD;TM=Y;SS=M; 3.25
 442643; U82756; Hs.3991; PRP4/STKWD splicing factor; WD40;SS=M; 3.25
 80 417525; R93355; Hs.192991; ESTs, Weakly similar to ALUB_HUMAN !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]; SH3,jg,pkinase,PH,spectrin,RhoGEF;SS=M; 3.25
 412283; BE089084; ; gb:QV3-BT0379-140100-058-g12 BT0379 Homo sapiens cDNA, mRNA sequence; ion_trans,RYDR,ITPR,MIR:none; 3.25
 411213; AA676939; Hs.69285; neuropilin 1; MAM,F5_F8_type_C,CUB,CUB,MAM,F5_F8_type_C; 3.25
 400352; AF227133; ; taste receptor, type 2, member 7; none;TM=Y;SS=M; 3.25

- 402974; ; Target Exon; Y_phosphatase, GnRH, hormone5, hormone4; 3.25
- 407644; D16815; Hs.37288; nuclear receptor subfamily 1, group D, member 2; hormone_rec.zf-C4; TM=M; SS=M; 3.25
- 421654; AW163267; Hs.108469; suppressor of var1 (S.cerevisiae) 3-like 1; helicase_C; SS=M; 3.25
- 438022; AW517524; Hs.135201; NOD2 protein; LRR, CARD, GTP_CDC, Viral_helicase1; TM=M; 3.24
- 449964; AW001741; Hs.24243; hypothetical protein FLJ10706; pkinase; TM=M; 3.24
- 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; EGF, sushi, trypsin, CUB, ABC_tran, ABC_membrane; SS=M; 3.24
- 427319; AW631495; Hs.27135; B-cell receptor-associated protein BAP29; filament; TM=Y; SS=M; 3.24
- 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RRN3;
aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_PI4_kinase, FAT, FATC, BclA, RUN; TM=M; 3.24
- 411887; AW182924; Hs.128790; ESTs; pkinase; TM=M; 3.24
- 430180; AA331406; Hs.75456; A kinase (PRKA) anchor protein 10; RGS; SS=M; 3.24
- 410267; AW978005; Hs.12600; N-ethylmaleimide-sensitive factor attachment protein, beta; none; NTF2; 3.23
- 410240; AL157424; Hs.61289; synaptotagmin 2; Exo_endo_phos, Syja_N, rrm, Gram-ve_porins; TM=M; 3.23
- 434510; AF143885; Hs.18190; EST; SH3, FCH, none; 3.22
- 422592; BE081857; Hs.94211; rcd1 (required for cell differentiation, S.pombe) homolog 1; none; PI-PLC-X, PH, PI-PLC-Y, C2; 3.22
- 439803; AA001021; Hs.6685; thyroid hormone receptor interactor 8; none; none; 3.22
- 448520; AB002367; Hs.21355; doublecortin and CaM kinase-like 1; pkinase, DCX; TM=M; 3.22
- 409245; AA361037; Hs.288036; tRNA isopentenylpyrophosphate transferase; Armadillo_seg; TM=M; 3.22
- 458946; AA009716; Hs.42311; ESTs; none; DSPc, Y_phosphatase; 3.22
- 409048; H59990; Hs.37699; ESTs; Armadillo_seg, IBB, none; 3.22
- 420357; U94333; Hs.97199; complement component C1q receptor; EGF, lectin_c, Tissue_fac, Xlnk, TIL; TM=Y; SS=M; 3.22
- 426230; AA367019; Hs.241395; protease, serine, 1 (trypsin 1); trypsin, toxin_4; SS=M; 3.21
- 411352; NM_002890; Hs.758; RAS p21 protein activator (GTPase activating protein) 1; SH2, SH3, C2, PH, RasGAP; TM=M; SS=M; 3.21
- 438333; R39382; Hs.25283; cyclin-dependent kinase 8; pkinase, none; 3.20
- 414202; BE275653; Hs.270379; transmembrane 6 superfamily member 1; 7tm_5, none; 3.20
- 429651; D79248; Hs.279870; ESTs; Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; MglE, none; 3.20
- 400987; ; C11000939.g[11464993]ref[1]NP_065260.1 gene for odorant receptor MOR83 [Mus musculus] glr; none; TM=Y; SS=M; 3.20
- 413760; Z25101; Hs.25127; Homo sapiens mRNA for KIAA1725 protein, partial cds; none; ank, ArfGp; 3.20
- 408468; AJ909712; Hs.93837; phosphatidylinositol transfer protein, membrane-associated; PX, PH, PLDc, PH, PLDc, PX; 3.20
- 409463; AJ458165; Hs.17296; hypothetical protein MGC2376; K_tetra; TM=M; 3.20
- 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; none; TM=M; 3.19
- 423798; AF047033; Hs.132904; solute carrier family 4, sodium bicarbonate cotransporter, member 7; HCO3_cotransp; TM=Y; SS=M; 3.19
- 407753; AL045916; Hs.293419; ESTs; Ephrin, none; 3.19
- 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 3.19
- 454128; AL031259; Hs.14639; programmed cell death 2; z-MYND; TM=M; 3.19
- 421202; AF193339; Hs.102506; eukaryotic translation initiation factor 2-alpha kinase 3; pkinase; TM=Y; SS=M; 3.19
- 446360; NA2553; Hs.267914; homolog of mouse transient receptor potential-phospholipase C-interacting kinase CHaK; hypothetical protein FLJ20117;
ion_trans, MHCK_EF2_kinase; TM=M; 3.18
- 458882; R34993; Hs.226666; ESTs; Moderately similar to I54374 gene NF2 protein [H.sapiens]; CRAL_TRIO, PKI; 3.18
- 424124; AA335609; Hs.7589; ESTs; Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]; pkinase, TBC; 3.18
- 444745; AF117754; Hs.11861; thyroid hormone receptor-associated protein, 240 kDa subunit; none; TM=M; 3.18
- 426399; AA652588; Hs.301348; Homo sapiens cDNA FLJ13271 fis, clone OVARC1001000; SH3, HST1_rep, none; 3.18
- 425836; AW955698; Hs.90960; ESTs; Cbl_N, Cbl_N2, Cbl_N3, UBA, zf-C3HC4, none; 3.18
- 403335; ; NM_021815; Homo sapiens solute carrier family 5 (choline transporter), member 7 (SLC5A7), mRNA; SSF; TM=Y; SS=M; 3.17
- 428788; AF082283; Hs.193516; B-cell CLL/lymphoma 10; CARD; TM=M; 3.17
- 429558; AJ391454; Hs.207251; nucleolar autoantigen (55kD) similar to rat synaptonemal complex protein; none; SS=M; 3.17
- 440248; AA876138; Hs.153136; ESTs; SH2, none; 3.17
- 423706; U95218; Hs.131924; G protein-coupled receptor 65; 7tm_1; TM=Y; SS=M; 3.17
- 429752; H52348; Hs.36636; ESTs; pkinase, pkinase; 3.17
- 446163; AA026880; Hs.25252; Homo sapiens cDNA FLJ13603 fis, clone PLACE1010270; none; NA; NA; 3.17
- 456773; AI038192; Hs.129764; EGF-like repeats and discoidin I-like domains 3; rrm, SH3, myosin_head, IQ, MyTH4, EGF, F5_F8_type_C, Band_41; TM=M; 3.17
- 434392; AW983709; Hs.250824; Homo sapiens cDNA: FLJ23435 fis, clone HRC12631; pkinase, none; 3.16
- 435972; W95088; Hs.114158; ESTs; pkinase, OPR, none; 3.16
- 441401; AJ824338; Hs.126891; ESTs; Tissue_fac; TM=M; SS=M; 3.16
- 410497; AL157648; Hs.157078; Homo sapiens cDNA FLJ12793 fis, clone NT2RP2002033; none; none; 3.16
- 401113; H25530; ; solute carrier family 22 (organic cation transporter), member 1-like; none; SS=M; 3.16
- 424833; NM_003894; Hs.153405; period (Drosophila) homolog 2; PAS; SS=M; 3.15
- 453880; AJ803166; Hs.28462; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; HSP70, none; 3.15
- 435391; AA704588; Hs.58934; ESTs; PIP5K, none; 3.15
- 428065; AJ634046; Hs.157313; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 3.15
- 452688; AA721140; Hs.49930; ESTs; Weakly similar to putative p150 [H.sapiens]; SH3, none; 3.15
- 426839; M74782; Hs.172689; Interleukin 3 receptor, alpha (low affinity); none; TM=M; SS=M; 3.15
- 421247; BE391727; Hs.102910; general transcription factor IIH, polypeptide 4 (52kD subunit); none; TM=M; 3.14
- 440249; AJ246590; Hs.249175; ESTs; TalD_DNase, pkinase, death, none; 3.14
- 406619; AK001015; Hs.55220; BCL2-associated ethanolamine 2; BAG; TM=M; 3.13
- 446135; AW130288; Hs.170318; hypothetical protein FLJ10147; hormone_rec, zf-C4; SS=M; 3.13
- 400440; X83957; Hs.83870; nebulin; SH3, Nebulin; 3.12
- 409099; AK000725; Hs.50579; hypothetical protein FLJ20718; Armadillo_seg; TM=M; 3.12
- 434237; AF119908; Hs.235518; hypothetical protein PRO2955; none; SS=M; 3.12
- 428179; AI127772; Hs.279696; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; pkinase, PX, pkinase_C; SS=M; 3.12
- 422824; NM_012108; Hs.121128; BCR downstream signaling 1; SH2, PH; TM=M; 3.11
- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA Library Homo sapiens cDNA clone 7B14E12, mRNA sequence; 7tm_1, zf-C3HC4, In3, SPRY, KRAB, zf-C2H2, rve, zf-B_box; TM=Y; SS=M; 3.11
- 435411; AW444619; Hs.138211; ESTs; none; pkinase; 3.11
- 424852; AI222779; Hs.144848; ESTs; adenylate kinase, SH2, pkinase, none; 3.11
- 441970; AW959918; Hs.155160; ESTs; rrm, zf-C2H2; 3.11
- 453370; AI705523; Hs.139336; ATP-binding cassette, sub-family C (CFTR/MRP), member 4; ABC_tran, ABC_membrane; TM=Y; 3.11
- 413285; BE078405; ; gb:QV2-BT0617-080300-071-g03 BT0617 Homo sapiens cDNA, mRNA sequence; GCV_T; SS=M; 3.10
- 429458; BE161832; Hs.292689; ESTs; pkinase, bZIP, Armadillo_seg, none; 3.10
- 401185; ; NM_021625; Homo sapiens vanilloid receptor-related osmotically activated channel; OTRPC4 protein (OTRPC4), mRNA; ank, ion_trans; TM=Y; 3.10
- 404537; Z25884; ; chloride channel 1, skeletal muscle (Thomsen disease, autosomal dominant); none; TM=Y; 3.10
- 417089; H52280; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone HEP03834; voltage_CLC, CBS, none; 3.09
- 450792; AA400323; Hs.183041; ESTs; none; ABC_tran; 3.09

- 420361; N92054; Hs.194718; zinc finger protein 265; zf-RanBP, 7tm_1; 3.09
 444040; AF204231; Hs.182982; golgin-67; SH3,C2,PH,RhoGEF,efhand;TM=M; 3.09
 416990; AF124145; Hs.80731; autocrine motility factor receptor; zf-C3HC4,CUE;TM=Y; 3.09
 442215; AI703172; Hs.129005; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; none,none; 3.09
 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothetical protein hc1 - mouse [M.musculus]; IRK,none; 3.09
 426523; AA382826; Hs.132793; ESTs; none;TM=M; 3.08
 419577; L36531; Hs.91296; integrin, alpha 8; integrin_A,FG-GAP;TM=Y; 3.08
 426618; AL036456; Hs.171374; smg GDS-ASSOCIATED PROTEIN; Armadillo_seg;TM=M; 3.08
 445133; AW157646; Hs.153506; ESTs; efhand,spectrin,GAG2,SH3,Plectin,RA,Xylose_isom,FilD,bZIP,Tropomyosin,Myc-LZ,M,Idh_C,CH,AIP3;TM=M; 3.08
 423681; AB023215; Hs.131525; Homo sapiens mRNA; cDNA DKFZp434E199 (from clone DKFZp434E199); partial cds; TTL;TM=M; 3.08
 428730; AA625947; Hs.25750; ESTs; HECT,none; 3.08
 427976; AW977808; Hs.80545; mitogen-activated protein kinase 8 interacting protein 2; Ribosomal_L37e,ptkinase; 3.08
 412448; L12964; Hs.73895; tumor necrosis factor receptor superfamily, member 9; TNFR_c6;TM=Y;SS=M; 3.08
 416814; AW192307; Hs.80042; dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylglucosyltransferase; Alg6_Alg8,7tm_1;TM=Y;SS=M; 3.08
 427395; AW298741; Hs.97851; ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]; none,aldedh,aakinas; 3.08
 436267; AW450938; Hs.180115; ESTs; none,PFK; 3.07
 422309; U79745; Hs.114924; solute carrier family 16 (monocarboxylic acid transporters), member 6; sugar_tr;TM=Y;SS=M; 3.07
 439238; N47305; Hs.46668; ESTs; 7tm_1;TM=Y;SS=M; 3.07
 458760; AI49631; Hs.111334; ferritin, light polypeptide; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.07
 424236; AW058114; Hs.7837; phosphoprotein regulated by mitogenic pathways; pkinase;TM=M; 3.06
 427286; AW732802; Hs.2132; epidermal growth factor receptor pathway substrate 8; SH3,TonB_boxC;TM=M; 3.06
 423878; AI907090; Hs.52891; hypothetical protein PRO1853; cystatin,ferritin,histone,HCO3_cotransp,SH3,RhoGAP,xan_ur_permease,FCH;SS=M; 3.06
 419270; NM_005232; Hs.89839; EphA1; fn3,ptkinase,SAM,EPH_1bd;TM=M;SS=M; 3.06
 450407; NM_000810; Hs.24969; gamma-aminobutyric acid (GABA) A receptor, alpha 5; Neur_chan_LBD,Neur_chan_memb;TM=Y; 3.06
 456249; AI206144; Hs.82508; HRIHFB2206 protein; none;SS=M; 3.06
 441560; F13386; Hs.7888; Homo sapiens clone 23736 mRNA sequence; pkinase,Recep_L_domain,Furin-like,YLP,none; 3.05
 446488; AB037782; Hs.15119; KIAA1361 protein; pkinase;SS=M; 3.05
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); pyr_redox;TM=M; 3.05
 425390; AI092634; Hs.156114; protein tyrosine phosphatase, non-receptor type substrate 1; ig;TM=Y;SS=M; 3.04
 409705; M37762; Hs.56023; brain-derived neurotrophic factor; NGF;SS=M; 3.04
 413962; AA331563; Hs.24678; sphingosine-1-phosphatase; PAP2;TM=Y; 3.04
 426578; R23027; gb:yt27e07.r1 Soares placenta Nb2HP Homo sapiens cDNA clone S', mRNA sequence; pkinase,none; 3.04
 438005; BE151746; gb:PM1-HT0305-061299-003-a06 HT0305 Homo sapiens cDNA, mRNA sequence; pkinase,UBA,KAI,none; 3.04
 438316; AA789249; Hs.80042; gb:a|27g08.s1 Soares_testis_NHT Homo sapiens cDNA clone 1391582 3', mRNA sequence; none,none; 3.04
 452850; H23230; Hs.22481; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; CBS,voltage_CLC,none; 3.03
 405266; ; Target Exon; arf,G-alpha;SS=M; 3.03
 402615; ; C1003844::gil6912550[ref]NP_036483.1| olfactory receptor, family 10, subfamily J, member 1; none;TM=Y;SS=M; 3.03
 422803; W28689; Hs.139041; ESTs; transmembrane4,none; 3.02
 439325; AF086139; Hs.150423; cyclin-dependent kinase 9 (CDC2-related kinase); pkinase,Mur_ligase,Mur_ligase_C; 3.02
 416389; AA180072; Hs.149846; Integrin, beta 5; integrin_B,none; 3.02
 418836; AI655499; Hs.161712; ESTs; pkinase,Activin_recpt,PDZ,ZUS,death; 3.02
 438996; AW748336; Hs.110613; KIAA0421 protein; none;TM=M; 3.02
 422676; D28481; Hs.1570; histamine receptor H1; 7tm_1;TM=Y;SS=M; 3.02
 450267; AW505538; Hs.243620; ESTs; pkinase,none; 3.01
 400566; ; Target Exon; none;TM=Y; 3.01
 407816; AW500857; Hs.40137; anaphase-promoting complex 1; meiotic checkpoint regulator; PI-PLC-X,C2,SH2,PH,SH3,PI-PLC-Y,PAN,none; 3.01
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase); Y_phosphatase,Band_41,PDZ;SS=M; 3.01
 417067; AJ001417; Hs.81086; solute carrier family 22 (extraneuronal monoamine transporter), member 3; sugar_tr;TM=Y;SS=M; 3.00
 403212; ; NM_019595:Homo sapiens intersecin 2 (ITSN2), mRNA. (CHRNA9), mRNA; SH3,efhand,C2,PH,RhoGEF;TM=M; 3.00
 410141; R7775; Hs.287657; Homo sapiens cDNA: FLJ21291 fls, clone COL01963; F5_F8_type_C,ptkinase,Ets,none; 3.00
 421059; AI654133; Hs.30212; thyroid receptor interacting protein 15; none,none; 3.00
 452335; AW188944; Hs.61272; ESTs; none,IRK; 2.99
 437644; AA748575; Hs.136748; lectin-like NK cell receptor; lectin_c;TM=Y;SS=M; 2.99
 435876; AW612586; Hs.160271; G protein-coupled receptor 48; 7tm_1,LRR,LRRNT;TM=Y;SS=M; 2.99
 429177; AA447527; Hs.207429; ESTs; 7tm_1,none; 2.99
 449289; BE466067; Hs.225660; ESTs; 3Beta_HSD,ptkinase; 2.99
 454701; AW854930; gb:PM0-CT0263-201099-003-f06 CT0263 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prol,none; 2.99
 409895; AW960597; Hs.129206; ESTs; pkinase,none; 2.98
 446860; AV660685; Hs.282953; ESTs; none,PP2C; 2.98
 438684; AA830105; Hs.194976; SH2 domain-containing phosphatase anchor protein 1; ig;TM=Y;SS=M; 2.98
 434164; AW207019; Hs.148135; serine/threonine kinase 33; pkinase;TM=M; 2.98
 403290; ; C10001011::gil4758212[ref]NP_004411.1| dual specificity phosphatase 8 [Homo sapiens] gil601; none;TM=M; 2.97
 433556; W56321; Hs.111460; calcium/calmodulin-dependent protein kinase (CaM kinase) II delta; pkinase,none; 2.97
 421990; T31811; Hs.110480; DC12 protein; GKAP,DUF159;TM=M; 2.97
 428315; AA688152; Hs.98505; ESTs; pkinase,none; 2.97
 411140; AW819463; gb:RCS-ST0293-061299-031-C07 ST0293 Homo sapiens cDNA, mRNA sequence; Choline_kinase,Carn_acyltransf,Sulfatase,Carn_acyltransf; 2.97
 453998; H47802; Hs.7557; FK506-binding protein 5; none,none; 2.97
 401342; ; Target Exon; none,none; 2.97
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); dNK,none; 2.96
 410976; R36207; Hs.25092; hypothetical protein MGC10744; none;TM=M;SS=M; 2.96
 431074; BE072772; Hs.153279; ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]; none,serpin; 2.96
 443829; AI087954; Hs.23348; S-phase kinase-associated protein 2 (p45); F-box,none; 2.95
 400356; AF227137; ; taste receptor, type 2, member 13; none;TM=Y;SS=M; 2.95
 422559; AW247696; Hs.155839; hypothetical protein MGC12934; adh_zinc.PGK,Semialdhyde_dh;SS=M; 2.95
 423482; BE280172; Hs.129228; galactokinase 2; GHMP_kinases;TM=M; 2.95
 438330; AW450572; Hs.257316; ESTs; pkinase,zf-C4,ERM,CNH,none; 2.95
 414581; AA256213; Hs.72010; ESTs; none,Carn_acyltransf,Choline_kinase,SCO1-SenC,Glycos_transf_3,Glycos_trans_3N; 2.95
 453058; AW612293; Hs.288684; Homo sapiens cDNA FLJ11750 fls, clone HEMBA1005568; SH2,SH3,C2,PH,RasGAP,none; 2.95
 430556; AW967807; Hs.13797; ESTs; HECT,none; 2.94
 400471; ; Target Exon; none;TM=M; 2.94
 419459; AW291128; Hs.278422; DKFZP586G1122 protein; Metallophos,7tm_1; 2.94
 407013; U35637; gb:Human nebulin mRNA, partial cds; SH3,Nebulin; 2.94
 421476; AW953805; Hs.21887; ESTs; Pwi,PAZ,Pwi; 2.94

- 426806; T19228; Hs.175272; hypothetical protein FLJ20093; ank,pkinase,UPF0073;SS=M; 2.94
 405588; ; NM_000299; Homo sapiens plakophilin 1 (ectodermal dysplasia/skin fragility syndrome) (PKP1), mRNA; Armadillo_seg;TM=M; 2.94
 443614; AV655386; Hs.7645; fibrinogen, B beta polypeptide; none;none; 2.94
 416737; AF154335; Hs.79691; LIM domain protein; LIM,PDZ;TM=M; 2.93
 428522; R10184; Hs.191987; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; none,ArfGap,PH,TNFR_c6; 2.93
 447818; W79940; Hs.21906; Homo sapiens clone 24670 mRNA sequence; none,pkinase; 2.93
 432925; AA878324; ; ESTs; none;none; 2.93
 443670; AW178935; Hs.238707; ESTs; RmaAD,DENN,dDENN,uDENN;TM=M; 2.93
 447555; AI391662; Hs.160963; Homo sapiens, clone MGC:12318, mRNA, complete cds; none;TM=M; 2.93
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; none;TM=M; 2.93
 417670; R07785; ; gby115c05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5' similar to contains Alu repetitive element;contains MSR1 repetitive element.; mRNA sequence; XYPPX,ABC_membrane,ABC_tran; 2.93
 424148; BE242274; Hs.1741; integrin, beta 7; integrin_B,EGF,metalbio,PSI;TM=Y;SS=M; 2.92
 439090; H65724; Hs.347158; gb:yr76a11.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 5', mRNA sequence; pkinase;none; 2.92
 408048; NM_007203; Hs.42322; A kinase (PRKA) anchor protein 2; Paralemmin;TM=M; 2.92
 428796; AU076734; Hs.193665; solute carrier family 28 (sodium-coupled nucleoside transporter), member 2; Nucleoside_tra2,BPD_transp_2;TM=Y; 2.92
 415272; AA164215; Hs.203186; ESTs; none,Exo_endo_phos,BNR,Atrophin-1,B56,pkinase,ig,TPR; 2.92
 424775; AB014540; Hs.153026; SWAP-70 protein; ehand,PH,Neuregulin;TM=M; 2.92
 439569; AW602168; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 2.92
 416680; AW444598; Hs.7940; RAPI, GTP-GDP dissociation stimulator 1; Armadillo_seg;TM=M; 2.91
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1; Somatomedin_B,Endonuclease,Phosphodiester;TM=Y;SS=M; 2.91
 400398; AF137396; Hs.283879; ubiquitin 3; 7tm_1,Abl;TM=Y;SS=M; 2.91
 435592; AI830490; Hs.1466; glycerol kinase; FGGY,FGGY_C;TM=M; 2.90
 400539; ; Target Exon; none;TM=M; 2.90
 403743; ; C1002604.gil8393668[ref]NP_058989.1 kinase interacting with leukemia-associated gene (st; none;TM=M; 2.90
 418913; AU046745; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Y_phosphatase,IMP4;none; 2.90
 428169; AJ928984; Hs.182793; golgi phosphoprotein 2; photoRC,UPF0118;TM=Y; 2.90
 403912; ; C5000394.gil12737280[ref]XP_006682.2 keratin 18 [Homo sapiens][S633; none;TM=M; 2.89
 431868; BE246400; Hs.285176; acetyl-Coenzyme A transporter; none;TM=Y; 2.89
 421558; AB011125; Hs.105749; KIAA0553 protein; none;TM=M; 2.89
 444100; AA383343; Hs.22116; CDC14 (cell division cycle 14, S. cerevisiae) homolog B; Y_phosphatase,DSPC;TM=M; 2.89
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled, 2; 7tm_1,SH2;TM=Y;SS=M; 2.89
 431512; BE270734; Hs.2795; lactate dehydrogenase A; lch,kdh_C,SH3,pkinase,UBA;TM=M; 2.89
 446601; AJ312783; Hs.155772; Homo sapiens thymic stromal co-transporter mRNA, complete cds; sugar_tr;TM=Y; 2.89
 420747; BE294407; Hs.99910; phosphofructokinase, platelet; PFK;TM=M; 2.88
 449459; BE546846; Hs.195048; ESTs; ank,ras,PH,ArfGap,HCO3_cotransp; 2.88
 405099; ; Target Exon; C2,PI-PLC-Y,PI-PLC-X;TM=M; 2.88
 445890; AF055019; Hs.21906; Homo sapiens clone 24670 mRNA sequence; pkinase,pkinase; 2.88
 401445; ; NM_021161; Homo sapiens potassium channel, subfamily K, member 10 (KCNK10), mRNA; ion_trans;TM=Y;SS=M; 2.87
 405480; ; Target Exon; none;none; 2.87
 400189; ; Eos Control; LRR,PPTA;TM=M; 2.87
 450125; AA005418; Hs.158186; ESTs; CIDE-N,7tm_1;none; 2.87
 432056; AB040973; Hs.272385; G protein-coupled receptor 72; 7tm_1;TM=Y;SS=M; 2.86
 423619; T48691; Hs.249159; adrenergic, alpha-2A-, receptor; 7tm_1,7tm_2;TM=Y;SS=M; 2.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; xan_ur_permease,RA; 2.86
 420035; F26726; Hs.187908; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; HATPase_c,MOZ_SAS,zf-C2H2; 2.86
 425480; AB023198; Hs.158135; KIAA0981 protein; PIP5K;SS=M; 2.86
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc finger protein, ESTs, STSs, GSSs and a putative CpG; none;TM=M; 2.86
 444595; AL121094; Hs.83572; hypothetical protein MGC14433; Y_phosphatase,SH2,Y_phosphatase,SH2; 2.85
 411331; AW837178; ; gb:QV1-LT0037-070300-100-d11 LT0037 Homo sapiens cDNA, mRNA sequence; SH2;none; 2.85
 410763; AF279145; Hs.8966; hypothetical protein FLJ21776; none;none; 2.85
 440617; AA894880; Hs.181181; ESTs; none;none; 2.85
 454071; AJ041793; Hs.42502; ESTs; 7tm_1;none; 2.85
 411040; AF007393; Hs.177574; protein-kinase, interferon-inducible double stranded RNA dependent inhibitor, repressor of (P58 repressor); HLH;TM=M; 2.85
 402183; ; NM_004491; Homo sapiens glucocorticoid receptor DNA binding factor 1 (GRF1), mRNA; none;SS=M; 2.85
 428753; AW939252; Hs.192927; hypothetical protein FLJ20251; none;TM=M; 2.84
 417070; Z19077; Hs.172004; 6tm; fn3,lg,SGXXSG,pkinase;TM=M; 2.84
 458456; AI122709; Hs.153609; ESTs; bZIP,Armadillo_seg,rm,NTF2;none; 2.84
 421226; AL096748; Hs.102708; DKFZP434A043 protein; Armadillo_seg,integrin_B,PSI,TIG;TM=M;SS=M; 2.84
 436733; BE327477; Hs.166941; ESTs; 7tm_3,oxidored_g5_N,Presenilin,PWT; 2.84
 427161; AJ024595; Hs.97508; a disintegrin and metalloproteinase domain 6; ig;TM=Y;SS=M; 2.84
 419462; AF071076; Hs.112255; nucleoporin 98kD; DEAD,helicase_C,Nucleoporin_FG,homobox;SS=M; 2.83
 413558; AA055369; Hs.75456; A kinase (PRKA) anchor protein 10; none;none; 2.83
 400749; ; NM_003105; Homo sapiens sortilin-related receptor, L(DLR class) A repeats-containing (SORL1), mRNA; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 2.83
 447388; AW630534; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; TB2_DP1_HVA22;TM=Y;SS=M; 2.83
 413243; AA769266; Hs.193657; ESTs; pkinase,zf-C4,ERM,CNH;none; 2.83
 423690; AA329648; Hs.23804; ESTs, Weakly similar to PNO099 son3 protein [H.sapiens]; ion_trans,IQ;none; 2.82
 447993; AW139525; Hs.170362; ESTs; none;none; 2.82
 423061; AI290473; Hs.44807; ESTs; integrin_B,Sema,PSI,TIG;none; 2.82
 440619; AW408586; Hs.91052; ESTs, Moderately similar to ALUS_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; abhydrolase_2;none; 2.82
 423497; U92642; Hs.129701; G protein-coupled receptor 45; 7tm_1;TM=Y;SS=M; 2.81
 446126; AW085909; Hs.10177; pleckstrin homology domain interacting protein; none;none; 2.81
 452488; N74921; Hs.184389; ESTs; none;TM=M; 2.80
 449515; AI653378; Hs.302012; ESTs; ion_trans;TM=Y;SS=M; 2.79
 443881; R64512; Hs.237146; hypothetical protein FLJ12752; none;none; 2.79
 449636; AI656608; Hs.281328; ESTs, Weakly similar to T00378 KIAA0641 protein [H.sapiens]; pkinase,hormone3;TM=Y;SS=M; 2.78
 424348; AB020523; Hs.266258; endonuclease G-like 1; Endonuclease;TM=M;SS=M; 2.78
 418844; M62982; Hs.1200; arachidonate 12-lipoxygenase; lipoxygenase,PLAT;TM=M; 2.78
 442233; AW967149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; MIF,sugar_tr;none; 2.78

- 450010; AW293801; Hs.255052; ESTs; ARID,7tm,1; 2.78
 452813; U54727; Hs.191445; ESTs; pkinase,Activin_recpt:none; 2.78
 418177; N44967; ; ESTs; pkinase:none; 2.78
 408014; AA723782; Hs.41749; protein kinase, cGMP-dependent, type II; cNMP_binding,pkinase;SS=M; 2.77
 448362; AA641767; Hs.21015; hypothetical protein DKFZp564L0864 similar to HIAT1; sugar_br;TM=Y;SS=M; 2.77
 423994; X01057; Hs.1724; Interleukin 2 receptor, alpha; sushi;TM=Y;SS=M; 2.77
 427342; AL110150; Hs.176680; Homo sapiens mRNA; cDNA DKFZp586D0724 (from clone DKFZp586D0724); none;NA;NA; 2.76
 447574; AF162666; Hs.18895; tousled-like kinase 1; pkinase;TM=M; 2.76
 442681; AI809182; Hs.130907; ESTs; transketolase,E1_dehydrog,transket_pyr,transketolase_C,pkinase; 2.75
 433637; AW024214; Hs.102307; ESTs; Na_sulph_symp_aa_permeases;TM=Y;SS=M; 2.75
 458997; AW937420; Hs.69662; ESTs; SH3,RhoGAP,FCH;TM=M; 2.75
 432284; AA532807; Hs.105822; ESTs; pkinase:none; 2.74
 406139; ; Target Exon; ig_Tub;TM=Y;SS=M; 2.74
 439518; W76326; ; gb:zd60d04.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5' similar to contains Alu repetitive element; mRNA sequence; Armadillo_seg:none; 2.74
 428536; AI143139; Hs.2288; visinin-like 1; ehfand;SS=M; 2.73
 400211; ; NM_003899; Homo sapiens PAK-interacting exchange factor beta (P85SPR), mRNA. VERSION NM_003897.1 GI; SH3,PH,RhoGEF,Terpene_synth;TM=M; 2.73
 402129; ; Target Exon; SH2,Peptidase_C9;TM=M; 2.73
 424238; AA337401; Hs.137635; ESTs; none;TM=M;SS=M; 2.73
 433834; AA620742; Hs.130786; ESTs; SPX,EXS;TM=Y; 2.73
 409339; AB020586; Hs.54037; ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function); Sulfatase,Phosphodiester;TM=M;SS=M; 2.73
 408163; AW779842; Hs.258217; ESTs; 7tm,1,zf-B_box,zf-C3HC4,7tm,1,zf-B_box,zf-C3HC4; 2.73
 422358; AL133030; Hs.115429; Homo sapiens mRNA for KIAA1666 protein, partial cds; SH3;TM=M; 2.73
 426409; AA594207; ; gb:nn29e01.s1 NCI_CGAP_Gas1 Homo sapiens cDNA clone 3; mRNA sequence; pkinase,Fibrillarin:none; 2.72
 400645; ; Target Exon; lig_chan,SBP_bac_3,ANF_receptor:none; 2.72
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; adenylatekinase:none; 2.71
 442572; AI001922; Hs.135121; hypothetical protein FLJ22415; none,HSP70; 2.71
 409317; U20165; Hs.53250; bone morphogenetic protein receptor, type II (BMPR2); pkinase,Activin_recpt;TM=M;SS=M; 2.71
 403201; ; Target Exon; none; 2.71
 459357; AW848211; ; gb:IL3-CT0214-150200-075-B11 CT0214 Homo sapiens cDNA, mRNA sequence; ABC_tran,ABC_membrane,lon_trans; 2.70
 439935; S75105; Hs.8358; glutamate receptor, ionotropic, kainate 2; ANF_receptor,lig_chan:none; 2.70
 414924; C06267; Hs.44247; ESTs; none:none; 2.69
 421008; BE269378; Hs.103147; hypothetical protein FLJ21347; DUF255; 2.69
 449951; AA004882; Hs.120904; ESTs; DED,Calsequestrin; 2.69
 411226; AI323022; ; gb:RC3-TT0005-191099-012-d04 TT0005 Homo sapiens cDNA, mRNA sequence; pkinase:none; 2.68
 417625; U59305; Hs.44708; Ser-Thr protein kinase related to the myotonic dystrophy protein kinase; pkinase,bZIP,G-gamma,K-box,pkinase_C;SS=M; 2.68
 408051; AI623351; Hs.172148; ESTs; PH,RhoGAP:none; 2.68
 412521; AW753481; Hs.294022; hypothetical protein FLJ14950; SH2;TM=M; 2.68
 413922; AI535895; Hs.221024; ESTs; lon_trans,RYDR,ITPR,MIR,UDPGT; 2.68
 432188; AI352952; Hs.2928; solute carrier family 7 (cationic amino acid transporter, y system), member 1; aa_permeases;TM=Y;SS=M; 2.67
 415516; F11411; ; gb:HSC2WF081 normalized infant brain cDNA Homo sapiens cDNA clone c-2wf08, mRNA sequence; lon_trans:none; 2.67
 419749; X73608; Hs.93029; sparco/osteonectin, cwcv and kazal-like domains proteoglycan (testican); kazal,thyroglobulin_1;SS=M; 2.66
 416095; AW014327; Hs.221951; ESTs; Weakly similar to I38022 hypothetical protein [H.sapiens]; ig,zf-C3HC4,Cbl_N,Cbl_N2,Cbl_N3:none; 2.66
 403609; ; C3001199;gb:J7494834[pat]JT15308 hypothetical protein B0286.2 - Caenorhabditis elegans[J41; 7tm,1,7tm,2,GPS,WIF;TM=Y;SS=M; 2.66
 458213; AL047521; Hs.12210; hypothetical protein FLJ13732 similar to tensin; pkinase:none; 2.66
 426158; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 3; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 2.66
 435410; AL135067; Hs.117182; ESTs; none,pkinase,RBD,DAG_PE-bind; 2.66
 437838; AI307229; Hs.184304; ESTs; CARD,ICE_p20,ICE_p10,HIT,voltage_CLC,CBS,HCCA_isomerase; 2.66
 430293; AI416988; Hs.238272; inositol 1,4,5-trisphosphate receptor, type 2; lon_trans,RYDR,ITPR,MIR:none; 2.65
 433090; AI720050; ; immortalization-upregulated protein; none;SS=M; 2.65
 432103; J15803; Hs.272458; protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (calcineurin A alpha); Metallophos;TM=M; 2.65
 435852; H72303; Hs.36011; ESTs; pkinase:none; 2.64
 433327; AI674779; Hs.126744; ESTs; none,7tm,1; 2.64
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; none,FMO-like; 2.64
 432251; AW972983; Hs.232165; polycythemia rubra vera 1; cell surface receptor; none;TM=M;SS=M; 2.63
 446963; AI862668; Hs.176333; ESTs; OMPdecase,Probosyltran,pkinase,RhoGEF,PH; 2.63
 444821; AA053564; Hs.12040; STE20-like kinase; pkinase;TM=M; 2.63
 436208; AK001451; ; CD2-associated protein; none:none; 2.63
 434370; AF130988; Hs.58346; ectodysplasin 1, anhidrotic receptor; death,Kunitz_BPTI;TM=Y;SS=M; 2.63
 439039; AI656707; Hs.48713; ESTs; pkinase:none; 2.63
 449656; AA002008; Hs.188533; ESTs; PIP5K:none; 2.63
 429341; X73874; Hs.2393; phosphorylase kinase, alpha 1 (muscle); none;TM=M; 2.62
 445174; AV652850; Hs.172004; ESTs; fn3,ig,SGXXSG:none; 2.62
 424950; AA602917; Hs.156974; ESTs; none,CDP-OH_P_transf; 2.62
 438141; AW946871; ; gb:RC2-ET0022-080500-012-d02 ET0022 Homo sapiens cDNA, mRNA sequence; SH2,STAT,STAT_bind,STAT_prot:none; 2.61
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, complete cds; pkinase,TBC,Rhodanese;TM=M; 2.61
 409264; NM_014937; Hs.52463; KIAA0966 protein; Syja_N;TM=M; 2.60
 458438; AI141520; Hs.151464; ESTs; Weakly similar to ALUC_HUMAN !!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]; pkinase:none; 2.60
 400719; ; NM_004055; Homo sapiens calpain 5 (CAPN5), mRNA. VERSION NM_004335.2 GI; C2,Peptidase_C2,Calpain_III;TM=M; 2.60
 427318; AF185081; Hs.175783; zinc transporter; Zip;TM=Y;SS=M; 2.59
 426086; T94907; Hs.188572; ESTs; PH,EtS,CH,spectrin,Ca_channel_B:none; 2.59
 430105; X70297; Hs.2540; cholinergic receptor, nicotinic, alpha polypeptide 7; Neur_chan_LBD,Neur_chan_memb,pkinase;TM=Y;SS=M; 2.58
 411495; AP000693; Hs.70359; KIAA0135 protein; HATPase_c,bZIP;TM=M; 2.58
 438167; R28363; Hs.24285; ESTs; none;TM=Y;SS=M; 2.58
 418749; N75147; Hs.22488; ESTs; none,zf-C2H2,KRAB,pkinase; 2.58
 454289; AL137554; Hs.49927; protein kinase NYD-SP15; dCMP_cyt_deam;TM=M; 2.58
 443605; H06865; Hs.134131; ESTs; ehfand,lon_trans:none; 2.57
 429429; AA829725; Hs.334437; hypothetical protein MGCA248; none,transmembrane4; 2.57
 403088; ; NM_003319; Homo sapiens titin (TTN), mRNA. mRNA; fn3,ig,SGXXSG;TM=M; 2.57
 409190; AJ076536; Hs.50984; sarcoma amplified sequence; transmembrane4;TM=Y;SS=M; 2.57
 426696; AW363332; Hs.171844; Homo sapiens cDNA: FLJ22296 fis, clone HRC04468; ig;TM=Y;SS=M; 2.56
 403328; ; Target Exon; Glyco_hydro_35;TM=M; 2.56

- 426167; AF039023; Hs.167496; RAN binding protein 6; Armadillo_seg.HEAT_PBS; 2.56
 428695; A1355647; Hs.189999; purinergic receptor (family A group 5); 7tm_1; TM=Y; SS=M; 2.54
 419285; D31887; Hs.89868; KIAA0062 protein; Zip; TM=Y; SS=M; 2.54
 415740; N80486; Hs.39911; Homo sapiens mRNA for FLJ00089 protein, partial cds; CBM_21; TM=M; 2.53
 403305; NM_006825; ; transmembrane protein (63kD), endoplasmic reticulum/Golgi intermediate compartment; pkinase; TM=Y; SS=M; 2.53
 443804; AL135352; Hs.255883; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; Peptidase_M18, Peptidase_M18_Y_phosphatase; 2.53
 450425; H06607; Hs.6099; ESTs; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N_hydrolase, none; 2.51
 401702; ; NM_001171; Homo sapiens ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (ABCC6), mRNA; ABC_tran, ABC_membrane; TM=Y; SS=M; 2.50
 439463; W69304; ; gb:zd4601.r1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone 5', mRNA sequence; fn3_Y_phosphatase, none; 2.50
 425975; AB011082; Hs.165559; organic cationic transporter-like 4; sugar_tr; TM=Y; 2.50
 443259; AW090601; Hs.69171; protein kinase C-like 2; pkinase, pkinase_C, HR1, none; 2.50
 400777; ; NM_007325; Homo sapiens glutamate receptor, ionotropic, AMPA 3 (GRIA3), transcript variant flip, mRNA; lig_chan, SBP_bac_3, ANF_receptor; TM=M; SS=Y; 2.49
 426044; AA502490; Hs.170290; ESTs; none, none; 2.48
 454564; AW807573; ; gb:MR1-ST0088-021299-004-g01 ST0088 Homo sapiens cDNA, mRNA sequence; pkinase, none; 2.48
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; KH-domain, TUDOR; TM=M; SS=M; 2.47
 426481; AW953941; ; gb:EST376014 MAGE resequences, MAGH Homo sapiens cDNA, mRNA sequence; Y_phosphatase, Band_41, DSPc, none; 2.46
 426005; AA377499; ; gb:EST90341 Synovial sarcoma Homo sapiens cDNA 5' end, mRNA sequence; tubulin, FKBP, COX6B, 7tm_1, tubulin_C; SS=M; 2.46
 424879; AA348013; Hs.273385; ESTs; arf, G-alpha, none; 2.46
 415156; X84908; Hs.78060; phosphorylase kinase, beta; none; TM=M; 2.46
 416508; R39769; ; ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; SH3, PDZ, Guanylate_kin, ZU5, none; 2.46
 408087; AW150645; ; gb:cg5407.x1 NCL_CGAP_Ui4 Homo sapiens cDNA clone 3', mRNA sequence; XYPPX, ABC_membrane, ABC_tran; 2.46
 433434; AA588429; ; gb:nc022b03.s1 NCL_CGAP_Py22 Homo sapiens cDNA clone 3', mRNA sequence; pkinase, DNA_mis_repair, HATPase_c; 2.45
 446768; AV660305; Hs.110286; ESTs; ICE_p20, DED, ICE_p10, ICE_p20, DED; 2.45
 437158; AW090198; ; KIAA1150 protein; none; NA; NA; 2.45
 430177; AW969233; Hs.302746; MSTP028 protein; K_tetra, none; 2.45
 422270; AF114494; Hs.114062; protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a; none; TM=Y; 2.45
 430680; AW138724; Hs.168974; ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Y_phosphatase, Adaplin_N_Y_phosphatase; 2.44
 446569; AW248031; Hs.155839; hypothetical protein MGC12934; adh_zinc, PGK, Semikahyde_dh; SS=M; 2.44
 411902; AW875344; ; gb:RC1-PT0009-220300-013-f06 PT0009 Homo sapiens cDNA, mRNA sequence; none, pkinase, ank; 2.43
 430057; AW450303; Hs.2534; bone morphogenetic protein receptor, type IA (BMPRI1A) (ALK-3); Activin_rec, pkinase; TM=Y; SS=M; 2.43
 446338; AI289121; Hs.206978; ESTs; none, SH3; 2.42
 426221; AB007881; Hs.110613; KIAA0421 protein; none, Ribosomal_S8; 2.42
 446796; AI652497; Hs.110103; RNA polymerase I transcription factor RRN3; none, none; 2.41
 428360; H10291; Hs.30974; ESTs; pkinase, PBD, none; 2.40
 428379; X06026; Hs.2259; CD3G antigen, gamma polypeptide (TIT3 complex); ITAM; TM=Y; SS=M; 2.40
 432488; AA551010; Hs.216640; ESTs; Na_sulph_symp, none; 2.40
 407235; D20569; Hs.169407; SAC2 (suppressor of actin mutations 2, yeast, homolog)-like; none, Ribosomal_S13, Galactosyl_T, Zip, adh_short, zfc-C3HC4; 2.40
 448595; AB014544; Hs.21572; KIAA0644 gene product; LRR, LRRCT; TM=Y; SS=M; 2.40
 428283; AI439096; Hs.323079; Homo sapiens mRNA; cDNA DKFZp564P116 (from clone DKFZp564P116); Y_phosphatase, fn3, Ig, none; 2.39
 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase, none; 2.38
 429549; AI333013; Hs.250505; retinoic acid receptor, alpha; none, zfc-C3HC4, BRCT, lig_chan; 2.38
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65557 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; Phosphodiester, Somatomedin_B, Endonuclease, none; 2.36
 417473; M55268; Hs.82201; casein kinase 2, alpha prime polypeptide; pkinase, ABC1; TM=M; 2.35
 453186; AK001708; Hs.32271; hypothetical protein FLJ110846; TK, DUF300; TM=Y; SS=M; 2.33
 447276; AL049795; Hs.17987; hypothetical protein MGC1203; none; TM=M; 2.33
 445310; AI242490; Hs.153290; Homo sapiens cDNA FLJ14318 f1s, clone PLACE3000402; none, pkinase; 2.31
 432942; AF083955; Hs.279852; G protein-coupled receptor; 7tm_1, globin; TM=Y; SS=M; 2.30
 434693; AW976001; Hs.337603; ESTs; none, none; 2.26
 452034; F12234; Hs.75893; ankyrin 3, node of Ranvier (ankyrin G); ZU5, death, none; 2.25
 423732; AF058056; Hs.132183; solute carrier family 16 (monocarboxylic acid transporters), member 7; sugar_tr; TM=Y; SS=M; 2.25
 404956; ; C1003210; gi|912582|ref|NP_036524.1| peflin [Homo sapiens] gi|6009487|dbj|BAA84922.1| (AB; none, P13_P14_kinase, P13K_C2, P13K_rbd, PX, P13Ka_C2; 2.24
 452183; NM_005694; Hs.28298; adaptor-related protein complex 4, beta 1 subunit; Adaptin_N_Y_phosphatase; 2.23
 420529; D25259; Hs.319844; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; pkinase, DAG_PE-bind, RBD, ras, DC1, GFP; TM=M; 2.21
 408808; BE074219; Hs.17230; hypothetical protein FLJ22087; Armadillo_seg; TM=M; SS=M; 2.21
 451932; AA360954; Hs.27268; Homo sapiens cDNA: FLJ21933 f1s, clone HEP04337; SH3, PH, RhoGEF; TM=M; 2.21
 432008; AW296791; Hs.193170; hypothetical protein FLJ21687; LIM, Synaptophysin, Ion_trans, KOW; 2.20
 455840; BE145897; ; gb:MR0-HT0208-221299-204-b07 HT0208 Homo sapiens cDNA, mRNA sequence; P13_P14_kinase, P13Ka, P13_P14_kinase, P13Ka; 2.19
 429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor type, R; Y_phosphatase; TM=Y; SS=M; 2.19
 430975; AA490055; ; gb:ab05b09.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone 3', mRNA sequence; adenylate kinase, Thymidylate_kin; TM=M; 2.17
 407174; T79938; Hs.77062; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 5; Ig, none; 2.16
 450921; AA098790; Hs.146245; ESTs, Moderately similar to T17242 hypothetical protein DKFZp586B1417.1 [H.sapiens]; none; NA; NA; 2.15
 427209; H05509; Hs.92423; KIAA1556 protein; pkinase; TM=M; 2.14
 401917; AL050149; ; RAN binding protein 3; Orexin, SH2, STAT, STAT_bind, STAT_prot, Ion_trans, PAC, PAS, none; 2.12
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 f1s, clone HEP11919; adenylate kinase, none; 2.07
 439520; W76548; Hs.336621; ESTs, Moderately similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; Ion_trans, none; 2.06
 410439; R35943; Hs.63758; transferrin receptor 2; PA; TM=Y; 2.05
 448696; AI564769; Hs.173070; EST, Weakly similar to ZN42_HUMAN ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZF-1) [H.sapiens]; none, zfc-C2H2; 2.04
 449543; AF070632; Hs.23729; Homo sapiens clone 24405 mRNA sequence; K_tetra, Ion_trans, none; 2.04
 453496; AA442103; Hs.33084; solute carrier family 2 (facilitated glucose/fructose transporter), member 5; sugar_tr; TM=Y; SS=M; 2.02
 443952; AI149106; Hs.143530; ESTs; pkinase, none; 2.02
 437589; AA761322; Hs.269662; ESTs; SH2, SH3, C2, PH, RasGAP, none; 2.02
 422637; AA399024; Hs.118836; myoglobin; globin; TM=M; 2.01
 450253; AL133047; Hs.24715; Homo sapiens mRNA; cDNA DKFZp434D0215 (from clone DKFZp434D0215); partial cds; SH3; TM=M; 1.97
 401984; ; C17000146; gi|2143629|pir|J157156 Ca2+-calmodulin-dependent protein kinase (EC 2.7.1.123) I; pkinase; 1.96
 453464; AJ884911; Hs.32989; receptor (calcitonin) activity modifying protein 1; none; TM=Y; 1.95
 417733; AL048678; Hs.82503; H.sapiens mRNA for 3'UTR of unknown protein; none; NA; NA; 1.94
 411450; H49819; Hs.127301; ESTs; pkinase, none; 1.82
 406303; ; C16009922; gi|7499103|pir|J20903 hypothetical protein F14F4.3b - Caenorhabditis elegans gi; ABC_tran, GTP_EFTU, PRK, ABC_membrane; TM=Y; 1.80
 425009; X58288; Hs.154151; protein tyrosine phosphatase, receptor type, M; fn3, Ig, Y_phosphatase, MAM; TM=Y; SS=M; 1.74

425280; U31519; Hs.1872; phosphoenolpyruvate carboxykinase 1 (soluble); PEPCK; TM=M; 1.65
 425958; AW163271; Hs.301839; intracellular antigen detected by monoclonal antibody K1-1; intracellular hyaluronan-binding protein; Y_phosphatase, DSPc; TM=M; 1.63
 432563; NM_013261; Hs.198468; peroxisome proliferative activated receptor, gamma, coactivator 1; nm; TM=M; 1.51

5 TABLE 49B

Key: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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Key CAT Number Accession

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 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398
 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071
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 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525
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 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027
 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821
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 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120
 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148
 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525
 AW975503 BE763276 H74234 AA687376
 AA229762 AA230035
 BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472
 AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768606
 BC012771 BG397153 BF366195 AA337277 AA319285 AW843252

5	410032 400263	1490765_1 18977_1	BE065985 BE066083 BE066008 BE066093 BE065944 Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AI562865 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL556664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166759 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
10	413227 426966	25501_86 349_1	BE072622 M79082 NM_025237 AF326739 AW771508 AI498457 AI493134 AI383985 AI498691 BF431247 AI580267 D79913 AF331844 AA393939 AI783624 AA969408 AI768408 AA393768 AA210987 D57294 AA214584 AA207006 D55572 BG028348 BF772844 H83066 AW817969 H90985 BF755039 AI858183 BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AL556850 AL576404 AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL566475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA840454 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 N79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 AW978432 AA830185 N67023 R80000 AL036458 AA358606 AW962990 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593767 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066 AI758223 AW469334 BF940841 AW080348 AI270363 AI055892 BE464168 BF431797 BE350144 BF448739 AI693409 BF432999 D62848 AA398070 AI383375 AW611490 AA715338 AA715284 AA715344 AV752763 AI032142 N30308 N22181 H95390 AW675632 X98248 NM_002959 AU127082 AU143346 BE327147 AI168442 AA426361 BF056336 AA418378 AI470560 AI365213 BI032745 BI032986 AA969895 AA23278 AW291971 AA418326 AI198417 AI337018 BI032747 AA888000 AU099083 AU129681 AL036861 AA418275 BF887436 BF767448 AA232975 BI094065 BI859449 AU079651 BF877391 AW902319 BF878798 BG281450 AA418268 BG770672 BE890328 BI520437 BE387505 AW375004 BI020046 BI033747 BF800905 BF869732 N99710 BF905459 BE715637 BE746496 BF918537 BF751392 BF751390 BF369123 BG949840 AA984366 H85743 AA959348 AI890196 T92267 AA018359 H38111 BM050097 BF692315 AW805907 AI547305 AA631091 BF845219 BG949806 T92310 BE277220 U44839 NM_004651 BC000350 BI458316 AU117940 BG759024 BG746694 BE799505 BG831537 AI816335 AA325352 AL547005 AW157038 AI859331 AI816186 AU150786 AL043549 AW162880 AU159233 AI143169 T03478 BE727648 AA764725 BE206603 AI369814 AI984369 AW157545 BE221486 H99016 AU159025 AU074496 AI494516 BE245950 AA704385 AA280862 AI479595 AI369776 BE671398 T05538 AA682249 BI677303 BE645335 AI359434 H92868 D52599 D53609 D54715 T06015 BE222174 AI954706 D53218 D53787 R69889 W68696 AI497670 R70771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 BI044097 AL555239 BF220278 AA081991 AI819544 AW001573 AW131600 AI858764 D52367 W22034 BG818979 BG024561 BE702779 BI458863 BI910399 BG707755 BF348284 H10055 BI086315 BE620574 H41088 BG119517 W23267 W21941 AA328817 X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 AI910663 BF905778 BG251264 AL562106 AI890538 AW769258 AI590391 AI913055 AW083235 AI078474 AI925022 AW504628 AW129725 BE466589 AW002786 AW591760 AI968816 AW006268 AW593767 BG236814 AW769893 AW407608 AW075982 AI248207 AI762509 AI812070 AI249937 AW083561 AW080697 BF663046 BG745612 BG979546 AW793245 BI014177 AL519126 BE675314 AW806520 BI870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 BE798121 R09703 BI013066 AV659361 BE075267 BF743302 AL549208 AI950002 AI224961 AJ471552 AI356537 AA768943 AA677028 AI358509 AI147596 AI208057 AI042009 AA156840 AA156603 AA151281 AA151341 N73171 AL540476 AI950893 BG960775 AL573355 D78831 C17898 D78863 AW747857 BI062758 AW629481 AA837630 AA557850 AA531132 AW973966 AW747856 AA203524 W88451 BE539344 AA361027 BF328781 BE011406 BE011437 BE011402 BE011395 BE011428 BE011421 BE011407 BM046773 AA224297 T33786 T08951 T09274 T08592 T30936 AA350905 NM_018485 AB038237 U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA482223 BM145813 BM194565 AI870824 BE973573 BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687 BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF228599 AW167268 AI990460 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15	417886 452098 452203	1031334_1 161393_1 2630_1	
20			
25	439096 425505 400208	1241997_1 1228213_1 16640_1	
30			
35	407305 443068 433075	2466880_1 18695_17 78_6	
40			
45	400252	2656_2	
50	400209	16640_1	
55	444825	19904_1	
60	414991 432236 417527 425845 455608 418512 407393 400178	1785136_1 1001131_1 2431831_1 1283068_1 1478902_1 12225_6 6807_1 840_4	
65			
70	410927	3618_2	
75	449343	14470_1	
80	432639 417479 426477 418342	1237887_1 2356588_1 1296538_1 295203_2	

400275	18707_1	NM_006513 BC009390 X91257 BC000716 BM450041 BI771139 AV710955 AU120415 AU141179 AU121081 BE409287 AU141397 AU122238 BI256788 BE386217 AU143368 AU133780 AU139704 BG531086 BE268235 BE545230 AU143414 AV761720 AU129842 AU143343 BE270064 BG473378 BE298813 BI772360 BE617354 AU140124 BE277005 BG745716 BE814960 AW161287 AV762084 BG898985 AW674875 AA313975 AV749916 AA374328 BM011248 AU098465 AW238888 BG940091 BG284599 AW410037 AA378483 D49914 AL573323 AL549819 AL572282 AL572871 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW10038 BI262249 BG284713 AI659394 AI093582 AW965846 AA652205 AI686014 AA654357 AU146982 AW273447 AW157715 AW574750 BG683509 AW687824 AI818522 AA703770 BE542873 AA515504 AU154982 AA831254 AA828521 AI088602 AA854654 AA190869 BF062816 AA464944 BG261335 AI003584 BG402820 AA932098 W68695 AW182900 W37334 AI073864 C17924 C18528 AI299318 BF154399 BG319570 BF764242 BF764209 AI620320 T06029 BF447193 F29285 AL548949 BI333775 BE743602 BE618230 BE268139 BF036434 BE562718 BG774381 AA659833 AA297649 AA010945 BG105512 BE269205 T32623 BG015679 AL518518 AL571178 AL538396 AI049861 AL581976 AV752041 W26586 BE181609 AI963016 BG057603 AI720256 AA844560 AA055570 BE618606 C17428 AI042174 N93945 N69743 BF795208 AW057940 BI091399 AW975179 AA909936 H28712 W65445 AL515439 W37117 H66514 T85737 W37369
5		
10		
15	414087 1632850_1 423387 2612_2	W19712 BE247277 L13288 AA928785 AI608912 AW872978 AA565655 AI022915 AI304920 AI564366 AI668793 AI094557 T60038 R72302 H45409 AA508805 R46356 AA418798 BM129553 BM129126 BM129292 BM128865 AI808418 AI689932 AI806573 BF431808 AW872985 AW166269 H73241 T16182 AI264547 R73391 R72085 R72840 T83751 X75299 BF754348 R94105 AW449839 R73300 NM_004624 AI797007 BE045543 BF110021 BF754250 T83923 AW884084 AA903896 AA418962 L20295 R72351 H45098 AA961010 R73210 R46451 AW884085 BI022902 BI763932 BI910138
20	412283 1163164_1 409745 MH1944_5	AW936035 AW935951 AW935789 AW935881 AW936018 AW935892 BE069084 BI030997 AA921874 AW188822 BI027862 AI347618 AI361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 AA150780 BI033518 BI027818 BG015789 BI033807 AA341445
25	413285 12794_9 426578 358276_1 438005 694209_2 454701 352355_1 411140 1071177_1 407013 2073_7 432925 225876_1 417670 2139587_1 400189 2140_1	BE078405 BE078404 BE168534 AV742719 R23027 R63874 AA381749 BG542693 D63271 T94955 AA774994 BF697879 BG984482 AW854930 AW854941 AW814115 AW814431 AW814190 BF325887 BF325890 BF985536 AW819463 AW819514 AW819517 AW819518 AW819609 U35637 AA192323 AA194508 BG011583 F25712 AL596820 BE185376 AA878324 AI619686 AI014377 T85948 R07785 T86972 Y08200 NM_004581 BC003093 BE733834 BI753321 BG773890 BF091906 BI917541 AI023762 AA587230 BF435086 AI264262 AI687392 AI810536
30		AW589886 AI244419 AA749261 AA535435 AW205689 AI765770 AI765431 C02465 AW305347 AI818456 AA322111 AW381845 AW381829 AV749407 AA811636 AU159893 AA603065 AA652542 AI468678 R49616 AW381863 BE389867 BE182387 BF087771 AA527551 AA134051 AA831504 AA134052 AI871759 AW089048 BI913532 AA367709 BG828155 BF093014
35	411331 1076355_1 418177 6503_2	AW837178 T77002 F13038 AK056654 AJ420421 AI127111 AA705921 AA749298 AA776967 AI343768 AW070583 AA766587 AA804876 AA460658 AA394137 W72279 AW071467 AI343843 AA393817 AW769379 AA861873 AA715043 AW512448 AJ452856 AI819873 T17354 AW779778 BF477620 AI783605
40		AI624523 AA261906 AA514931 BI964124 AW576481 AI864544 AA490863 AA860972 BI953076 AI632879 AA291985 AA255873 BI826686 BI953833 Z38970 BI495302 BI495301 AI784395 AU185472 AA652150 AA652026 D20449 BI088167 BI260636 BE869946 AI935271 BI792882 AI762915 AI809275 AI813351 BF447139 AI052069 AI057127 AA398950 AA291984 AA292934 AA262543 BF760287 R64455 R72980 H90786 BE698016 AW959314 BI031449 AL574617 AA776284 AA393770 BM455617 BI602104 BI793150 N36710 H59529 BI005937 BI600748 BF085914 BF085907 BF835429 BF835210 BF085926 AA226136 BF836829 BF836606 BM007373 AI369807 BF085930 W25119 BI252884 BI001270 BE549079 BF238403 R56934
45	439518 23842_1 400211 3532_1	AF086341 W76326 W72300 NM_003899 D63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW028198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA897814 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AL535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876
50		AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044534 AA258853 BI037915 AA448037 BM461769 BI826686 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439551 AW264418 AA577618 AI802954 AA902292 AA468752 AI380374 AA722690 AI867708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746
55		AA447634 AI282427 F22456 T15901 AA825298 AW007436 BE934303 BG981939 AW373814 BM151638 AW956921 BM150080 BM153173 BM147451 BF953992 AA916696 AW444933 M78398 AW581147 AW608258 AA651910 AA132152 AW806295 T30326 D20054 AA310837 T06543 BM194508 BM193225 BM469348 AW964920 AA325930 BI833527 AW952193 AA738189 AA321051 BG987199 BF953967 T08890 BE869543 BG742857 BG986885 AA456880 BG001842 BF809452 AW892083 BF944342 T49551 W69981 BF764519 T15869 AA132030
60	426409 320121_1 459357 1086411_1 411226 1073516_1 415516 1875286_1 433090 7504_2 436206 31207_1	AW954027 AA377709 AW848421 T71427 T62567 AW833022 AW833054 H20760 R15237 Z43915 BF372479 F11411 AB038318 BC008888 BE905346 BE301941 AA705936 AW014954 BE378742 AI720050 BE395327 BG951204 AK001451 AU151098 AW515540 AW439618 AI671555 AW304953 AA565885 AI829434 AW590882 AI889234 AW117522 AA847824 AI636224 AA883540 AA169387 AW771571 AI130803 BF438773 AA088710 AI972691 AI972638 AI762358 AI473907 AI925905 AA502277 BG943806 BG218468 AA194853 AU128875 AA306025 BG986896
65	438141 1173217_1 439463 23351_1 454564 1061820_1 426481 1229053_1 426005 MH790_19	AA778849 AW946871 AW946782 AW946855 AF086283 W69200 W69304 AW807573 AW807572 AW963941 AA379825 AW963944 AA379564 NM_054014 X52220 BC005147 BI551326 AI393601 AW592611 AA608921 AA731598 W96331 AW590007 AI076813 AI022644 AA158365 AI699321 AI146747 AW296894 H85337 AA017692 AA354519 AA018512 D20081 R02704 AA825671 AA017651 AL135600 R02585 AA018849 BG749616 BF689840 R85326 AA677955 AA702354 AI076645 AI057359 H53178 W66484 H53074 BG988909 AW962456 AA367326 AA377499
70	416508 1974161_1 408087 633688_1 433434 194862_1 437158 59575_1	R39769 T53143 H60012 AW150645 AW811024 AW811148 AW811068 BF812525 AW504832 AI972567 AA588429 AI299594 AL050088 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021958 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847
75		AW875344 AW875287 AW875285 AW875286 BF381295 AW875402 AW875400 BE145815 BE145897 BF349721 DE145885 AK057266 BI767614 BI828586 AW069362 BI829572 AI826091 BI819382 AL040402
80	411902 1141058_1 455840 1518844_1 430975 56593_2	

TABLE 49C

5	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	NL_position
10	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	401027	7230983	Minus	70407-70554,71060-71160
	400991	8096825	Plus	159197-159320
	406137	9166422	Minus	30487-31058
	404083	9944029	Minus	16650-17082
15	404440	7528051	Plus	80430-81581
	400792	7382433	Plus	134339-134593
	404289	2769644	Plus	15049-15286,30267-30457
	401083	3242744	Plus	33192-33360
	402211	7689783	Minus	67414-68229
20	402705	8782736	Plus	69961-90114,90773-90895,91131-91261
	402233	7690102	Plus	90281-91477
	405370	2078469	Minus	38980-39111
	400846	9188605	Plus	39310-39474
	405484	5922025	Plus	199214-199579,199672-199920,200262-20049
25	401345	9926424	Plus	148042-148392
	400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807,
	406364	9256114	Minus	50715-50833
	405490	7705240	Plus	20683-20850
	400755	8119083	Minus	120084-120889
30	404276	9885189	Plus	127624-127856
	402915	7406502	Minus	140-276
	405616	5649378	Minus	2782-3308
	400847	9188605	Plus	44643-44835
	402328	4464283	Minus	13758-13922,14558-14752
35	405369	2078469	Minus	34183-34357,35686-35751
	400845	9188605	Plus	34428-34612
	403716	7239669	Plus	66899-87122
	402447	9796640	Plus	47605-47729,51696-51821,52070-52257,5330
	404140	9843520	Plus	37761-38147
40	405516	9454624	Plus	112707-112876,113676-113854
	405110	8096888	Minus	118940-119100
	403608	8308266	Minus	121321-121476
	401241	4827300	Minus	30503-30844,31056-31248
	405102	8076881	Minus	120922-121296
45	404185	4572584	Minus	129171-129327
	405545	1054740	Plus	118677-118807,119091-119296,121626-12182
	405411	3451356	Minus	17503-17778,18021-18290
	405602	4753260	Plus	44647-44778
	403391	9438337	Plus	42410-42544,83317-83540,86840-86922,8797
50	403869	7280046	Minus	34379-34583
	404942	7382153	Plus	92095-92252
	403142	9444521	Plus	89285-90131
	400844	9188605	Plus	24746-24872,25035-25204
	402704	8782736	Plus	37368-37493
55	402833	8918545	Plus	26987-27778
	401851	7770425	Minus	148443-146684,147794-147971,148351-14848
	401242	4827300	Minus	32616-32863
	401943	4914397	Plus	65925-66371
	402807	6456148	Minus	101542-101660,103476-103656
60	402603	9909396	Minus	141663-141852
	405328	3253114	Plus	21399-21583
	402974	9653349	Plus	124035-124321
	400987	8086488	Minus	22052-22185
	403335	8588884	Plus	112307-112524,114074-114703
65	401113	9966541	Minus	19419-19959
	401185	9625304	Minus	177393-177691
	404537	8247909	Minus	188775-189573
	405266	4156171	Minus	63337-63552
	402615	9926801	Plus	131390-132157
70	400566	9884730	Plus	64486-64714
	403212	7630897	Minus	156037-156210
	403290	8083176	Plus	19288-20076
	401342	9908882	Plus	3095-3242
	400471	9931670	Minus	105629-105760
75	405588	5002511	Plus	46180-46366
	400539	7574902	Plus	8559-8721
	403743	7652003	Minus	136463-136646
	403912	7710730	Minus	72000-72290,72431-72700,72929-73199
	405099	8074292	Minus	114365-114514,128635-128831
80	401445	8218584	Minus	93700-93886
	405480	2766593	Plus	33325-33659
	402183	7658390	Minus	100618-104258
	400749	7331445	Minus	9162-9293
	406139	9166768	Minus	72397-72602

5	402129	7704953	Minus	166156-166365
	400645	8117693	Minus	58471-58716
	403201	9958297	Minus	109782-109934
	403609	8308266	Minus	125974-126320
	400719	8118911	Minus	44579-44656,45294-45487,46449-46641
	403088	8954241	Plus	169894-170193,170504-170806
	403328	8469086	Minus	120428-120703
	403305	8099945	Plus	114632-114805
10	401702	1871197	Minus	68182-68325
	400777	8131663	Plus	70745-71121
	404956	7387343	Plus	55883-56203
	401917	9502466	Plus	25054-25229
	401984	4454511	Plus	103825-104024
15	406303	8575868	Plus	173622-173786

20 Table 50A lists about 414 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 85th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

25 Table 51A lists about 518 genes up-regulated in seminomatous testicular cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" seminomatous testicular cancer level was set to the 85th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 Table 52A lists about 673 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 2. The "average" testicular cancer level was set to the 75th percentile amongst testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 Table 53A lists about 735 genes up-regulated in testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" testicular cancer to "average" normal adult tissues was greater than or equal to 3. The "average" testicular cancer level was set to the 95th percentile amongst testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

45 Table 54A lists about 476 testis-specific genes downregulated in testicular cancer (non-seminomatous and seminomatous). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio (R1) of normal testis to normal adult tissues was greater than or equal to 3. R1 was calculated as the mean number of interquartile range values over the median normal adult body tissue expression among normal testicular samples. The ratio (R2) of "average" normal testis to "average" testicular cancer among these genes was greater than or equal to 2. The "average" normal testis level was set to the 50th percentile amongst normal testis. The "average" normal testicular cancer level was set to the 95th percentile amongst testicular cancer samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

50 Table 55A lists about 586 genes up-regulated in non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" non-seminomatous mixed germ cell testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" non-seminomatous mixed germ cell testicular cancer level was set to the 95th percentile amongst non-seminomatous mixed germ cell testicular cancers. The "average" normal adult testicular tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

60 Table 56A lists about 812 genes up-regulated in seminomatous testicular cancer compared to normal adult testicular tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" seminomatous testicular cancer to "average" normal adult testicular tissues was greater than or equal to 4. The "average" seminomatous testicular cancer level was set to the 50th percentile amongst seminomatous testicular cancers. The "average" normal adult tissue level was set to the 95th percentile amongst non-malignant testicular tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant normal testicular tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 50A:

65 Pkey: Uniqua Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UniGeneID: UniGene number
UniGene Title: UniGene gene title
R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult tissues

70	Pkey	ExAccn	UniGene	UniGene Title	R1
	432666	AW204069		ESTs, Weakly similar to unnamed protein	74.60
	432730	A1066520	Hs.131358	ESTs	50.55
	450581	AF081513	Hs.25195	TGF-beta 4	47.85
75	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	44.05
	423458	A1204212		ESTs	36.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	30.60
	448981	A1968719	Hs.195387	ESTs	26.40
	407710	AW022727	Hs.23616	ESTs	24.00
80	429486	AF155827	Hs.203953	hypothetical protein FLJ10339	19.35
	451106	BE382701	Hs.25960	N-MYC oncogene	18.85
	417407	AA923278	Hs.290906	ESTs, Weakly similar to proleuse (H.sapi	18.40
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	18.25

	424578	AK001973	Hs.150890	hypothetical protein	17.88
	418756	AA252254	Hs.226949	ESTs	17.20
	404996			Target Exon	16.15
5	447534	AW953935	Hs.288655	ESTs	15.80
	456847	AJ360456	Hs.37776	ESTs	15.00
	446979	AJ654443	Hs.197683	ESTs	14.80
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	14.75
	452838	U65011	Hs.30743	preferentially expressed antigen in mela	14.70
10	449322	AJ638616	Hs.196566	ESTs	14.35
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	12.95
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	12.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi	12.55
15	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.43
	406547			Target Exon	12.35
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	12.10
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	11.65
	408908	BE296227	Hs.250822	serine/threonine kinase 15	11.55
20	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	11.05
	430576	AF084866		gb:Homo sapiens envelope protein RIC-3 (10.08
	426866	U02330	Hs.172816	neuregulin 1	10.05
	446791	AI632278	Hs.195922	ESTs	10.05
	433159	AB035898	Hs.150587	kinesin-like protein 2	9.85
25	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.95
	427521	AW973352		ESTs	8.92
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	8.90
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.52
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
30	408465	AW196940	Hs.253277	ESTs	8.47
	444971	AI651116	Hs.148659	ESTs	8.35
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	8.00
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.95
35	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	7.75
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.65
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	7.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	7.36
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	7.25
40	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	7.22
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.13
	435918	AF263538	Hs.86232	growth differentiation factor 3	7.13
	412537	AL031778		nuclear transcription factor Y, alpha	7.08
45	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	7.05
	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.88
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	437052	AA861697	Hs.120691	ESTs	6.75
50	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.72
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.71
	457465	AW301344	Hs.122908	DNA replication factor	6.62
	442832	AW206560	Hs.253569	ESTs	6.54
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	6.30
55	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	6.30
	448588	AI970276	Hs.156905	KIAA1676	6.12
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	6.09
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fls, clone HE	5.95
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	5.85
60	443068	AI188710		ESTs	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	441287	AW293132	Hs.131373	ESTs	5.80
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	5.76
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
65	436902	AW247145	Hs.192729	ESTs	5.70
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.56
	436812	AW298067		gb:UH-BW0-ajp-g-09-0-UI.s1 NCI_CGAP_Su	5.55
70	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	5.51
	431354	BE046956	Hs.251673	DNA (cytosine-5)-methyltransferase 3 be	5.51
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	AI571514	Hs.133022	ESTs	5.45
	435663	AI023707	Hs.134273	ESTs	5.40
75	427567	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fls, clone NT	5.40
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.21
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	5.15
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.12
80	427961	AW293165	Hs.143134	ESTs	5.05
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.05
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!	5.00
	418477	AW022983		gb:EST374154 MAGE resequences, MAGG Homo	5.00
	418378	AW952081			4.95

	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.94
	443537	D13305	Hs.203	cholecystokinin B receptor	4.92
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	4.90
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
5	423642	AW452650	Hs.157148	hypothetical protein MGC13204	4.80
	449592	AI655494	Hs.195718	ESTs	4.75
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	4.73
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.68
10	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.60
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-i	4.48
	402145			Target Exon	4.48
15	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	4.47
	453289	AI188161	Hs.144527	ESTs	4.45
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	4.40
	422689	AW856655		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	4.32
20	426427	M86699	Hs.169840	TTK protein kinase	4.30
	420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	4.20
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.18
	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (4.15
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.10
25	438188	AA779975	Hs.128859	ESTs	4.10
	435514	AW592804		ESTs	4.10
	442333	AI650877	Hs.129302	ESTs	4.05
	413627	BE182082	Hs.246973	Intron of Bicaudal D homolog 1	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
30	448038	AW015073	Hs.232026	ESTs, Weakly similar to ROS2_HUMAN 52 KD	4.00
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	3.95
	419423	D26488	Hs.90315	KIAA0007 protein	3.95
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	3.95
	441553	AA281219	Hs.121296	ESTs	3.95
35	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.91
	409757	NM_001898	Hs.123114	cystatin SN	3.89
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.88
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	3.85
	403780			C4001759:gil133250[sp]P19474[RO52_HUMAN	3.84
40	421917	AB028943	Hs.109445	KIAA1020 protein	3.84
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary osta	3.84
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	3.82
	410193	AJ132592	Hs.59757	zinc finger protein 281	3.80
	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	3.80
45	415829	AW450198	Hs.163742	ESTs	3.78
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.77
	439780	AL109888		gb:Homo sapiens mRNA full length insert	3.70
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	3.68
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.66
50	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	3.65
	420900	AL045633	Hs.44269	ESTs	3.65
	426572	AB037783	Hs.170623	hypothetical protein FLJ11183	3.65
	426496	D31765	Hs.170114	KIAA0061 protein	3.60
	452461	N78223	Hs.108106	transcription factor	3.60
55	418379	AA218940	Hs.137516	fidgeline-like 1	3.50
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	3.45
	419384	AA490866	Hs.39429	ESTs	3.44
	453932	AW006303	Hs.329298	ESTs, Weakly similar to (define not ava	3.43
60	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	3.41
	422094	AF129535	Hs.272027	F-box only protein 5	3.40
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.40
	423198	M81933	Hs.1634	cell division cycle 25A	3.39
	424153	AA451737	Hs.141496	MAGE-like 2	3.38
65	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.37
	443715	AI583187	Hs.9700	cyclin E1	3.34
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.34
	449571	AW016812	Hs.200266	ESTs	3.34
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.31
70	452807	AA028933	Hs.162434	ESTs	3.31
	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	3.30
	421650	AA781795	Hs.122587	ESTs	3.30
	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	3.28
	438494	AA908678	Hs.130183	ESTs	3.23
75	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.22
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosis	3.18
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.18
80	442618	R56222	Hs.26514	ESTs	3.17
	415799	AA653718	Hs.225841	DKFZP434D193 protein	3.17
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.15
	450431	AW136797	Hs.266041	ESTs	3.13
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.12

	430835	AI240006	Hs.192326	ESTs	3.12
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.10
	417791	AW965339	Hs.111471	ESTs	3.10
	434609	R76593		gb:yi60c11.1.r1 Soares placenta Nb2HP Homo	3.05
5	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.04
	411975	AI916058	Hs.144583	ESTs	3.01
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fls, clone NT	2.99
	440207	AI371978	Hs.128326	ESTs	2.98
10	435726	BE535787	Hs.113170	ESTs	2.97
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.97
	450149	AW969781	Hs.132863	Zic family member 2 (odd-paired Drosophi	2.95
	435373	AW665538	Hs.117689	ESTs	2.93
	452571	W31518	Hs.34665	ESTs	2.93
15	454679	AW813110		gb:CM4-ST0189-051099-021-f05 ST0189 Homo	2.91
	414972	BE263782	Hs.77695	KIAA0008 gene product	2.90
	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.90
	420092	AA814043	Hs.88045	ESTs	2.89
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	2.89
20	434414	AI798376		gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens	2.87
	422746	NM_004484	Hs.119651	glypican 3	2.87
	446258	AI283476	Hs.263478	ESTs	2.86
	444371	BE540274	Hs.239	forkhead box M1	2.86
	409517	X90780		tropoin I, cardiac	2.85
25	414034	U89277	Hs.305985	early development regulator 1 (homolog o	2.84
	443169	AI038687	Hs.133338	ESTs	2.84
	447519	U46258	Hs.339665	ESTs	2.84
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	2.84
	406687	M31126		matrix metalloproteinase 11 (stromelysin	2.83
30	416201	AA467752	Hs.195161	ESTs	2.83
	412140	AA219591	Hs.73825	RAB6 interacting, kinesin-like (raklines	2.83
	457191	AI376228		Friend leukemia virus integration 1	2.82
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.81
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	2.80
35	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp43480425 (f	2.75
	427719	AI393122	Hs.134726	ESTs	2.75
	451684	AF216751	Hs.26813	CDA14	2.75
	414590	NM_000506	Hs.76530	coagulation factor II (thrombin)	2.74
40	442032	AW016786		ESTs	2.73
	437123	AL049285	Hs.302053	Homo sapiens mRNA; cDNA DKFZp564M193 (fr	2.72
	446528	AI076640	Hs.15243	nucleolar protein 1 (120kD)	2.72
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	2.71
	438180	AA808189	Hs.272151	ESTs	2.70
	453500	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	2.70
45	423765	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.69
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	2.69
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	2.68
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.67
	445413	AA151342	Hs.12677	CGI-147 protein	2.66
50	448769	N66037	Hs.38173	ESTs	2.66
	411022	AW936378		gb:QV4-DT0021-301299-071-f05 DT0021 Homo	2.65
	423600	AI633559	Hs.310359	ESTs	2.65
	447175	AI365208	Hs.293606	ESTs	2.65
	414151	AW976468	Hs.257245	ESTs	2.65
55	448877	AI583696	Hs.253313	ESTs	2.62
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	2.61
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	2.61
	449665	AI655391	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	2.61
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	2.60
60	429228	AI553633		ESTs	2.60
	410929	H47233	Hs.30643	ESTs	2.59
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	2.58
	446142	AI754693	Hs.145968	ESTs	2.56
	445093	AI207197		ESTs	2.56
65	413686	AI469213	Hs.71404	ESTs	2.55
	447733	AF157482	Hs.19400	MAD2 (mitotic arrest deficient, yeast, h	2.55
	420218	AW958037		ribosomal protein L4	2.55
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	2.55
	414312	AA155694	Hs.191060	ESTs	2.55
70	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synthet	2.55
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	2.52
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	2.51
	435096	AA664977		gb:nu73b07.s1 NCI_CGAP_Ah1 Homo sapiens	2.50
	422468	AA355210		gb:EST63589 Jurkat T-cells V Homo sapien	2.50
75	449576	AW014631	Hs.225068	ESTs	2.50
	415684	D59356		sorbitol dehydrogenase	2.50
	452226	AA024898	Hs.157103	ESTs	2.50
	421451	AA291377	Hs.50831	ESTs	2.50
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.50
80	418203	X54942	Hs.83758	CDC28 protein kinase 2	2.49
	453941	U39817	Hs.36820	Bloom syndrome	2.49
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.49
	449655	AI021987	Hs.59970	ESTs	2.49

	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	2.49
	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	2.48
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	2.48
5	445363	NM_005993	Hs.12570	tubulin-specific chaperone d	2.47
	452404	AW450675	Hs.212709	ESTs	2.46
	444823	BE262989	Hs.12045	putative protein	2.46
	427675	AW138190	Hs.180248	zinc finger protein 124 (HZF-16)	2.45
	444159	AF116846	Hs.10431	dead ringer (Drosophila)-like 2 (bright	2.45
10	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	2.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.45
	433183	AF231338	Hs.222024	transcription factor BMAL2	2.45
	447350	AI375572		v-erb-a avian erythroblastic leukemia vi	2.45
	428728	NM_016625	Hs.191381	hypothetical protein	2.43
15	407325	AA291180	Hs.328476	ESTs, Weakly similar to alternatively sp	2.43
	410276	AI554545		angiopoietin-2	2.42
	444670	H58373	Hs.332938	hypothetical protein MGC5370	2.42
	419029	AA233397	Hs.326290	hypothetical protein FLJ12581	2.42
	437908	AI082424		ESTs	2.41
20	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.41
	425202	AW962282	Hs.152049	ESTs, Weakly similar to I38022 hypotheti	2.40
	425212	AW962253	Hs.171618	ESTs	2.39
	423787	AJ295745	Hs.236204	nuclear pore complex protein	2.38
	425601	AW629485	Hs.140720	GSK-3 binding protein FRAT2	2.38
25	449676	AW380579	Hs.209657	ESTs	2.38
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.37
	453227	AW135862	Hs.243991	ESTs	2.37
	417833	AW003251	Hs.86264	hypothetical protein FLJ14549	2.36
	451999	AW176401	Hs.27424	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.36
30	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	2.35
	418866	T65754		gbryc11c07.s1 Stralagene lung (937210) H	2.35
	410060	NM_001448	Hs.58367	glypican 4	2.35
	449138	AW294215	Hs.195631	ESTs	2.35
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.35
35	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	2.35
	436481	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	2.34
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	2.34
	407818	AL021938	Hs.40154	Jumonji (mouse) homolog	2.34
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	2.33
40	401704			NM_021195*:Homo sapiens claudin 6 (CLDN6	2.33
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (I	2.32
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.32
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	2.31
	429271	AF039850	Hs.198515	dead ringer (Drosophila)-like 1	2.30
45	432865	AI753709	Hs.152484	ESTs, Weakly similar to I38022 hypotheti	2.30
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	2.30
	448755	AW503807	Hs.21907	histone acetyltransferase	2.30
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	2.29
50	441031	AI110684	Hs.7645	fibrinogen, B beta polypeptide	2.29
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.28
	407289	AA135159	Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	2.27
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.26
	401220			branched chain aminotransferase 1, cytos	2.26
55	453985	N44545	Hs.251865	ESTs	2.25
	414890	BE281095	Hs.77573	uridine phosphorylase	2.25
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.25
	418140	BE613836	Hs.83551	microfibrillar-associated protein 2	2.25
	424765	AA428211		hypothetical protein FLJ14033 similar to	2.25
60	419278	AU076799	Hs.1247	apolipoprotein A-IV	2.24
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	2.24
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	2.23
	417273	AK002209	Hs.81831	Homo sapiens cDNA FLJ11347 fis, clone PL	2.23
	449722	BE280074	Hs.23960	cyclin B1	2.22
65	443184	AI638728	Hs.131973	ESTs	2.22
	416391	AI878927	Hs.79284	mesoderm specific transcript (mouse) hom	2.21
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	2.21
	435045	BE297155	Hs.143698	ESTs	2.21
	414883	AA926960		CDC28 protein kinase 1	2.21
70	446323	AI288274	Hs.345792	ESTs	2.20
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.20
	448757	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	2.20
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	2.20
	418973	AA233056	Hs.191518	ESTs	2.20
75	413582	AW295647	Hs.71331	hypothetical protein MGC5350	2.20
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	2.20
	443748	AW206447		gb:UL-H-B11-atg-g-02-0-UL.s1 NCL_CGAP_Su	2.20
	415989	AI267700		ESTs	2.20
	400195			NM_007057*:Homo sapiens ZW10 interactor	2.20
80	428878	AA436884	Hs.48926	ESTs	2.20
	431805	NM_014053	Hs.270594	FLVCR protein	2.19
	446839	BE091926	Hs.16244	mitotic spindle coiled-coil related prot	2.19
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	2.18
	417389	BE260964	Hs.82045	midkine (neurite growth-promoting factor	2.18

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	2.18
	413992	W26276	Hs.104557	RNA, U2 small nuclear	2.18
	412722	AI343300	Hs.15091	ESTs	2.18
	409089	NM_014781	Hs.50421	KIAA0203 gene product	2.17
	430809	AI791150	Hs.262009	ESTs, Moderately similar to I38022 hypot	2.17
	405542			C19000728*:g 12585552 sp Q9Y2Q1 Z257_HU	2.17
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.17
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothi	2.17
10	425580	L11144	Hs.1907	galanin	2.16
	439398	AA284267	Hs.221504	ESTs	2.16
	452833	BE559681	Hs.30736	KIAA0124 protein	2.15
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	2.15
	444863	AW384082	Hs.104879	serine (or cysteine) proteinase inhibito	2.15
	449410	AA001356	Hs.18159	ESTs	2.15
15	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypothi	2.15
	427953	AA417944	Hs.44331	ESTs	2.15
	422281	M36803	Hs.346935	hemopexin	2.15
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	2.14
20	444960	AI611317	Hs.341531	ESTs	2.14
	415890	H08225	Hs.268712	ESTs	2.14
	402099			ENSP000000217725*:Laminin alpha-1 chain p	2.14
	427779	AA906997	Hs.180780	TERRA protein	2.14
	453005	AW055308	Hs.31803	ESTs, Weakly similar to N-WASP [Hsapien	2.14
25	422170	AI791949	Hs.112432	anti-Mullerian hormone	2.14
	414161	AA136106	Hs.184852	KIAA1553 protein	2.14
	437623	D63880	Hs.5719	chromosome condensation-related SMC-asso	2.13
	449810	AB008681	Hs.23994	activin A receptor, type IIB	2.11
	450663	H43540	Hs.25292	ribonuclease H1, large subunit	2.11
30	419525	T79257	Hs.1259	asialoglycoprotein receptor 2	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.10
	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	2.10
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	2.10
	430821	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr	2.09
35	418552	AF198254	Hs.86088	IGF-II mRNA-binding protein 1	2.09
	408291	AB023191	Hs.44131	KIAA0974 protein	2.09
	425474	Z48054	Hs.158084	peroxisome receptor 1	2.09
	453028	AB006532	Hs.31442	RecQ protein-like 4	2.09
	447831	AI433293	Hs.164115	ESTs	2.08
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.08
	429166	AB033096	Hs.197668	KIAA1270 protein	2.08
	432446	AA542845	Hs.294088	GAJ protein	2.08
	417866	AW067903	Hs.82772	collagen, type XI, alpha 1	2.07
	431093	AB031038	Hs.301704	eomesodermin (Xenopus laevis) homolog	2.07
45	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.07
	449569	AI656634	Hs.195389	ESTs	2.07
	429999	AI761902	Hs.99597	ESTs	2.06
	420552	AK000492	Hs.98806	hypothetical protein	2.06
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	2.05
50	406137			NM_000179*:Homo sapiens mutS (E. coli) h	2.05
	413833	Z15005	Hs.75573	centromere protein E (312kD)	2.05
	450375	AA009647		a disintegrin and metalloproteinase doma	2.05
	409066	AA052980	Hs.66960	ESTs	2.05
	425700	AF076292	Hs.159251	forkhead box H1	2.05
55	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	2.05
	409093	BE243834	Hs.50441	CGI-04 protein	2.05
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.04
	408446	AW450669	Hs.45068	hypothetical protein DKFZp434I143	2.04
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.04
60	429840	AA458699	Hs.99496	ESTs	2.03
	409717	AW452871	Hs.56043	CGI-115 protein	2.02
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.02
	448275	BE514434	Hs.20830	kinesin-like 2	2.02
	432731	R31178	Hs.287820	fibronectin 1	2.02
65	405157			NM_003213*:Homo sapiens TEA domain famil	2.02
	425274	BE281191	Hs.155462	minichromosome maintenance deficient (mi	2.01
	423739	AA398155	Hs.97600	ESTs	2.01
	421310	AW630087	Hs.103315	trinucleotide repeat containing 1	2.00
	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	2.00
70	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	2.00
	407259	L02256		gb:Human Fab fragment binding syncytial	2.00

TABLE 50B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
		BG215094 BG198867 BG196332 BG208220 BG212418

5	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603
	427521	513212_1	AJ352469 BE061601 BI062752 AW818206 BF887722
	427486	684159_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
	412537	14066_1	AA548736 AA768578 AI539081 AW025957 AF736837 N79575 AW594357 AA480892
10			BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
			AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114
			AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364
			BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793
			AA382556 AW235763 AA927051 AI862075 BE886691 BE619282
	443068	18695_17	AV752763 AI032142 N30308 N22181 H95390 AW675632
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 AI690673
	418477	4172_1	BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
			AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424
15	418378	1227421_1	AA218925 AW962081 AA354237
	422689	874209_1	AW954733 AA315006 AW856665
	435514	132288_1	AA683356 AW592804 AI150287
	439780	49082_1	AL109588 R23665 R26578
	434609	14739_1	AF147390 R76593 R76594
20	454679	174325_1	AW813110 BF771370 BF771371 AW813113 AW003381
	434414	35978_1	AF134164 BF809407 AA218567 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
			AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 BF754298
			AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
			BF854337
25	409517	4537_1	NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070
			C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04458 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255
			T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339
	406687	0_0	M31126
	457191	1389182_1	AI216469 AI354789 AA446136 H24336 AA446443 AI376228 R48940
30	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
			AW840571
	413646	1525656_1	BE155042 BE155040 BE154987 BE155012
	442032	15407_1	BF223060 BF222818 AI950472 AW016786 AI207136 AI969730 BF222890 AI633857 AI968711 AA974235 AI352637
	411022	1066666_1	AW936378 AW936544 AW813513
35	429228	215430_1	BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620
			AW969605 AI553633
	445093	175963_1	AI207197 BF773544 AW196462
	420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
			AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727
40	435096	125215_1	H30075 AA664977 AW975278
	422468	216674_1	AW962701 AA310998 AW962699
	415684	18695_18	BF666746 C59356 BG678312 N56640 AA166861
	447350	2267324_1	AI375572 AI480404 BF430912 T06882
	410276	641443_1	AA083514 AI554545 AW169852 AI363822 AI633826 AI656026 AI765624 AA147545 AA147552
45	437908	13268_11	AJ740586 AA771806 BE500995 AW204531 AI082424 AI033879 BF093176 AA771764 D38676
	418866	245947_1	T65754 AA229658 AA229857
	424765	6857_1	AK021881 AU145974 AU145787 C16964 AA428211 AU119698 AA993264 BF999192 AW903017 AA346559 AU119446 AW581679 AA991677
			AW898165 AW386878 AW890957 Z18340
50	414883	8371_2	AF274943 BG494894 AI719075 AA908783 AI935150 AI422691 AA910544 AA583187 BM272167 AI828996 AA527373 AW972459 AI831350
			AA772418 AI033892 AA100926 AU154749 AI459432 AI423513 AI094597 AA740817 AI991988 AI090262 AI312104 BI256707 AA459522 AA416871
			AI075239 AI339996 AA701623 AI139549 AI336880 AA633648 AI989380 AI362835 AA399239 AI146955 BF514270 N92892 AI348243 AI278887
			AA459292 AI494230 BF507531 AI492600 AA962596 AW813002 AA293140 AA235549 BF108854 AA954344 N49682 AI457100 AW589407
			AW300758 BE220715 BE220698 BE569091 BM009647 BF900351 AI537692 AI203723 AI857576 AA584410 AW371667 BM172363
	443748	669881_1	BM467830 AI084433 AW208447 AI400976 AI248530 R16553
55	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF090208 BF909980 BF095153
			BG285837 AI720344 BF541715 AA355086 AA172236
	400195	16894_2	BM477554 BM423987 BC020979 AF067656 NM_007057 BI869291 BG468263 BG760599 BI261788 AA855060 BE257094 BF212452 BE888249
			BI259219 AW409765 BE089556 AL564377 BI258884 AW440401 AL578460 AL578434 AL556136 BG036804 AL531381 AW371767 BG610641
			BF102552 BE294929 BF792282 BG121657 BG502285 BG777493 AL584510 AW770358 AA573448 AA564001 AA969560 AW078946 AW750065
60			AL573860 AA143778 H99221 AA969210 AW103401 AW750073
	450375	16559_3	BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410
			H59605 BE157601 AA113758
65	TABLE 50C		
	Pkey:	Unique number corresponding to an Eos probe set	
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.	
	Strand:	Indicates DNA strand from which exons were predicted.	
70	NL_position:	Indicates nucleotide positions of predicted exons.	
	Pkey	Ref	Strand NL_position
	404996	6007890	Plus 37999-38145,38652-38998,39727-39872,4055
	406547	7711513	Minus 172780-174358
75	402145	8018280	Plus 113086-114800
	403780	8076989	Plus 93160-93409
	403432	9719611	Minus 68204-68392
	401704	3097841	Plus 24712-25374
	403433	9719611	Minus 72225-72437
80	401220	9929324	Minus 48079-48279
	406542	7711499	Plus 117335-118473
	402099	8117697	Plus 121553-121742,123265-123423
	406137	9166422	Minus 30487-31058

405157 9965228 Plus 156363-156502,157573-157746

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TABLE 51A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of seminomatous testicular cancer compared to normal adult tissues

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Pkey	ExAccn	UnigeneID	Unigene Title	R1
418696	AW959433	Hs.326290	hypothetical protein FLJ12581	56.62
432666	AW204069		ESTs, Weakly similar to unnamed protein	49.00
432730	AI066520	Hs.131358	ESTs	37.64
426534	U58096	Hs.2051	testis specific protein, Y-linked	37.60
428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	32.70
420367	AA259090	Hs.257028	ESTs	29.98
420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	26.50
437052	AA861697	Hs.120591	ESTs	26.42
407710	AW022727	Hs.23616	ESTs	23.85
420528	AF130728	Hs.98586	doublesex and mab-3 related transcript	23.12
424578	AK001973	Hs.150890	hypothetical protein	22.27
420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	22.06
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	20.46
429486	AF155827	Hs.203963	hypothetical protein FLJ10339	18.44
434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	15.92
430252	AI638774	Hs.105328	testes development-related NYD-SP20	15.44
423458	AI204212		ESTs	15.28
438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	15.26
427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	14.84
427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	12.98
426427	M86699	Hs.169840	TTK protein kinase	12.44
420401	AK001907	Hs.97464	hypothetical protein	12.40
406937	U14622		gb:Human transketolase-like protein gene	11.60
430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	11.55
425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	11.52
418477	AW022983		gb:d46h12.y1 Morton Fetal Cochlea Homo	10.94
434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	10.78
436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCL CGAP_Su	10.54
437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	10.40
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	10.32
421241	X91817	Hs.102866	transketolase-like 1	10.14
410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	10.02
418134	AA397769	Hs.86617	ESTs	9.76
433159	AB035898	Hs.150587	kinesin-like protein 2	9.56
433975	AA971953	Hs.122055	ESTs	9.36
422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	9.30
410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	9.22
431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	9.16
436899	AA764852		ESTs	8.76
426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.76
424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	8.64
408908	BE296227	Hs.250822	serine/threonine kinase 15	8.50
413627	BE182082	Hs.246973	Intron of Bicaudal D homolog 1	8.42
425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	8.30
415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.14
408728	AL137379	Hs.47125	hypothetical protein FLJ13912	8.14
406547			Target Exon	8.02
424153	AA451737	Hs.141496	MAGE-like 2	7.90
434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.64
437421	AA917062		ESTs	7.53
409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	7.50
419423	D26488	Hs.90315	KIAA0007 protein	7.38
428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	7.38
431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	7.32
430676	AF084866		gb:Homo sapiens envelope protein RUC-3 (7.29
436608	AA628980	Hs.192371	down syndrome critical region protein DS	7.25
435206	AI432364	Hs.160594	ESTs	7.20
414972	BE263782	Hs.77695	KIAA0008 gene product	7.12
407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	7.10
426518	Z43039	Hs.170198	KIAA0009 gene product	7.10
436513	AJ278110	Hs.125507	DEAD-box protein	7.04
427521	AW973352		ESTs	6.96
423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	6.92
422232	D43945	Hs.113274	transcription factor EC	6.90
420047	AI478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	6.83
431041	AA490967	Hs.197955	KIAA0704 protein	6.76
427335	AA448542	Hs.251677	G antigen 7B	6.58
422797	AB033064	Hs.236463	KIAA1238 protein	6.55
418379	AA218940	Hs.137516	ridgetin-like 1	6.46

5	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	6.45
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.44
	422665	AJ011812	Hs.119018	transcription factor NRF	6.38
	433701	AW445023	Hs.15155	ESTs	6.34
	436909	AA907120		ESTs	6.28
10	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	6.27
	429228	AI553633		ESTs	6.26
	419384	AA490866	Hs.39429	ESTs	6.23
	435514	AW592804		ESTs	6.08
	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	5.90
15	430835	AI240006	Hs.192326	ESTs	5.89
	438188	AA779975	Hs.128859	ESTs	5.88
	429120	AK001673	Hs.195530	hypothetical protein FLJ10811	5.80
	408758	NM_003686	Hs.47504	exonuclease 1	5.78
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	5.70
20	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.67
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	5.64
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	5.58
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.58
	419556	U29615	Hs.91093	chitinase 1 (chitinotrioidase)	5.55
25	438494	AA908878	Hs.130183	ESTs	5.52
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	5.52
	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	5.48
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	5.45
	413623	AA825721	Hs.246973	intron of Bicaudal D homolog 1	5.36
30	402145			Target Exon	5.30
	414136	AA812434		SMC2 (structural maintenance of chromoso	5.28
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	5.22
	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	5.16
	408460	AA054726	Hs.285574	ESTs	5.14
35	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.12
	420900	AL045633	Hs.44269	ESTs	5.08
	426496	D31765	Hs.170114	KIAA0061 protein	5.01
	407122	H20276	Hs.31742	ESTs	5.00
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	4.95
40	402199			Target Exon	4.90
	409103	AF251237	Hs.112208	XAGE-1 protein	4.90
	416859	H43437	Hs.80305	hypothetical protein MGC14258	4.84
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	4.82
	410929	H47233	Hs.30643	ESTs	4.73
45	417886	AA214584		ESTs	4.73
	426223	AW977812	Hs.130391	ESTs	4.72
	409421	AA199883	Hs.67624	ESTs	4.72
	428249	AA130914	Hs.183291	zinc finger protein 268	4.71
	429999	AI761902	Hs.99597	ESTs	4.68
50	431721	AB032996	Hs.268044	KIAA1170 protein	4.68
	408321	AW405882	Hs.44205	coristatin	4.67
	419197	N48921	Hs.27441	KIAA1615 protein	4.66
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	4.64
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	4.64
55	427119	AW880562	Hs.272525	ESTs	4.64
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.64
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.64
	409066	AA062980	Hs.66960	ESTs	4.62
	416201	AA467752	Hs.195161	ESTs	4.53
60	433330	AW207084	Hs.132816	hypothetical protein MGC14801	4.52
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	4.50
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	4.46
	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.46
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.34
65	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	4.32
	418971	AA360392	Hs.87113	ESTs	4.30
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (4.29
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.21
	415717	AA167270	Hs.130435	ESTs	4.18
70	423198	M81933	Hs.1634	cell division cycle 25A	4.12
	433849	BE465884	Hs.280728	ESTs	4.12
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	4.11
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	4.07
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.07
75	414725	AA769791		ring finger protein 21, interferon-respo	4.05
	408291	AB023191	Hs.44131	KIAA0974 protein	4.05
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.04
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.04
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.03
80	421917	AB028943	Hs.109445	KIAA1020 protein	4.02
	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	4.02
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	4.01
	436360	AI962796	Hs.156100	ESTs	4.00
	438624	AA889055	Hs.123468	ESTs	3.99
	434609	R76593		gb:Y160c11.1 Soares placenta Nb2HP Homo	3.92
	411945	AL033527	Hs.92137	L-myc-2 protein(MYCL2)	3.90
	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.90

	413833	Z15005	Hs.75573	centromere protein E (312kD)	3.90
	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.88
	438456	AA913381	Hs.20594	ESTs	3.88
5	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	3.87
	412537	AL031778		nuclear transcription factor Y, alpha	3.86
	418661	NM_001949	Hs.1189	E2F transcription factor 3	3.85
	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	3.83
	422094	AF129535	Hs.272027	F-box only protein 5	3.82
10	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.80
	416350	AF188625	Hs.189507	phospholipase A2, group IID	3.78
	426054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	3.76
	401435			C14000397*:gij7499898 pir T33295 hypoth	3.76
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	3.74
	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	3.70
15	409089	NM_014781	Hs.50421	KIAA0203 gene product	3.70
	426067	AW664691	Hs.97053	ESTs	3.67
	415584	D59356		sorbitol dehydrogenase	3.66
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.62
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	3.62
20	427761	AA412205	Hs.140996	ESTs	3.61
	433641	AF080229		gb:Human endogenous retrovirus K clone 1	3.60
	418216	AA662240	Hs.283099	AF15q14 protein	3.59
	438180	AA808189	Hs.272151	ESTs	3.58
	424281	AA766243		gb:aa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	3.56
25	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	3.55
	428878	AA436884	Hs.48926	ESTs	3.54
	438885	AI886558	Hs.184987	ESTs	3.53
	416445	AL043004	Hs.79337	KIAA0135 protein	3.52
	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.51
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	3.49
	427298	AA400495		ESTs	3.48
	420218	AW958037		ribosomal protein L4	3.40
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	3.40
35	410420	AA224053	Hs.172405	cell division cycle 27	3.40
	432809	AA565509	Hs.131703	ESTs	3.36
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	3.34
	421373	AA808229	Hs.46677	ESTs	3.34
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.31
40	418830	BE513731	Hs.88959	hypothetical protein MGC4816	3.30
	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.30
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.26
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypothi	3.22
45	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	3.21
	434288	AW189075	Hs.116265	fibrillin3	3.20
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.19
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.17
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.17
	420161	AI683069	Hs.120817	ESTs	3.17
50	414618	AI204600	Hs.96978	hypothetical protein MGC10764	3.16
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	3.14
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitosi	3.14
	423419	R55336	Hs.23539	ESTs	3.13
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.12
55	408092	NM_007057	Hs.42650	ZW10 Interactor	3.12
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.12
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	3.12
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.12
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.11
60	420552	AK000492	Hs.98806	hypothetical protein	3.11
	402408			NM_030920*:Homo sapiens hypothetical pro	3.10
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	3.10
	415829	AW450198	Hs.163742	ESTs	3.09
	423739	AA398155	Hs.97600	ESTs	3.07
65	418459	R85436	Hs.268814	ESTs	3.07
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.07
	437257	AI283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	3.06
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.06
	420524	AB010575	Hs.98547	amiloride-sensitive cation channel 3, te	3.06
70	433023	AW864793		thrombospondin 1	3.04
	421633	AF121860	Hs.106260	sorting nexin 10	3.04
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.04
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	3.03
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.03
75	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (3.03
	425312	AA354940	Hs.145958	ESTs	3.02
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.01
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.01
	432446	AA542845	Hs.294088	GAJ protein	3.01
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.00
80	436902	AW247145	Hs.192729	ESTs	3.00
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.00
	430056	X97548	Hs.228059	KRAB-associated protein 1	2.98
	427617	D42063	Hs.199179	RAN binding protein 2	2.98

	406367		NM_022357:Homo sapiens putative metallo	2.97
	418866	T65754	gb:yc11c07.s1 Striatogene lung (937210) H	2.97
	435918	AF263538	growth differentiation factor 3	2.97
5	436511	AA721252	Hs.86232 ESTs	2.96
	402680		Hs.291502 Target Exon	2.96
	414161	AA136106	Hs.184852 KIAA1553 protein	2.95
	427239	BE270447	ubiquitin carrier protein	2.95
	433683	AI817723	Hs.22678 hypothetical protein FLJ21832	2.94
10	417576	AA339449	Hs.82285 phosphoribosylglycinamide formyltransfer	2.94
	402299		Target Exon	2.92
	420697	AA827705	Hs.26605 ESTs	2.90
	427719	AI393122	Hs.134726 ESTs	2.90
	419131	AA406293	Hs.109526 ESTs	2.89
	410048	W76467	Hs.343874 proline oxidase homolog	2.89
15	427314	AB033024	Hs.175475 KIAA1198 protein	2.89
	424315	AW614850	Hs.193384 putative 28 kDa protein	2.88
	430335	D80007	Hs.239499 KIAA0185 protein	2.87
	410361	BE391804	Hs.62661 guanylate binding protein 1, Interferon-	2.87
	413686	AI469213	Hs.71404 ESTs	2.87
20	429183	AB014604	Hs.197955 KIAA0704 protein	2.86
	430292	AK000634	Hs.238270 hypothetical protein FLJ20627	2.86
	422726	U11690	Hs.1572 facio-genital dysplasia (Aarskog-Scott sy	2.86
	437834	AA769294	gb:nz36g03.s1 NC1_CGAP_GCB1 Homo sapiens	2.86
25	435159	AA668879	Hs.116649 ESTs	2.84
	428361	NM_015905	Hs.183858 transcriptional intermediary factor 1	2.84
	430388	AA356923	Hs.240770 nuclear cap binding protein subunit 2, 2	2.84
	434070	AF116652	Hs.270087 hypothetical protein PRO0813	2.83
	429323	NM_001649	Hs.2391 apical protein, Xenopus laevis-like	2.83
	433247	AB040948	Hs.142856 KIAA1515 protein	2.82
30	415884	H22966	Hs.13471 ESTs	2.82
	427668	AA298760	Hs.180191 hypothetical protein FLJ14904	2.82
	437162	AW005505	Hs.5464 thyroid hormone receptor coactivating pr	2.81
	401091		decay accelerating factor for complement	2.81
35	425601	AW629485	Hs.140720 GSK-3 binding protein FRAT2	2.79
	428597	AK000147	Hs.295909 hypothetical protein FLJ10700	2.79
	417705	AW134952	Hs.175220 hypothetical protein FLJ14541	2.79
	438243	AI581311	ESTs	2.78
	418203	X54942	Hs.83758 CDC28 protein kinase 2	2.78
40	410704	BE076754	gb:CM1-BT0601-180200-121-b10 BT0601 Homo	2.77
	429063	AW363845	Hs.322903 ESTs, Weakly similar to A46010 X-linked	2.76
	427147	AA398587	Hs.97414 ESTs	2.76
	430552	AA176374	Hs.243886 nuclear autoantigenic sperm protein (his	2.76
	437660	W31708	Hs.55304 ESTs	2.74
45	425237	U07695	Hs.155227 EphB4	2.72
	419335	AW960146	Hs.284137 hypothetical protein FLJ12888	2.72
	426386	AA748850	Hs.125830 bladder cancer overexpressed protein	2.70
	423123	NM_012247	Hs.124027 SELENOPHOSPHATE SYNTHETASE ; Human selen	2.70
	430968	AW972830	gb:EST384925 MAGE resequences, MAGL Homo	2.70
50	420596	NM_002692	Hs.99185 polymerase (DNA directed), epsilon 2	2.68
	419741	NM_007019	Hs.93002 ubiquitin carrier protein E2-C	2.68
	401464		histone deacetylase 5	2.68
	411856	H67899	Hs.4190 Homo sapiens cDNA: FLJ23269 fis, clone C	2.68
	411365	M76477	Hs.289082 GM2 ganglioside activator protein	2.68
55	419029	AA233397	Hs.326290 hypothetical protein FLJ12581	2.67
	421654	AW163267	Hs.105469 suppressor of var1 (S.cerevisiae) 3-like	2.66
	421535	AB002359	Hs.105478 phosphoribosylformylglycinamide synthase	2.66
	423453	AW450737	Hs.128791 CGI-09 protein	2.66
	412673	AL042957	Hs.31845 ESTs	2.65
60	410006	AW732308	Hs.57783 eukaryotic translation initiation factor	2.65
	434159	AW135214	Hs.191828 ESTs	2.65
	427260	AA663848	gb:ae70b06.s1 Striatogene schizo brain S1	2.64
	439053	BE244588	Hs.6456 chaperonin containing TCP1, subunit 2 (b	2.64
	414706	AW340125	Hs.76989 KIAA0097 gene product	2.64
65	433979	AA620999	gb:ag03a08.s1 Soares_testis_NHT Homo sap	2.64
	403969		ENSP00000034683:Zinc finger protein 131	2.64
	420582	BE047878	Hs.99093 Homo sapiens chromosome 19, cosmid R2837	2.64
	418355	L42563	Hs.1165 ATPase, H7 transporting, nongastric, alp	2.63
	411127	AA668995	Hs.218329 hypothetical protein	2.62
70	437205	AL110232	Hs.279243 Homo sapiens mRNA; cDNA DKFZp564D2071 (f	2.62
	412123	BE251328	Hs.73291 hypothetical protein FLJ10881	2.61
	436481	AA379597	Hs.5199 HSPC150 protein similar to ubiquitin-con	2.60
	408446	AW450669	Hs.45068 hypothetical protein DKFZp434I143	2.59
	437033	AW248364	Hs.5409 RNA polymerase I subunit	2.58
	418592	X99226	Hs.284153 Fanconi anemia, complementation group A	2.58
75	415585	R59946	Hs.184852 KIAA1553 protein	2.57
	424800	AL035588	Hs.153203 MyoD family inhibitor	2.57
	426470	AA528794	Hs.128644 ESTs	2.57
	426919	AL041228	ELAV (embryonic lethal, abnormal vision,	2.56
80	421209	AJ010230	Hs.102576 ret finger protein-like 1 antisense	2.56
	437495	AA452378	Hs.146668 Homo sapiens mRNA; cDNA DKFZp547J125 (fr	2.56
	401837		NM_025109:Homo sapiens hypothetical prot	2.56
	428743	AL080060	Hs.301549 Homo sapiens mRNA; cDNA DKFZp564H172 (fr	2.56
	422809	AK001379	Hs.121028 hypothetical protein FLJ10549	2.55

	418648	AW979223	Hs.292478	ESTs	2.55
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	2.54
	430345	AK000282	Hs.239681	hypothetical protein FLJ20275	2.54
5	424075	AI807320	Hs.227630	RE1-silencing transcription factor	2.54
	428728	NM_016625	Hs.191381	hypothetical protein	2.53
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	2.52
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	2.52
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	2.52
10	422406	AF025441	Hs.116206	Opa-interacting protein 5	2.52
	433228	F28212	Hs.14953	KIAA1491 protein	2.51
	411943	BE502436	Hs.7962	ESTs, Weakly similar to S44608 C02F5.6 p	2.51
	426181	AA371422	Hs.334371	hypothetical protein MGC13096	2.50
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	2.50
	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	2.48
15	419750	AL079741	Hs.183114	Homo sapiens cDNA FLJ14236 fis, clone NT	2.48
	408209	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	2.47
	435726	BE535787	Hs.113170	ESTs	2.47
	404068			Target Exon	2.46
20	403137			NM_005381: Homo sapiens nucleolin (NCL),	2.46
	434276	AF123659	Hs.93605	leucine zipper, putative tumor suppressor	2.46
	422283	AW411307	Hs.114311	CDC45 (cell division cycle 45, S.cerevis	2.46
	429652	AA766810	Hs.259290	ESTs	2.45
	416204	AW972270	Hs.195161	ESTs	2.45
	414713	BE465243	Hs.12664	ESTs	2.44
25	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.44
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	2.44
	435244	N77221	Hs.187824	ESTs	2.44
	402679			NM_000478: Homo sapiens alkaline phosphat	2.43
30	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	2.42
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	2.41
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	2.41
	410855	X97795	Hs.66718	RAD54 (S.cerevisiae)-like	2.41
	423232	BE244625	Hs.125742	leucine-rich neuronal protein	2.40
35	427578	AI591305	Hs.169084	ESTs, Highly similar to TUL3_HUMAN TUBBY	2.40
	409934	R91601	Hs.190466	hypothetical protein FLJ22584	2.39
	423787	AI295745	Hs.236204	nuclear pore complex protein	2.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	2.39
	438869	AF075009		gb: Homo sapiens full length insert cDNA	2.38
40	434981	AW182577	Hs.293077	ESTs	2.38
	417911	AA333387	Hs.82916	chaperonin containing TCP1, subunit 6A (2.38
	409210	AA251812	Hs.51120	cathelicidin antimicrobial peptide	2.37
	424425	AB031480	Hs.146824	SPR1 protein	2.37
	411885	AA452636	Hs.131057	ESTs, Moderately similar to CRGD_HUMAN G	2.37
45	421567	AJ272137	Hs.198265	matrix metalloproteinase 25	2.37
	425159	NM_004341	Hs.154868	carbamoyl-phosphate synthetase 2, aspart	2.37
	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	2.36
	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	2.36
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppressor	2.36
50	410968	AA199907	Hs.67397	homeo box A1	2.36
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	2.36
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	2.36
	412389	AW947655		gb:RCO-MT0003-140300-031-b07 MT0003 Homo	2.35
	419359	AL043202	Hs.90073	chromosome segregation 1 (yeast homolog)	2.35
55	403780			C4001759:gil133250[sp]P19474[RO52_HUMAN	2.34
	437681	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain faml	2.34
	400205			NM_006265: Homo sapiens RAD21 (S. pombe)	2.34
	433160	AW207002	Hs.134342	TASP for testis-specific adriamycin sens	2.34
	432606	NM_002104	Hs.3056	granzyme K (serine protease, granzyme 3;	2.34
60	425331	AW962128		gb:EST374201 MAGE resequences, MAGG Homo	2.33
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	2.33
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	2.32
	418821	AA436002	Hs.183161	ESTs	2.32
	437437	AA226869		hypothetical protein DKFZp762L0311	2.32
65	413437	BE313164	Hs.75361	gene from NF2/meningioma region of 22q12	2.31
	425848	BE242709	Hs.159637	valyl-HRNA synthetase 2	2.30
	435532	AW291488	Hs.117305	Homo sapiens, clone IMAGE:3682908, mRNA	2.30
	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	2.30
	409342	AU077058	Hs.54089	BRCA1 associated RING domain 1	2.29
70	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	2.29
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	2.29
	417115	AW952792	Hs.334612	small nuclear ribonucleoprotein polypept	2.28
	412721	AW183165	Hs.95600	ESTs	2.28
	404071			C12000514:gil7302471[gb]AAF57556.1[AE	2.27
75	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.26
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	2.26
	424935	AI655010	Hs.120363	hypothetical protein MGC15634	2.26
	415791	H09366	Hs.78853	uracil-DNA glycosylase	2.26
	431667	AA812573	Hs.246787	ESTs	2.26
80	424169	AA336399	Hs.153797	ESTs	2.25
	436540	BE397032	Hs.14468	hypothetical protein MGC14226	2.25
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	2.24
	403242			Target Exon	2.24
	414732	AW410976	Hs.77152	minichromosome maintenance deficient (S.	2.24

	421002	AF116030	Hs.100932	transcription factor 17	2.24
	438833	BE612940	Hs.88252	ESTs	2.24
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	2.23
5	433844	AA610175	Hs.179647	Homo sapiens cDNA FLJ12195 fis, clone MA	2.23
	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S.	2.23
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	2.23
	421016	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	2.23
	436251	BE515065	Hs.296585	nucleolar protein (KKE/D repeat)	2.23
10	418826	AK000375	Hs.88820	HDCMC28P protein	2.23
	428612	AA770001		ESTs	2.22
	433220	AI076192	Hs.131933	ESTs	2.22
	422225	BE245652	Hs.118281	zinc finger protein 266	2.22
	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	2.22
15	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.22
	408665	T88845	Hs.112200	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.22
	408116	AA251393	Hs.289052	Homo sapiens, Similar to RIKEN cDNA 5430	2.21
	420062	AW411096	Hs.94785	TGF(beta)-induced transcription factor 2	2.21
	432820	AI554057	Hs.152477	ESTs	2.21
20	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	2.21
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.20
	407275	AI364186		gb:qw34h07.x1 NC1_CGAP_U14 Homo sapiens	2.20
	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	2.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	2.20
25	433598	H24201	Hs.247423	adducin 2 (beta)	2.19
	409101	NM_004297	Hs.50612	guanine nucleotide binding protein (G pr	2.19
	435541	AA687361	Hs.221318	ESTs	2.19
	412019	AA485890	Hs.69330	Homo sapiens cDNA FLJ13835 fis, clone TH	2.19
	418753	BE217818	Hs.87016	hypothetical protein FLJ22938	2.19
30	435461	AI075846	Hs.133996	ESTs	2.19
	402260			NM_001436*:Homo sapiens fibrillarin (FBL	2.18
	421098	AI697901	Hs.192425	ESTs	2.18
	400587			C10000649*:gij7296574[gb]AAAF51857.1 (AE	2.18
	407832	AW976516	Hs.283707	Homo sapiens cDNA: FLJ21354 fis, clone C	2.18
35	427159	U80735	Hs.173654	PAX transcription activation domain inte	2.17
	405770			NM_002362:Homo sapiens melanoma antigen,	2.17
	412722	AI343300	Hs.15091	ESTs	2.16
	414334	AA824298	Hs.21331	hypothetical protein FLJ10036	2.16
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	2.16
40	417420	T85150	Hs.268814	ESTs	2.16
	421308	AA687322	Hs.192843	leucine zipper protein FKSG14	2.16
	412851	AI826502	Hs.97269	ESTs	2.16
	414702	L22005	Hs.76932	cell division cycle 34	2.16
	409670	AI368109		KIAA1855 protein	2.16
45	419926	AW900992	Hs.93796	DKFZP586D2223 protein	2.15
	417863	AB000450	Hs.82771	vaccinia related kinase 2	2.15
	434750	BE019254	Hs.4112	t-complex 1	2.15
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	2.15
	418574	N28754		M-phase phosphoprotein 9	2.15
50	409019	AW385412		myosin regulatory light chain 2, smooth	2.15
	416508	R11499	Hs.189716	ESTs	2.14
	436027	AI864053	Hs.39972	ESTs, Weakly similar to 138588 reverse t	2.14
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	2.13
	422805	AA436989	Hs.121017	H2A histone family, member A	2.13
55	410284	U50939	Hs.61828	amyloid beta precursor protein-binding p	2.13
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	2.12
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	2.12
	433252	AB040957	Hs.151343	KIAA1524 protein	2.12
	416819	U77735	Hs.80205	pim-2 oncogene	2.12
60	437218	AL117497	Hs.58185	ESTs, Weakly similar to T42727 prolifera	2.12
	407239	AA076350	Hs.67846	leukocyte immunoglobulin-like receptor,	2.12
	433947	AA927996	Hs.112876	ESTs, Weakly similar to AF129535 1 F-box	2.11
	424727	AW590378	Hs.152519	hypothetical protein FLJ20674	2.11
	435703	AW630133	Hs.83313	GK003 protein	2.11
65	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.11
	422192	AA305159	Hs.113019	fts485	2.11
	407961	AW672939	Hs.41694	origin recognition complex, subunit 2 (y	2.10
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.10
	414151	AW976468	Hs.257245	ESTs	2.10
70	434789	AW292515	Hs.194317	ESTs, Weakly similar to T08680 hypotheti	2.10
	424196	AL133660	Hs.142926	Homo sapiens beta cysteine string protei	2.10
	408831	AF090114	Hs.48433	endocrine regulator	2.10
	414733	BE514535	Hs.77171	minichromosome maintenance deficient (S.	2.09
	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	2.09
75	409637	AA323948	Hs.55407	Homo sapiens mRNA; cDNA DKFZp434K0621 (f	2.09
	403532			NM_024638:Homo sapiens hypothetical prot	2.09
	432141	BE410964	Hs.272736	nuclear receptor binding protein	2.08
	409014	H83115	Hs.49760	origin recognition complex, subunit 6 (y	2.08
	410575	BE207480	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	2.08
80	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	2.08
	418755	Y14443	Hs.88219	zinc finger protein 200	2.08
	406137			NM_000179*:Homo sapiens muIS (E. coli) h	2.07
	409893	AW247090	Hs.57101	minichromosome maintenance deficient (S.	2.07
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	2.07

5	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	2.07
	417230	U40998	Hs.81728	unc119 (C.elegans) homolog	2.07
	425966	NM_001761	Hs.1973	cyclin F	2.07
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	2.06
	407162	N63855	Hs.142634	zinc finger protein	2.06
	422382	D79988	Hs.115778	KIAA0166 gene product	2.06
	402677			NM_000478:Homo sapiens alkaline phosphat	2.06
	433017	Y15067	Hs.279914	zinc finger protein 232	2.05
10	424677	U09414		zinc finger protein 137 (clone pHZ-30)	2.05
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	2.05
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.05
	402678			Target Exon	2.05
	408146	R45621	Hs.81057	hypothetical protein MGC2718	2.05
15	420027	AF009746	Hs.94395	ATP-binding cassette, sub-family D (ALD)	2.04
	427447	T65414	Hs.6647	Homo sapiens cDNA FLJ13088 fis, clone NT	2.04
	433219	AB040916	Hs.24106	KIAA1483 protein	2.04
	431126	AF085243	Hs.283619	zinc finger protein 236	2.04
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	2.04
20	419669	AJ007041	Hs.92236	KIAA0304 gene product	2.04
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	2.03
	426242	AL096727	Hs.168249	Homo sapiens mRNA; cDNA DKFZp434B104 (fr	2.02
	432185	AA221032	Hs.272838	hypothetical protein FLJ10494	2.02
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	2.02
25	408636	BE294925	Hs.46680	CGI-12 protein	2.02
	420005	AW271106	Hs.133294	ESTs	2.02
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	2.02
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	2.02
	425358	AL079658	Hs.338207	FK506 binding protein 12-rapamycin assoc	2.01
30	409617	BE003760	Hs.55209	Homo sapiens mRNA; cDNA DKFZp434K0514 (f	2.01
	438450	AI050866	Hs.65853	nodal, mouse, homolog	2.00
	431629	AU077025	Hs.265827	interferon, alpha-inducible protein (clo	2.00
	424934	U75370	Hs.153880	polymerase (RNA) mitochondrial (DNA dire	2.00
	436291	BE568452	Hs.344037	protein regulator of cytokinesis 1	2.00
35	414251	AL042306	Hs.97689	VASA protein	2.00

TABLE 51B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
45	432666	144_7
	423458	30480_1
	418477	4172_1
50	436812	659779_1
	436899	1000797_1
	437421	978654_1
	430676	60836_2
55	427521	513212_1
	436909	596835_1
	429228	216430_1
60	435514	132288_1
	422689	874209_1
	421974	864120_1
	414136	30243_1
65	417886	1031334_1
	418235	888897_1
	414725	19377_1
70	434609	14739_1
	408065	101881_1
	412537	14066_1
75	415684	18695_18
	433641	35983_1
80	424281	892055_1

5	427298	115241_1	AA933717 BF061897 AW628327 AA641788 AA400495
	420218	191547_1	AW958037 R42557 AJ337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756
	418049	12052_4	AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA255527 BE089727
	433023	3970_8	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 FD2234 AA584711 BI222234
	418866	245947_1	AV731417 R42406 H04995 T98498 R12489 R12577 R42405
10	427239	20459_2	BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148
			AI968683 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871
			T65754 AA229658 AA229857
			AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334809 AI802853 AI345036 AI348921 AI340734 AI307478
15			AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
			AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072495 AW071420
			AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
			AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
			BF178773 BF718645 AW074866 BE857822
20	437834	294580_1	BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749296
			AA769294 AW749297 AW749295 AW749292 BE002573
	438243	2532601_1	AI581311 AA781682 AA781678
	410704	1054673_1	AW877458 AW877524 BE067922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
25			AW840571
	430968	1237115_1	AW972830 AA489820 AA527647 AA570362
	427260	11272_50	AA401424 AA400100 AA663848
	433979	2076469_1	N50454 AA620999 T16375
	426919	347372_1	BI917595 AI203314 AL041228 AV727959 D61361 D82004 BI753157 AA961066 AI990307 BF439651 AI453076 AI376075 AI014836 AI018308
30	438869	52134_1	AW183530 AA393346 AA935601 AA628633 AI150282 AI028574 AI217182 AA431478 AW087473 AW900295 H50055 AL041229 BI917726
	412389	1174403_1	AF075009 R63109 R63068
	400205	2538_1	AW947655 AW984020
			NM_006265 D38551 X98294 BM477931 BM461566 AU123557 AU133303 AU134649 AW500421 BM172439 AW500587 AW503665 AW504355
			AW503640 BM152454 AW505260 AI815984 AW504075 AW500716 AL597310 BC001229 BM474371 AA984202 AU135205 BE090841 AW163750
35			BF747730 BF898637 AI206506 AV660870 AV692110 AW386830 AV656831 N84710 AW993470 BF086802 BF758454 BG960772 BF757769
			BI870853 BE018627 C75436 AW148744 BF757753 BG622067 BE909924 AA708208 BG530266 BF968015 AW992930 BF888862 BG536628
			AA143164 AW748953 BG489922 BF885190 BF889005 BF754781 BF800003 BM476529 AI627668 AW028126 AL046011 BF590668 AI017447
			AA579936 AI367597 AA699622 BE280597 AI24620 AI082548 AW274985 AA677870 AI056767 BE551689 AA287642 H94499 AI752427 AI652365
			AW002374 AW062651 AA360834 N68822 AU135442 AU125960 Z78334 BE545813 AI092115 BF312771 BF242859 BG533616 BG533761
40			BG164745 BG492433 BM473183 AA172043 AA172069 AU157092 AU151353 AU155318 BE302211 AI375022 AA085641 AU157923 H88858
			AA132730 AA115113 AA909781 AI475256 AA424206 AW572383 AW084296 AI184820 AI469178 AA782432 H92184 AA340562 BF195818
			AA852821 AW576342 AA827107 AA173317 AW190014 AI918514 AA729372 AA729718 AI055958 AA331424 BE328601 AA515690 BI018896
			AW628277 AA748368 AA626222 BG492636 AW380620 BF800058 AW370956 AA290909 R25587 BG952995 BF801437 AA172077 AU155890
			AU149783 AI720904 AA902936 AA865727 AI470830 AV740677 AA142982 AA482485 AU145485 AW576399 AU156042 R63448 BF246427
45			BE928472 D25910 BF758439 BF968785 BE565238 AA355981 AI906607 BG291148 BG533096 BG532888 BF030886 BG613756 BE928471
			BG574501 AA187596 AA361196 T95557 BG531446 BG527242 BG527513 BG611106 AA085995 BF847252 BG024608 BE540261 BG531236
			AL579993 BG108733 BG483503 BG571032 BG492505
	425331	1227464_1	AA427363 AW962128 AA335353
	437437	6087_1	BC009352 BC014630 AU131857 AL527140 AU131768 BI769362 BI753220 AU129886 AU128771 AA314135 AU126819 AI333799 AA479336
50			AA258503 AL597351 AL359619 BG697218 BI254283 AI743846 AA236444 AA397533 AA247450 AI051464 AI224533 AU153442 AU151001
			AU152621 AU151829 AU153069 AW269958 AU154195 AI862754 AI589780 AW273839 AI338155 AI126632 BE046048 AA976930 AI289304
			AI625961 AI222288 AI280054 AA973329 AI524262 AI242371 AA296517 AI567865 AI590681 AJ346616 AW247913 AI422051 AI475352 AI689531
			AW469308 AW198034 AA936939 AU151059 AU148134 AA486419 AU151953 AI830968 BI493265 BI493264 AU149861 BE268763 AV763495
			AW962827 BM480300 AA226869 AI529368 BM451957 AU132714 BI871319 AA380739 BI911351 BF795906 BE548853 AW579751
55	430183	17316_1	AK055746 AA039909 BE183282 W60721 AA648687 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852
			BF173139 BE010038
	430504	5477_6	BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AJ440295 H52800 BE218790 AI681575
			AW300064 AW262133 H21568 AI363015 AI884914 H86948
	428612	1383189_1	AA770001 AA431112 AA432126
60	409670	8882_8	AI625045 AW504152 AI469086 AA905873 AW504662 AW136114 AI927270 BE041754 AI548386 AA662655 AA400052 AI143501 AI744934
			AJ400147 AJ381657 AA676551 AA974367 AW117437 AI570383 AI242456 AI274581 AA678138 R49939 AI393926 AA345854 AW605850 AI869780
			AW391171 R77044
	418574	12009_2	AW955043 AI990326 AA776406 AI016250 AW451882 AA843678 BF916900 AW945895 AI979339 N23129 W70051 AA322672 N23137
	409019	32320_4	BM480413 N28908 H37992 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085196
65	430935	15297_3	AJ093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285
			BC017923 AA789302 AW466994 BF513878 AI819642 AI184913 AW468044 AI220572 AW072916 AI280239 AJ473611 AW841126 D60937
			AA489195 N59350 AA693435 BG531204 AA484243 AW514092
	424677	2518_37	U09414 NM_003438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW509708

TABLE 51C

Pkey:	Unique number corresponding to an Eos probe set
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

75	Pkey	Ref	Strand	NL_position
	405547	7711513	Minus	172780-174358
	402145	8018280	Plus	113086-114800
	402199	8576116	Minus	84187-84744
	401435	8217934	Minus	54508-55233
	402408	9796239	Minus	110326-110491
	405367	9256126	Minus	58313-58489
80	402680	8113438	Plus	137634-137768, 139702-139893, 140475-14059
	402299	6693370	Plus	23367-25175
	401091	9958240	Plus	94760-94898

5	401464	6682291	Minus	170688-170834
	403969	8569909	Plus	31237-31375,32405-32506
	401837	7630990	Minus	120993-121095,121660-121729
	404068	3168621	Minus	18123-18766
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402679	8113438	Plus	132079-132216
	403780	8076989	Plus	93160-93409
	404071	7210053	Minus	167354-167859,168810-168920,169000-16910
10	403242	7637817	Minus	11297-12511
	402260	3399665	Minus	113765-113910,115653-115765,116808-11694
	400587	9887626	Plus	25435-25588,25668-25747
	405770	2735037	Plus	61057-62075
	403532	8076842	Minus	81750-81901
15	406137	9166422	Minus	30487-31058
	402677	8113438	Plus	22135-22309,23063-23238
	402678	8113438	Plus	37395-37514,37866-37981

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TABLE 52A:

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

25 Unigene Title: Unigene gene title

R1: Ratio of testicular cancer (non-seminomatous and Seminomatous) compared to normal adult testicular tissues

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
30	414438	AI879277	Hs.76136	thioredoxin	51.77
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	49.93
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	49.20
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	44.46
	438091	AW373062		nuclear receptor subfamily 1, group I, m	40.70
35	406658	AI920965	Hs.77961	major histocompatibility complex, class	39.64
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	38.70
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	38.25
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	37.50
	430542	AI557486	Hs.119122	ribosomal protein L13a	37.22
40	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	35.98
	432730	AI066520	Hs.131358	ESTs	35.25
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	31.69
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	31.33
	417088	M54915	Hs.81170	pim-1 oncogene	31.20
45	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	29.93
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	29.35
	426295	AW367283		zinc finger protein 6 (CMPX1)	29.32
	406856	AW515336	Hs.29797	ribosomal protein L10	28.83
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	27.99
50	440207	AI371978	Hs.128326	ESTs	27.75
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	26.95
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.90
	420367	AA259090	Hs.257028	ESTs	26.50
	429978	AA249027		ribosomal protein S6	26.43
55	440440	Z28925	Hs.7188	sera domain, immunoglobulin domain (Ig),	26.36
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	26.23
	412636	NM_004415		desmoplakin (DPI, DPII)	26.15
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	25.25
	446899	NM_005397	Hs.16426	podocalyxin-like	25.25
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	25.15
	406656	M16714	Hs.89643	major histocompatibility complex, class	25.13
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	24.78
	423961	D13666	Hs.136348	periostin (OSF-2os)	24.48
	425543	R23313	Hs.334895	ribosomal protein L10a	24.38
65	420676	AI434780	Hs.4248	vav 2 oncogene	24.18
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	23.96
	440869	NM_014297	Hs.7486	protein expressed in thyroid	23.80
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	23.56
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	23.22
70	446827	AI973016	Hs.15725	hypothetical protein SBB148	22.93
	449571	AW016812	Hs.200266	ESTs	22.83
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	22.81
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	22.68
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	22.45
75	422714	AB018335	Hs.119387	KIAA0792 gene product	22.45
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	22.30
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.69
	406648	AA563730	Hs.277477	major histocompatibility complex, class	21.58
	446588	AI970276	Hs.156905	KIAA1676	21.23
80	433423	BE407127	Hs.8997	heat shock 70kd protein 1A	21.19
	429490	AI971131	Hs.23689	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.70
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	20.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	20.57

	420754	W79431	Hs.346911	ribosomal protein L22	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	20.15
	424800	AL035588	Hs.153203	MyoD family inhibitor	20.10
5	412915	AW087727	Hs.74823	NM_004541: Homo sapiens NADH dehydrogenas	20.01
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	19.89
	410143	AA188169		KIAA1191 protein	19.41
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	19.08
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.03
10	425535	AB007937	Hs.158287	KIAA0468 gene product	18.78
	411573	AB029000	Hs.70823	KIAA1077 protein	18.63
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.53
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	18.52
	412379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	18.50
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2/G5	18.50
15	429183	AB014604	Hs.197955	KIAA0704 protein	18.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	18.44
	450377	AB033091		KIAA1265 protein	18.40
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.15
20	440528	BE313555	Hs.7252	KIAA1224 protein	18.05
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothi	17.98
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	17.80
	414582	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	17.75
	428782	X12830	Hs.193400	interleukin 6 receptor	17.48
25	415221	W07418	Hs.78225	annexin A1	17.47
	429614	AJ371172	Hs.211539	hypothetical protein MGC4248	17.40
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	17.30
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	17.14
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	17.13
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	17.10
30	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	17.03
	425996	W67330		hypothetical protein AL110115	16.98
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	16.98
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	16.98
35	427521	AW973352		ESTs	16.93
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.93
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	16.53
	449338	H73444	Hs.394	adrenomedullin	16.36
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	16.23
40	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	16.21
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	16.15
	427691	AW194426	Hs.20726	ESTs	16.13
	406785	AW161678	Hs.111334	ferritin, light polypeptide	16.11
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	16.10
45	451106	BE382701	Hs.25960	N-MYC oncogene	16.09
	408380	AF123050	Hs.44532	diubiquitin	16.00
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	15.93
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	15.69
50	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	15.64
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	15.55
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	15.55
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	15.53
	410185	BE294068	Hs.737	immediate early protein	15.49
55	422105	AI929700	Hs.111680	endosulfine alpha	15.23
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	15.23
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	15.05
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	15.02
	426552	BE297660	Hs.170328	moesin	14.96
60	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.88
	436860	H12751	Hs.5327	PRO1914 protein	14.85
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	14.84
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	14.78
	412623	R28898	Hs.74170	metallothionein 1E (functional)	14.70
65	408989	AW361666	Hs.49500	KIAA0746 protein	14.53
	426234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypothi	14.48
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	14.31
	410325	AB023154	Hs.82264	KIAA0937 protein	14.23
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	14.20
70	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase II	14.19
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	14.18
	426996	AW568934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.13
	447211	AL161961	Hs.17767	KIAA1554 protein	14.08
	417426	NM_002291	Hs.82124	laminin, beta 1	14.08
75	414420	AA043424	Hs.76095	immediate early response 3	14.04
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.02
	454413	AI653672	Hs.40092	PNAS-123	13.93
	452651	AI218918	Hs.30209	KIAA0854 protein	13.86
80	450581	AF081513	Hs.25195	TGF-beta 4	13.85
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.78
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.63
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.59
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.57
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	13.53

	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	13.43
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	13.41
	447534	AW953935	Hs.288655	ESTs	13.33
5	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.31
	428065	AI634046	Hs.157313	ESTs	13.30
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	13.28
	436398	H87136	Hs.5174	ribosomal protein S17	13.18
	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	12.93
10	452436	BE977546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	12.90
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	12.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	12.90
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	12.89
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.83
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	12.79
15	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	12.78
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	12.75
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	12.73
	430630	AW269920	Hs.2621	cystatin A (stafin A)	12.68
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	12.65
20	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	12.50
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	12.48
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	12.43
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.43
25	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	12.41
	412247	AF022375	Hs.73793	vascular endothelial growth factor	12.41
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	12.40
	435876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mito	12.38
	432409	AA806538	Hs.130732	KIAA1575 protein	12.33
30	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.33
	419384	AA490866	Hs.39429	ESTs	12.33
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	12.32
	432805	X94630	Hs.3107	CD97 antigen	12.32
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	12.25
35	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB88_HUMAN RAS-R	12.13
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	12.12
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	12.03
	402145			Target Exon	12.01
	407179	AA206465		thymosin, beta 4, X chromosome	12.00
40	433208	AW002834	Hs.24095	ESTs	11.95
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.90
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	11.83
	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	11.75
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	11.75
45	427761	AA412205	Hs.140996	ESTs	11.68
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	11.58
	436075	BE090176	Hs.179902	transporter-like protein	11.50
	440774	AI420611	Hs.153934	ESTs	11.35
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	11.25
50	419223	X60111	Hs.1244	CD9 antigen (p24)	11.08
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	11.08
	444656	AI277924	Hs.145199	ESTs	10.98
	420943	AI718702	Hs.279930	major histocompatibility complex, class	10.96
	450294	H42587	Hs.238730	hypothetical protein MGC10823	10.92
55	413686	AI469213	Hs.71404	ESTs	10.83
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	10.78
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	10.75
	407252	AA659037	Hs.163780	ESTs	10.75
	445929	AI089560	Hs.323401	dpy-30-like protein	10.70
	451864	N20370	Hs.69547	ESTs	10.69
60	429307	AU076592	Hs.198951	jun B proto-oncogene	10.64
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	10.63
	447519	U46258	Hs.339665	ESTs	10.63
	417365	D50683	Hs.82028	transforming growth factor, beta recepto	10.59
65	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	10.55
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	10.54
	437103	AW139408	Hs.152940	ESTs	10.50
	449961	AW265634	Hs.133100	ESTs	10.50
	441244	BE612935	Hs.184052	PP1201 protein	10.49
70	450139	AK001838		serum/glucocorticoid regulated kinase	10.48
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	10.48
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rheokin, clone	10.47
	446682	AW205532	Hs.211198	ESTs	10.43
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.43
75	430068	AA484964		gb:zx80110.s1 Soares ovary tumor NbHOT H	10.40
	424950	AA602917	Hs.156974	ESTs	10.40
	434442	AA737415		ESTs	10.33
	438089	W05391		nuclear receptor subfamily 1, group I, m	10.33
	432559	AW452948	Hs.257631	ESTs	10.30
80	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	10.30
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	10.28
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	10.27
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	10.27
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	10.23

	445245	AB032973	Hs.12461	LCHN protein	10.18
	446488	AB037782	Hs.15119	KIAA1361 protein	10.15
	410611	AW954134	Hs.20924	KIAA1628 protein	10.15
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	10.14
5	416926	H03109	Hs.263395	HT018 protein	10.07
	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	10.05
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	10.04
	411975	AI916058	Hs.144583	ESTs	10.03
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	10.00
10	408784	AW971350	Hs.63386	ESTs	9.95
	444795	AI933356	Hs.160316	ESTs	9.93
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.90
	400440	X83957	Hs.83870	nebulin	9.90
	414829	AA321568	Hs.77436	pleckstrin	9.88
15	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.88
	426827	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase	9.85
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	9.83
	446795	AI797713	Hs.156471	ESTs	9.78
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	9.67
20	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	9.65
	419904	AA974411	Hs.18672	ESTs	9.63
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	9.63
	414405	AI362533		KIAA0306 protein	9.58
25	418840	AI821614	Hs.185831	ESTs	9.53
	453716	AA037675	Hs.152675	ESTs	9.50
	415323	BE269352	Hs.949	neutrophil cytosolic factor 2 (65kD, chr	9.50
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.45
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	9.45
30	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	9.43
	434423	NM_006769	Hs.3844	LIM domain only 4	9.43
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	9.43
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	9.42
	410397	AF217517	Hs.63042	DKFZp564J157 protein	9.37
35	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	9.37
	434524	AA635931	Hs.249716	ESTs	9.36
	422960	AW890487		cadherin 13, H-cadherin (heart)	9.35
	414774	X02419	Hs.77274	plasminogen activator, urokinase	9.32
	411960	R77776	Hs.18103	ESTs	9.30
40	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	9.28
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.28
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.27
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	9.27
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypoteti	9.25
45	427968	AI857607	Hs.181301	cathepsin S	9.23
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	9.23
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	9.23
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	9.18
	417315	AI080042	Hs.180450	ribosomal protein S24	9.18
50	421098	AI697901	Hs.192425	ESTs	9.18
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.18
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	9.17
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	9.17
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.15
55	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	9.14
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.13
	426689	BE245550	Hs.171825	basic helix-loop-helix domain containing	9.12
	420099	D80011	Hs.95140	KIAA0189 gene product	9.10
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	9.08
	441436	AW137772	Hs.185980	ESTs	9.08
60	448019	AW947164	Hs.195541	ESTs, Moderately similar to I38022 hypot	9.08
	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	9.08
	430556	AW967807	Hs.13797	ESTs	9.07
	450147	AW373713	Hs.146324	CGI-145 protein	9.06
	442806	AW294522	Hs.149991	ESTs	9.05
65	431187	AW971146	Hs.293187	ESTs	9.05
	449971	AA807346	Hs.288591	Homo sapiens cDNA FLJ14296 fis, clone PL	9.03
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	9.03
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	9.02
70	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	9.00
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.99
	432314	AA533447	Hs.312989	ESTs	8.98
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.95
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	8.94
75	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	8.93
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.90
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	8.90
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.89
	417228	AL134324	Hs.7312	ESTs	8.88
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	8.88
80	422616	BE300330	Hs.118725	selenophosphate synthetase 2	8.88
	438980	AW502384		gb:U1-HF-BR0p-aka-f-12-0-U1.r1 NIH_MGC_5	8.85
	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	8.85
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	8.85

	430592	AJ224864	Hs.9688	leukocyte membrane antigen(LRC1)	8.83
	445612	N94126	Hs.12969	hypothetical protein	8.80
	427254	AL121523	Hs.97774	ESTs	8.80
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.80
5	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	8.79
	430162	AW450843	Hs.346348	ESTs	8.75
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	8.73
	446659	AI335361	Hs.226376	ESTs	8.73
	447198	D61523	Hs.283435	ESTs	8.73
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	8.70
	401091			decay accelerating factor for complement	8.68
	442832	AW206560	Hs.253569	ESTs	8.68
	442495	AI184717		ESTs	8.63
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	8.63
15	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	8.61
	447674	BE270840	Hs.19192	cyclin-dependent kinase 2	8.59
	425580	L11144	Hs.1907	galanin	8.55
	449656	AA002008	Hs.188633	ESTs	8.55
	412093	BE242691	Hs.14947	ESTs	8.54
20	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.54
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.53
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	8.51
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	8.45
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	8.45
25	425284	AF155568		NS1-associated protein 1	8.45
	441623	AA315805		desmoglein 2	8.43
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	8.42
	441021	AW578716	Hs.7644	H1 histone family, member 2	8.40
	446630	AW384793	Hs.15740	Homo sapiens mRNA: cDNA DKFZp434E033 (fr	8.40
30	417621	AV654694	Hs.82316	Interferon-induced, hepatitis C-associat	8.35
	433655	AL036559	Hs.3463	ribosomal protein S23	8.33
	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.32
	446975	BE246446	Hs.16895	ubiquitin-activating enzyme E1-like	8.31
35	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.30
	414662	AL036058	Hs.76807	major histocompatibility complex, class	8.30
	414601	AV660804	Hs.301417	AHNAK nucleoprotein (desmoyokin)	8.29
	406699	L06505	Hs.182979	ribosomal protein L12	8.28
	443684	N20617	Hs.194397	leptin receptor	8.28
	442821	BE391929	Hs.8752	transmembrane protein 4	8.26
40	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	8.24
	435968	AW161481	Hs.111577	integral membrane protein 3	8.23
	440327	R12581	Hs.191146	ESTs	8.23
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	8.22
	435684	NM_001290	Hs.4980	LIM domain binding 2	8.16
45	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	8.15
	427523	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3	8.14
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown H.s	8.13
	448094	H24387	Hs.32061	ESTs, Weakly similar to I38022 hypotheti	8.10
	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	8.09
50	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	8.08
	412645	AW444433	Hs.138061	Homo sapiens, Similar to hypothetical pr	8.07
	423523	AW299828	Hs.193580	ESTs	8.03
	426759	AI590401	Hs.21213	ESTs	8.03
55	426780	BE242284	Hs.172199	adenylate cyclase 7	8.03
	426215	AW963419	Hs.155223	stanniocalcin 2	8.03
	435748	AA699756	Hs.117335	ESTs	8.00
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	8.00
	447500	AI381900	Hs.159212	ESTs	8.00
60	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	8.00
	428728	NM_016625	Hs.191381	hypothetical protein	8.00
	434511	R28982	Hs.18106	ESTs	7.99
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	7.98
	424875	AI187945	Hs.199310	ESTs	7.95
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	7.95
65	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	7.93
	425277	NM_001241	Hs.155478	cyclin T2	7.91
	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	7.90
70	407013	U35637	Hs.83870	gb:Human nebula mRNA, partial cds	7.90
	429999	AI761902	Hs.99597	ESTs	7.90
	445493	AI915771		metallothionein 1E (functional)	7.89
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.88
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	7.88
	453485	BE620712	Hs.33026	hypothetical protein PP2447	7.87
75	434159	AW135214	Hs.191828	ESTs	7.85
	432666	AW204069		ESTs, Weakly similar to unnamed protein	7.83
	430915	AA488953		gb:aa55e05.r1 NCL_CGAP_GCB1 Homo sapiens	7.83
	425913	AA365799		SEC22, vesicle trafficking protein (S. c	7.80
80	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	7.80
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	7.79
	435905	AW997484	Hs.5003	KIAA0456 protein	7.78
	406663	U24683		immunoglobulin heavy constant mu	7.78
	427395	AW298741	Hs.97661	ESTs, Moderately similar to I38022 hypot	7.78

	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	7.75
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	7.75
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 f1s, clone MA	7.73
5	422900	AA641201	Hs.222051	ESTs	7.73
	432598	AJ341227	Hs.157106	ESTs	7.72
	449322	AI638616	Hs.195566	ESTs	7.71
	416987	D86957	Hs.80712	KIAA0202 protein	7.67
	410800	BE280421	Hs.94499	ESTs	7.67
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	7.67
10	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.65
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.65
	401466			vesicle-associated membrane protein 4	7.65
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	7.64
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.63
15	457250	AA811987	Hs.125779	ESTs	7.63
	412949	AJ471639	Hs.71913	ESTs	7.63
	406819	AA908472		gb:og82a10.s1 NCI_CGAP_Ov8 Homo sapiens	7.62
	441612	AJ802629	Hs.113660	Homo sapiens cDNA FLJ11631 f1s, clone HE	7.62
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	7.61
20	435937	AA830893	Hs.119769	ESTs	7.60
	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	7.60
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.60
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	7.56
	418134	AA397769	Hs.86617	ESTs	7.55
25	451812	X81889	Hs.152151	plakophilin 4	7.55
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.54
	429083	Y09397	Hs.227817	BCL2-related protein A1	7.54
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	7.52
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.52
30	407784	AW139585	Hs.12708	ESTs	7.52
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	7.50
	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrate-	7.50
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 f1s, clone PL	7.48
	446013	A1360167	Hs.152774	ESTs	7.48
35	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 f1s, clone C	7.48
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	7.45
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 f1s, clone H	7.45
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	7.44
40	447082	T85314	Hs.54629	thioredoxin-like	7.43
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 f1s, clone H	7.43
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.43
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	7.43
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypothe	7.43
45	436394	AA531187	Hs.126705	ESTs	7.39
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	7.39
	446258	AJ283476	Hs.263478	ESTs	7.38
	410570	AJ133096	Hs.64593	ATP synthase, H transporting, mitochondr	7.37
	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.36
50	435541	AA687361	Hs.221318	ESTs	7.35
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	7.35
	408057	BE244560	Hs.342307	hypothetical protein FLJ10330	7.35
	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.35
	418336	BE179882		glutathione peroxidase 3 (plasma)	7.35
	448877	AJ583696	Hs.253313	ESTs	7.35
55	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 f1s, clone NT	7.35
	444838	AV651680	Hs.208558	ESTs	7.33
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	7.31
	424677	U09414		zinc finger protein 137 (clone pHZ-30)	7.30
60	441878	AJ801869	Hs.127982	ESTs	7.29
	406542			C19000728*.gij12585552sp Q9Y2Q1 Z257_HU	7.28
	408418	AW963897	Hs.44743	KIAA1435 protein	7.28
	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	7.26
	442492	AA528489	Hs.234518	ribosomal protein L23	7.25
65	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	7.25
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	7.25
	426501	AW043782	Hs.293616	ESTs	7.25
	411251	R19774	Hs.22835	HHGP protein	7.25
	444670	H58373	Hs.332938	hypothetical protein MGC5370	7.25
	418117	AJ922013	Hs.83496	linker for activation of T cells	7.24
70	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 f1s, clone H	7.24
	434817	AA082118	Hs.102737	golliath protein	7.23
	419970	AW612022		ESTs	7.23
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 f1s, clone HE	7.23
75	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	7.23
	433891	AA613792		gb:mo97h03.s1 NCI_CGAP_Pr2 Homo sapiens	7.21
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	7.21
	430314	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	7.20
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.20
80	441224	AJ076964	Hs.7753	calumenin	7.18
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.18
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	7.15
	447341	AF106941	Hs.18142	arrestin, beta 2	7.15
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 f1s, clone A	7.14

	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	7.14
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	7.13
	421633	AF121860	Hs.106260	sorting nexin 10	7.10
	410668	BE379794	Hs.159651	hypothetical protein	7.09
5	435812	AA700439	Hs.188490	ESTs	7.08
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	7.08
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	7.08
	417165	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C	7.06
	408605	AF025374	Hs.46465	T-cell, Immune regulator 1	7.06
10	416401	N80139	Hs.268916	ESTs	7.05
	415799	AA653718	Hs.225841	DKFZP434D193 protein	7.05
	415995	NM_004573		phospholipase C, beta 2	7.05
	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.05
	417535	AA203569	Hs.191482	ESTs	7.04
15	449567	AI990790	Hs.188614	ESTs	7.03
	429355	AW973253	Hs.292689	ESTs	7.03
	442460	NM_014135	Hs.8345	PRO0641 protein	7.03
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	7.03
	430280	AA361258	Hs.237868	interleukin 7 receptor	7.03
20	426124	AI268389	Hs.250697	phosphatidylinositol glycan, class F	7.02
	442685	AB033017	Hs.8594	KIAA1191 protein	7.01
	433735	AA608955	Hs.109653	ESTs	7.00
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.98
25	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.96
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	6.95
	409956	AW103364	Hs.727	Inhibin, beta A (activin A, activin AB a	6.95
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.93
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	6.93
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.93
30	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	6.93
	451838	AW005866	Hs.193969	ESTs	6.91
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCL_CGAP_Su	6.90
	443749	R38828	Hs.143463	ESTs	6.90
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.90
35	427919	AA173942	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	6.90
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.90
	435655	AW105663	Hs.6947	HSPC069 protein	6.90
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	6.85
40	418259	AA215404		ESTs	6.85
	407244	M10014		fibrinogen, gamma polypeptide	6.85
	418832	X04011	Hs.88974	cytochrome b-245, beta polypeptide (chro	6.83
	441321	H17182	Hs.7771	B-cell associated protein	6.80
	433162	AI025842		ESTs	6.80
45	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.80
	434372	AA631373		gb:np86c01.s1 NCL_CGAP_Thy1 Homo sapiens	6.80
	456629	AW891965		histone deacetylase 3	6.78
	430283	BE391688		RAB7, member RAS oncogene family	6.77
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	6.76
50	406858	AI865720	Hs.29797	ribosomal protein L10	6.75
	429582	AI569068	Hs.22247	ESTs	6.75
	401113			solute carrier family 22 (organic cation	6.75
	449576	AW014631	Hs.225068	ESTs	6.75
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	6.72
55	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.72
	430451	AA836472	Hs.297939	cathepsin B	6.72
	410503	AW975746	Hs.188652	KIAA1702 protein	6.70
	415682	AI347128	Hs.191870	ESTs	6.70
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	6.70
60	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	6.70
	457073	AA233210	Hs.179943	ribosomal protein L11	6.69
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	6.68
	436137	AI056769	Hs.133512	ESTs	6.68
	425787	AA363867	Hs.155029	ESTs	6.67
	437802	AI475995	Hs.122910	ESTs	6.65
65	432636	AA340864	Hs.278562	claudin 7	6.65
	407340	AA810168	Hs.284289	vitiligo-associated protein VIT-1	6.65
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	6.65
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	6.63
	441355	AI822034	Hs.137097	ESTs	6.63
70	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	6.63
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	6.63
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	6.62
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	6.60
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	6.60
75	449057	AB037784	Hs.22941	KIAA1363 protein	6.60
	446979	AI654443	Hs.197683	ESTs	6.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	6.60
	424868	AI568170	Hs.96886	ESTs	6.59
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	6.58
80	451603	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H	6.58
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.58
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	6.57
	450256	AA286687	Hs.24724	MFH-amplified sequences with leucine-ric	6.56

	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	6.56
	444207	AI565004		calhepsin D (lysosomal aspartyl protease	6.55
	418459	R85436	Hs.268814	ESTs	6.55
5	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	6.55
	406745	AW511970	Hs.279860	tumor protein, translationally-controlle	6.55
	446173	BE565849	Hs.14158	copine III	6.53
	436566	BE545586	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	6.53
	423825	NM_004402	Hs.133089	DNA fragmentation factor, 40 kD, beta po	6.53
10	443441	AW291196	Hs.92195	ESTs	6.51
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	6.50
	431971	BE274907	Hs.77385	myosin, light polypeptide 6, alkali, smo	6.50
	450219	AI826999	Hs.224624	ESTs	6.50
	408896	AI610447	Hs.48778	niban protein	6.50
15	442618	R56222	Hs.26514	ESTs	6.49
	422773	AB026962	Hs.301552	KIAA1039 protein	6.48
	413663	BE247585	Hs.75462	BTG family, member 2	6.48
	418905	BE539674		actinin, alpha 4	6.48
	405086			NM_006662: Homo sapiens Snf2-related CBP	6.45
20	446520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	6.45
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.45
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	6.45
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	6.43
	426496	D31765	Hs.170114	KIAA0061 protein	6.43
25	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	6.42
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	6.41
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.40
	435918	AF263538	Hs.86232	growth differentiation factor 3	6.38
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	6.38
30	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.38
	436716	AI433540		gb:ti69g05.x1 NCI_CGAP_Kd11 Homo sapien	6.38
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	6.38
	413326	H88621	Hs.19762	ESTs, Weakly similar to KIAA1140 protein	6.38
	441970	AW959918	Hs.73737	ESTs	6.38
35	430835	AI240006	Hs.192326	ESTs	6.38
	414890	BE281095	Hs.77573	uridine phosphorylase	6.37
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	6.37
	414768	AW376989	Hs.259855	elongation factor-2 kinase	6.36
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	6.36
40	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	6.35
	432586	AA568548		ESTs	6.35
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	6.35
	420012	AW957955	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	6.35
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.35
45	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.35
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JCS238 galactosy	6.35
	437296	AA350994	Hs.20281	KIAA1700	6.35
	427747	AW411425	Hs.180655	serine/threonine kinase 12	6.33
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	6.33
50	410387	AI277367	Hs.47094	ESTs	6.33
	413677	AW503116	Hs.301819	zinc finger protein 146	6.31
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	6.31
	443634	H73972	Hs.134460	ESTs	6.30
	409453	AI885516	Hs.95612	ESTs	6.29
55	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	6.29
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.29
	410532	TS3088	Hs.155376	hemoglobin, beta	6.28
	428453	AB011110	Hs.184367	GTPase activating protein-like	6.27
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	6.26
60	458965	AA010319	Hs.60389	ESTs	6.25
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	6.25
	426797	AW936268	Hs.342849	ADP-ribosylation factor-like 5	6.25
	412528	AI123478	Hs.32112	ESTs	6.25
	410079	U94362	Hs.58589	glycogenin 2	6.25
65	427477	AW973119	Hs.178391	ribosomal protein L44	6.24
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.24
	435961	BE293127	Hs.263722	GTT1 protein	6.23
	424090	X99699	Hs.139262	XIAP associated factor-1	6.23
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.23
70	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	6.23
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	6.23
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	6.22
	428773	BE256238	Hs.193163	bridging Integrator 1	6.20
	436372	AW972301	Hs.310286	ESTs	6.19
75	440719	AA150869	Hs.26267	ATP-dependant interferon response protei	6.18
	406685	M18728		gb:Human nonspecific crossreacting antig	6.18
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	6.17
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	6.16
	458659	AW749895	Hs.332520	Homo sapiens mRNA: cDNA DKFZp434A1014 (f	6.15
80	406806	AW088535		ribosomal protein, large, P0	6.15
	420151	AA255931	Hs.186704	ESTs	6.14
	413441	AI929374	Hs.75357	Src-like-adaptor	6.13
	449317	AW293413	Hs.132906	19A24 protein	6.13
	421568	W85858	Hs.99804	ESTs	6.13

5	435919	AI052189	Hs.114104	ESTs	6.13
	417353	AA375752	Hs.348140	Homo sapiens mRNA: cDNA DKFZp586F1822 (I	6.13
	448946	AI652855	Hs.23363	hypothetical protein FLJ10983	6.13
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.13
	406857	AA613726	Hs.29797	ribosomal protein L10	6.11
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	6.11
	425095	AW014160	Hs.182585	KIAA1276 protein	6.10
	435756	AI418466	Hs.33655	ESTs	6.10
10	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	6.10
	413813	M96956	Hs.75561	teratocarcinoma-derived growth factor 1	6.10
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22155 fis, clone H	6.10
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	6.08
	447832	AI433357		ESTs	6.08
	434421	AI915927	Hs.34771	ESTs	6.08
15	437438	AL359620	Hs.14217	hypothetical protein DKFZp762P2111	6.08
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	6.08
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	6.07
	433339	AF019226	Hs.8036	glioblastoma overexpressed	6.06
20	435511	AA683336	Hs.189046	ESTs	6.06
	423458	AI204212		ESTs	6.06
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.06
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	6.06
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	6.06
25	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	6.05
	432925	AA878324	Hs.264750	ESTs	6.05
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	6.05
	449810	AB008681	Hs.23994	activin A receptor, type IIB	6.04
	406797	AI432224		ribosomal protein L6	6.04
30	450157	AW981576	Hs.60178	ESTs	6.03
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.03
	407635	AW370213	Hs.295232	ESTs, Moderately similar to A46010 X-link	6.03
	453331	AI240665		ESTs	6.03
	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	6.02
35	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isom	6.01
	409945	AW015935	Hs.122642	ESTs	6.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	6.00
	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	6.00
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	6.00

TABLE 52B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

45	Pkey	CAT Number	Accession
50	438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW898628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI660794 AI344784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095608 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF956933 BG623563 AV646254 AA463522 BI003244 AI299190 AW04186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BI039626 BI037700 R00353 BF155184 N98343 N79072 H01812 T55581
60	426295	510_1	BE880923 BG390191 AW470082 AW014585 AI423255 BI714731 BG054894 AW780248 N31683 AW664132 AW467353 AI983152 AA617918 BF447795 AI088357 AA807328 AA576970 AI741153 AI755003 AI474016 AI422030 AI348114 AW997085 BM271753 AI363147 BM311311 AI146640 AI246771 AW512619 AI359020 BG054897 AI292234 AI215830 AI283836 C06205 AW503423 AW272680 N33205 AW873021 AA070724 AI753886 AW192487 AI087151 AA658909 AI346368 AI335677 AA825442 AW440066 AW131357 AW513210 AI082314 AI085455 BE551404 AA780704 AW008596 AI796964 AA917471 AI400531 AA668526 N72207 AI306482 AW440562 AI084687 AA347280 AA063536 BF477389 AI241662 AA931543 AA484310 AA812486 AI032216 AA665779 AI916336 AI350590 BF198106 AI433377 AI300638 AI672626 AI282741 AI351487 AW105544 AA973627 AW517914 AA715424 AA508454 BF334080 AI274618 AW367201 AW572619 AW469088 AA382095 AI368364 AI146934 AI357180 AI361181 BI911347 BI871044 AA136325 BF084010 BF084007 AA335788 AI920878 AA805614 BE932941 AI678261 C75308 AI148479 BE178174 W88513 BM013627
70	429978	35194_2	BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612657 AI339558 AI919424 AI377532 AI354441 AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918684 AW963196 C06195 AI678018
75	412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI755807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999989 BF368816 BE184924 BE159646 BE714632 BE184948 BG985845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723

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			BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548
			AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA053629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399

			D54161 R73016 D55021 B1857200 H83444 B1016954 D54163 R15563 B1818664 BE152207 B1048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200 AW972830 AA489820 AA527647 AA570362 BE739425 AA514221 AA865491 A1828293 AA470456 A1276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 A1432496 A1470335 A1247243 BG533994 AA513783 A1887309 AA528036 AW972006 AW873028 A1924914 A1818810 AW152378 AW084946 A1521413 A1669583 BE932521 A1581370 BE180238 AW089750 AW771461 AW089714 A1590949 A1819148 AA731056 BF815234 BF911506 AA235803 AA485373 A1735658 AW393133 AW073080 A1707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 A1807430 A1676072 AA837010 A1452482 A1625817 AW241750 BE048616 A1290928 A1680714 AA485530 BE175687 AV648513 AW130312 A1000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524654 AA490345 A1244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 A1565004 AW819026 BE843092 AV686437 AV723049 BG616948 A1911647 A1743490 A1091096 BE857251 A1962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 A1749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BM459076 AA533027 A1127512 A1368802 AA533141 AA700560 AW576028 A1610851 A1435361 BM129172 AW474544 BM128899 A1814292 AW502039 AA531243 BF941858 AW502037 AA702337 A1419854 AA662755 AA934364 A1300510 A1291136 AA505263 A1144527 A1076919 A1633534 A1242473 AA938561 BG055372 AA512894 A1671356 AA962403 BF808010 AA663911 AA847056 AA513301 AA369063 AA377265 BG291206 AA402298 AA885766 AW801002 AA302280 A1305842 AW800873 AA302492 AA478427 A1817291 AW801104 AW801028 AA865744 BF155979 A1374743 AA478431 A1159846 A1369757 A1800672 BF435788 AA255451 A1937707 AW006198 A1280363 BF062434 AW801115 A1919181 F28413 W04214 AW152380 AW901567 AW901570 AA886371 AA384251 A1302845 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 B108170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 A1142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605 A1433540 AA804981 AA728984 BG015794 BE158357 BE158358 BE158360 BE158362 BE158351 BE158355 BC022881 AU150944 BG750783 AW754175 AW857737 A1911659 A1050036 AA554053 A1826259 AA568548 A1732997 AA977633 AA865818 M18728 AW088535 A1889321 AA954221 A1337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA857965 A1625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 A1149335 AA936925 AA581684 AA954198 AW238461 A1281504 A1265812 AA583267 AW236162 AA876535 AW304296 AW474334 A1559415 A1589241 A1660952 AA641137 A1431696 A1688844 AA552513 AA564954 AW090553 A1205612 A1245753 AA954883 AA947909 A1866014 AW971213 AA493925 AA493567 AA878339 AA934462 A1628543 A1433357 AW772732 B1918168 AW779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 A1203107 R35004 F07491 R25094 R35360 BC018070 BG702493 A1204212 AA460929 AA93606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418 BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 B1596425 AA115605 A1589155 BF439839 BG188832 A1359615 BG190473 A1024233 BF439574 AW118065 A1672797 AA610042 BG212008 A1204382 R70913 AA033534 AA781036 A1627278 AA307285 AA034218 BG482748 AW162429 B1602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555 AA423826 AA115129 AA18107 A1432224 AW276890 A1499346 AA937014 AA653573 A1318525 A1246219 AA961591 A1270640 BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 R75732 B1057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 AA626915 AA746952 A1161014 AA098554 BG572534 A1803329 A1809932 A1808765 AA411449 A1378760 AA976929 A1378620 AA909684 R75632 A1360919 A1350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 A1240665 BF989591 B1056086 BG001590 BF107035 BE219720 BF475241 A1571723 BE219848 B1789268 A1224899 AA724864 AW771467 AA480255 AW845616 A1440295 H52800 BE218790 A1681575 AW300064 AW262133 H21568 A1363015 A184914 H86948
5	430968 444207	1237115_1 9172_3	
10			
15	418905	517_1	
20			
25	436716 413703 432586 440129 406685 406806	2472838_1 376077_1 6633_1 2607882_1 0_0 0_0	
30			
35	431155 447832 449625	1235742_1 1036795_1 249224_1	
40	423458 455263	30480_1 26143_1	
45	406797 453331	0_0 16559_1	
50			
55			TABLE 52C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.
60	Pkey 402474 402145 401091 401466 406542 401113 405086	Ref 7547175 8018280 9958240 6682292 7711499 9965541 8072509	Strand Minus Plus Plus Plus Plus Minus Plus NL_position 53526-53628,55755-55920,57530-57757 113086-114800 94760-94898 28748-29023 117335-118473 19419-19959 73864-73841,74081-74217,74610-74779,7492
65			
70			TABLE 53A: Pkey: Unique Eos probeset identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Unigene Title: Unigene gene title R1: Ratio of testicular cancer (non-seminomatous and seminomatous) compared to normal adult tissues
75	Pkey 432666 452838 418696 432730 450581	ExAccn AW204069 U65011 AW959433 A1066520 AF081513	UnigenelD Hs.30743 Hs.326290 Hs.131358 Hs.25195 Unigene Title ESTs, Weakly similar to unnamed protein preferentially expressed antigen in mela hypothetical protein FLJ12581 ESTs TGF-beta 4 R1 78.20 75.45 58.80 51.80 48.40
80			

	426534	U58096	Hs.2051	testis specific protein, Y-linked	44.05
	423458	AI204212		ESTs	36.60
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	34.65
	420367	AA259090	Hs.257028	ESTs	32.60
5	451106	BE382701	Hs.25960	N-MYC oncogene	30.10
	437052	AA861697	Hs.120591	ESTs	29.35
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	29.05
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	28.45
	420347	AL033539	Hs.97124	Human DNA sequence from clone RP1-309H15	28.25
10	407710	AW022727	Hs.23616	ESTs	26.86
	448981	AI968719	Hs.195387	ESTs	26.40
	429486	AF155827	Hs.203963	hypothetical protein FLJ10339	25.55
	420528	AF130728	Hs.98586	doublesex and mab-3 related transcriptio	25.10
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	23.70
15	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.95
	454077	AC005952	Hs.37062	insulin-like 3 (Leydig cell)	21.73
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	20.15
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	19.65
	424578	AK001973	Hs.150890	hypothetical protein	19.16
20	427335	AA448542	Hs.251677	G antigen 7B	19.05
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	18.95
	432938	T27013	Hs.3132	steroidogenic acute regulatory protein	18.86
	449322	AI638616	Hs.196566	ESTs	18.30
	430691	C14187	Hs.157208	aristaeless-related homeobox protein ARX	18.00
25	430676	AF084866		gb:Homo sapiens envelope protein RIC-3 (17.96
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	17.41
	418756	AA252254	Hs.226949	ESTs	17.20
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Ciona savignyi	16.20
	447534	AW953935	Hs.288655	ESTs	16.04
30	407122	H20276	Hs.31742	ESTs	15.95
	446979	AI654443	Hs.197683	ESTs	15.90
	406547			Target Exon	15.70
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	15.65
	456847	AI360456	Hs.37776	ESTs	15.50
35	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	15.00
	452291	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi	14.95
	408908	BE296227	Hs.250822	serine/threonine kinase 15	14.65
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	14.20
	422828	AL133396		prion protein 2 (dublet)	14.08
40	433330	AW207084	Hs.132816	hypothetical protein MGC14801	14.05
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	14.05
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	13.90
	418134	AA397769	Hs.86617	ESTs	13.85
	454438	AA224053	Hs.172405	cell division cycle 27	13.70
45	449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	13.40
	426427	M86699	Hs.189840	TTK protein kinase	13.35
	437789	AI581344	Hs.127812	ESTs, Weakly similar to T17330 hypotheti	13.20
	419384	AA490866	Hs.39429	ESTs	13.10
	418477	AW022983		gb:d146h12.y1 Morton Fetal Cochlea Homo	12.85
50	453922	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1	12.80
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	12.78
	430521	NM_016383	Hs.242183	HOM-TES-85 tumor antigen	12.72
	443068	AI188710		ESTs	12.65
	437099	N77793	Hs.48659	ESTs, Highly similar to S14458 laminin a	12.60
55	420401	AK001907	Hs.97464	hypothetical protein	12.50
	410361	BE391804	Hs.62661	guanylate binding protein 1, interferon-	12.50
	431494	AA991355	Hs.298312	hypothetical protein DKFZp434A1315	12.45
	406937	U14622		gb:Human transketolase-like protein gene	12.25
60	439451	AF086270	Hs.278554	heterochromatin-like protein 1	12.10
	404996			Target Exon	11.86
	424905	NM_002497	Hs.153704	NIMA (never in mitosis gene a)-related k	11.85
	444619	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-in	11.60
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	11.55
	421241	X91817	Hs.102866	transketolase-like 1	11.50
65	414972	BE263782	Hs.77695	KIAA0008 gene product	11.45
	426866	U02330	Hs.172816	neuregulin 1	11.37
	433159	AB035898	Hs.150587	knesin-like protein 2	11.35
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	11.24
	440207	AI371978	Hs.128326	ESTs	11.12
70	407276	AI951118	Hs.326736	Homo sapiens breast cancer antigen NY-BR	11.10
	450142	AW207469	Hs.24485	chondroitin sulfate proteoglycan 6 (bama	11.05
	449576	AW014631	Hs.225068	ESTs	10.95
	414251	AL042306	Hs.97689	VASA protein	10.95
	422956	BE545072	Hs.122579	ECT2 protein (Epithelial cell transformi	10.90
75	435812	AW298067		gb:U1-HBW0-ajp-g-09-0-ULs1 NCI_CGAP_Su	10.85
	427521	AW973352		ESTs	10.81
	408728	AL137379	Hs.47125	hypothetical protein FLJ13912	10.80
	442832	AW206560	Hs.253569	ESTs	10.62
	436899	AA764852		ESTs	10.60
80	428949	AA442153	Hs.104744	hypothetical protein DKFZp434J0617	10.55
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	10.45
	435206	AI432364	Hs.160594	ESTs	10.15
	433975	AA971953	Hs.122055	ESTs	10.10

	446791	AJ632278	Hs.195922	ESTs	10.05
	422232	D43945	Hs.113274	transcription factor EC	10.00
	420047	AJ478658	Hs.94631	brefeldin A-inhibited guanine nucleotide	9.71
5	434334	AA912476	Hs.116750	Homo sapiens cDNA FLJ13221 fis, clone NT	9.50
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.44
	438188	AA779975	Hs.128859	ESTs	9.30
	418973	AA233056	Hs.191518	ESTs	9.25
	413627	BE182082	Hs.246973	intron of Bicaudal D homolog 1	9.25
10	422689	AW856655		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	9.15
	436608	AA628980	Hs.192371	down syndrome critical region protein DS	9.11
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	9.08
	426518	Z43039	Hs.170198	KIAA0009 gene product	9.05
	440968	N36327		gb:yx82b05.r1 Soares melanocyte 2NbHM Ho	9.05
15	440952	AI291804	Hs.118101	ESTs	9.05
	427469	AA403084	Hs.269347	ESTs, Weakly similar to 2109260A B cell	9.05
	442618	R56222	Hs.26514	ESTs	8.96
	419423	D26488	Hs.90315	KIAA0007 protein	8.95
	428153	AW513143	Hs.98367	SRY (sex determining region Y)-box 17 (S	8.80
20	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	8.76
	444971	AI651116	Hs.148659	ESTs	8.75
	436513	AJ278110	Hs.125507	DEAD-box protein	8.60
	427486	AA974433		fibroblast growth factor 4 (heparin secr	8.59
	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	8.58
25	428847	AI954833	Hs.98881	ESTs	8.57
	408465	AW196940	Hs.253277	ESTs	8.54
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	8.53
	440527	AV657117	Hs.184164	ESTs, Moderately similar to S65657 alpha	8.50
	439570	T79925	Hs.269165	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.50
30	450480	X82125	Hs.25040	zinc finger protein 239	8.50
	425266	J00077	Hs.155421	alpha-fetoprotein	8.50
	453884	AA355925	Hs.36232	KIAA0186 gene product	8.42
	413318	AU076607	Hs.75285	inter-alpha (globulin) inhibitor, H2 pol	8.35
	430835	AI240006	Hs.192326	ESTs	8.33
35	416859	H43437	Hs.80305	hypothetical protein MGC14258	8.30
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	8.26
	407340	AA810168	Hs.284289	villigo-associated protein VIT-1	8.25
	449260	AA741180	Hs.29879	ESTs	8.25
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	8.18
40	448844	AI581519	Hs.177164	FGENESH predicted novel cell surface pr	8.17
	431840	AA634908	Hs.2860	POU domain, class 5, transcription facto	8.14
	428479	Y00272	Hs.334562	cell division cycle 2, G1 to S and G2 to	8.14
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	8.03
	425572	AB011076	Hs.158307	undifferentiated embryonic cell transcri	7.98
45	410420	AA224053	Hs.172405	cell division cycle 27	7.90
	453878	AW964440	Hs.19025	DC32	7.75
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	7.66
	453913	AW004683	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	7.65
	421974	AA301270		gb:EST14192 Testis tumor Homo sapiens cD	7.65
50	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	7.65
	451950	AW292317	Hs.213307	ESTs	7.60
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	7.59
	435514	AW592804		ESTs	7.55
	431041	AA490967	Hs.197955	KIAA0704 protein	7.55
55	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.51
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	7.38
	409421	AA199883	Hs.67624	ESTs	7.35
	449433	AI672096	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	7.35
	458570	AW971698	Hs.12627	TJ6 protein	7.30
60	441287	AW293132	Hs.131373	ESTs	7.30
	434609	R76593		gb:yi50c11.r1 Soares placenta Nb2HP Homo	7.25
	432239	X81334	Hs.2936	matrix metalloproteinase 13 (collagenase	7.25
	441425	AA933590	Hs.28937	homeobox protein from AL590526	7.25
	446293	AI420213	Hs.149722	LIM domain transcription factor LIM-1 (h	7.21
65	414136	AA812434		SMC2 (structural maintenance of chromoso	7.20
	409089	NM_014781	Hs.50421	KIAA0203 gene product	7.19
	422938	NM_001809	Hs.1594	centromere protein A (17kD)	7.18
	441421	AA356792	Hs.334824	hypothetical protein FLJ14825	7.15
	452226	AA024898	Hs.157103	ESTs	7.15
70	435918	AF263538	Hs.86232	growth differentiation factor 3	7.14
	418661	NM_001949	Hs.1189	E2F transcription factor 3	7.10
	436360	AI962796	Hs.156100	ESTs	7.10
	442950	AI500417	Hs.46764	ESTs	7.00
	415684	D59356		sorbitol dehydrogenase	7.00
75	448336	R53848	Hs.44976	ESTs	7.00
	453183	AW086185	Hs.223856	ESTs	7.00
	444434	NM_004849	Hs.11171	APG5 (autophagy 5, S. cerevisiae)-like	6.95
	422665	AJ011812	Hs.119018	transcription factor NRF	6.95
	437421	AA917062		ESTs	6.95
80	428916	AF003001	Hs.194562	telomeric repeat binding factor (NIMA-in	6.94
	408045	AW138959	Hs.245123	ESTs	6.90
	448588	AI970276	Hs.156905	KIAA1676	6.89
	433764	AW753676	Hs.39982	zinc finger protein RINZF (NM_023929)	6.85
	439760	AL109588		gb:Homo sapiens mRNA full length insert	6.85

	449911	AI262106	Hs.12653	ESTs	6.85
	417791	AW965339	Hs.111471	ESTs	6.80
	424085	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40	6.75
5	453160	AI263307		H2B histone family, member L	6.75
	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	6.75
	425427	AI652662	Hs.157205	branched chain aminotransferase 1, cytos	6.73
	447254	NM_004153	Hs.17908	origin recognition complex, subunit 1 (y	6.70
	418379	AA218940	Hs.137516	fidgin-like 1	6.70
10	407366	AF026942	Hs.17518	gb:Homo sapiens clg33 mRNA, partial sequ	6.70
	414618	AI204600	Hs.96978	hypothetical protein MGC10764	6.69
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	6.66
	428743	AL080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	6.65
	442717	R88362	Hs.180591	ESTs, Weakly similar to T23976 hypotheti	6.65
	433247	AB040948	Hs.142856	KIAA1515 protein	6.65
15	430647	AC003682	Hs.127988	ESTs, Weakly similar to Z211_HUMAN ZINC	6.65
	417886	AA214584		ESTs	6.64
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	6.62
	412537	AL031778		nuclear transcription factor Y, alpha	6.61
20	426614	AA411925	Hs.301960	ESTs	6.57
	457465	AW301344	Hs.122908	DNA replication factor	6.52
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	6.50
	440801	AA906366		ESTs	6.50
	453116	AI276680	Hs.146086	ESTs	6.50
	436909	AA907120		ESTs	6.50
25	402199			Target Exon	6.50
	419556	U29615	Hs.91093	chitinase 1 (chitotriosidase)	6.46
	421285	NM_000102	Hs.1363	cytochrome P450, subfamily XVII (steroid	6.41
	438494	AA908678	Hs.130183	ESTs	6.41
30	418592	X99226	Hs.284153	Fanconi anemia, complementation group A	6.40
	408758	NM_003686	Hs.47504	exonuclease 1	6.40
	442671	AI005668	Hs.130673	EST	6.40
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	6.38
	413833	Z15005	Hs.75573	centromere protein E (312kD)	6.35
35	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	6.33
	441878	AI801869	Hs.127982	ESTs	6.31
	429120	AK001673	Hs.196530	hypothetical protein FLJ10811	6.31
	418221	Z45514	Hs.83775	DiGeorge syndrome gene D	6.30
	410166	AK001376	Hs.59346	hypothetical protein FLJ10514	6.30
40	421650	AA781795	Hs.122587	ESTs	6.30
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.28
	408291	AB023191	Hs.44131	KIAA0974 protein	6.26
	438180	AA808189	Hs.272151	ESTs	6.25
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	6.25
45	427510	Z47542	Hs.179312	small nuclear RNA activating complex, po	6.20
	423642	AW452650	Hs.157148	hypothetical protein MGC13204	6.20
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.18
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	6.12
	426223	AW977812	Hs.130391	ESTs	6.10
50	445038	AI635444	Hs.143917	dJ467N11.1 protein	6.10
	419197	N48921	Hs.27441	KIAA1615 protein	6.09
	453775	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	6.05
	436902	AW247145	Hs.192729	ESTs	6.05
	429228	AI553833		ESTs	5.99
55	457065	AI476318	Hs.192480	ESTs	5.90
	426572	AB037783	Hs.170523	hypothetical protein FLJ11183	5.90
	449132	BE045641	Hs.197573	ESTs	5.90
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	5.89
	423728	AW891294	Hs.132136	solute carrier family 4, sodium bicarbon	5.85
60	457289	AW573204	Hs.137078	ESTs	5.85
	433849	BE465884	Hs.280728	ESTs	5.85
	412642	BE244598	Hs.809	hepatocyte growth factor (hepapoietin A;	5.85
	438450	AI050866	Hs.65853	nodal, mouse, homolog	5.81
	428301	AW628666	Hs.98440	ESTs, Weakly similar to I38022 hypotheti	5.80
65	408750	BE294069	Hs.93581	hypothetical protein FLJ10512	5.77
	415947	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	5.77
	408460	AA054726	Hs.285574	ESTs	5.75
	442461	AW062564	Hs.285833	Homo sapiens cDNA: FLJ22135 fis, clone H	5.75
	416747	AW876523	Hs.15929	hypothetical protein FLJ12910	5.75
	428249	AA130914	Hs.183291	zinc finger protein 268	5.74
70	419635	NM_005033	Hs.91728	polymyositis/scleroderma autoantigen 1 (5.72
	402145			Target Exon	5.71
	447178	AW594641	Hs.192417	ESTs	5.70
	458814	AI498957	Hs.170861	ESTs, Weakly similar to Z195_HUMAN ZINC	5.65
75	442980	AA857025	Hs.8878	kinesin-like 1	5.65
	419131	AA406293	Hs.109526	ESTs	5.60
	450254	NM_004885	Hs.99231	neuropeptide G protein-coupled receptor;	5.60
	441627	AA947552	Hs.58086	branched chain aminotransferase 1, cytos	5.60
	440304	BE159984	Hs.125395	ESTs	5.60
80	440553	AA889416	Hs.344043	Homo sapiens cDNA FLJ14459 fis, clone HE	5.58
	442333	AI650877	Hs.129302	ESTs	5.58
	453941	U39817	Hs.36820	Bloom syndrome	5.57
	415799	AA653718	Hs.225841	DKFZP434D193 protein	5.57
	413623	AA825721	Hs.246973	intron of Bicuculal D homolog 1	5.55

	427147	AA398587	Hs.97414	ESTs	5.55
	451050	AW937420		ESTs	5.55
	450113	A1683098	Hs.200868	ESTs, Moderately similar to ALU7_HUMAN A	5.54
5	418678	NM_001327	Hs.167379	cancer/testis antigen (NY-ESO-1)	5.54
	437812	A1582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisou	5.53
	431354	BE046956	Hs.251673	DNA (cytosine-5-)-methyltransferase 3 be	5.51
	449592	A1655494	Hs.195718	ESTs	5.50
	445517	AF208855	Hs.12830	hypothetical protein	5.50
10	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	5.48
	430044	AA464510	Hs.152812	ESTs	5.47
	437036	A1571514	Hs.133022	ESTs	5.47
	423006	U29700	Hs.123014	anti-Mullerian hormone receptor, type II	5.46
	409103	AF251237	Hs.112208	XAGE-1 protein	5.45
	420900	AL045633	Hs.44269	ESTs	5.45
15	437257	A1283085	Hs.290931	ESTs, Weakly similar to YFJ7_YEAST HYPOT	5.45
	440738	A1004650	Hs.225674	WD repeat domain 9	5.45
	412723	AA648459	Hs.335951	hypothetical protein AF301222	5.45
	441122	H56777	Hs.121084	eppin-3	5.42
	414151	AW976468	Hs.257245	ESTs	5.40
20	435663	A1023707	Hs.134273	ESTs	5.40
	448986	H42169	Hs.347310	hypothetical protein FLJ14627	5.39
	433701	AW445023	Hs.15155	ESTs	5.39
	443486	NM_003428	Hs.9450	zinc finger protein 84 (HPF2)	5.35
	440842	AA907288	Hs.130173	ESTs	5.35
25	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	5.34
	401837			NM_025109:Homo sapiens hypothetical prot	5.32
	423739	AA398155	Hs.97600	ESTs	5.31
	424315	AW614850	Hs.193384	putative 28 kDa protein	5.31
30	453900	AW003582	Hs.226414	ESTs, Weakly similar to ALU8_HUMAN ALU S	5.30
	415717	AA167270	Hs.130435	ESTs	5.30
	428329	AA426091	Hs.98453	ESTs, Moderately similar to R27328 2 [H.	5.26
	427119	AW880562	Hs.272525	ESTs	5.25
	432117	AL036195	Hs.2909	protamine 1	5.24
35	446837	AW273055	Hs.156598	ESTs	5.23
	442007	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34	5.21
	422797	AB033064	Hs.236463	KIAA1238 protein	5.19
	446258	A1283476	Hs.263478	ESTs	5.18
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	5.17
40	445413	AA151342	Hs.12677	CGI-147 protein	5.17
	449670	F07693	Hs.85603	Homo sapiens mRNA; cDNA DKFZp434K2172 (f	5.16
	436211	AK001581	Hs.334828	hypothetical protein FLJ10719; KIAA1794	5.15
	429629	BE501732	Hs.30622	Homo sapiens cDNA FLJ13010 fis, clone NT	5.15
	424235	NM_003181	Hs.143507	T brachyury (mouse) homolog	5.15
45	448038	AW015073	Hs.232026	ESTs, Weakly similar to RO52_HUMAN 52 KD	5.15
	430272	X04898	Hs.237658	apolipoprotein A-II	5.14
	422094	AF129535	Hs.272027	F-box only protein 5	5.13
	420424	AB033036	Hs.97594	KIAA1210 protein	5.13
	447924	A1817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.10
50	422631	BE218919	Hs.118793	hypothetical protein FLJ10688	5.10
	453448	AL036710	Hs.209527	ESTs	5.10
	438378	AW970529	Hs.86434	hypothetical protein FLJ21816	5.06
	418235	BE072634		gb:PM4-BT0548-171299-001-h08 BT0548 Homo	5.05
	427961	AW293165	Hs.143134	ESTs	5.05
55	441553	AA281219	Hs.121286	ESTs	5.05
	429999	A1761902	Hs.99597	ESTs	5.04
	426496	D31765	Hs.170114	KIAA0081 protein	5.02
	410929	H47233	Hs.30843	ESTs	5.01
	448757	A1366784	Hs.48820	TATA box binding protein (TBP)-associate	5.01
60	457107	AA418246	Hs.185796	ESTs, Weakly similar to Z184_HUMAN ZINC	5.00
	408332	H91230	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	5.00
	440138	AB033023	Hs.318127	hypothetical protein FLJ10201	5.00
	407568	AA740964	Hs.62699	ESTs	5.00
	409798	AA248587	Hs.30237	ESTs, Weakly similar to ALUB_HUMAN !!!!	5.00
65	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	5.00
	416350	AF188625	Hs.189507	phospholipase A2, group IID	4.99
	452197	AW023595	Hs.232048	ESTs	4.98
	420333	AJ001383	Hs.97084	lymphocyte antigen 94 (mouse) homolog (a	4.97
	403780			C4001759:gil133250[sp]P19474[RO52_HUMAN	4.97
70	418378	AW962081		gb:ESTJ74154 MAGE resequences, MAGG Homo	4.95
	418894	W73921	Hs.50743	ESTs	4.95
	426623	AA382826	Hs.132793	ESTs	4.95
	443537	D13305	Hs.203	cholecystokinin B receptor	4.94
	414812	X72755	Hs.77367	monokine induced by gamma interferon	4.94
75	453716	AA037675	Hs.152675	ESTs	4.90
	402299			Target Exon	4.90
	411945	AL033527	Hs.92137	L-myc-2 protein (MYCL2)	4.89
	414034	U89277	Hs.305985	early development regulator 1 (homolog o	4.87
	409066	AA062980	Hs.56960	ESTs	4.85
80	437496	AA452378	Hs.146668	Homo sapiens mRNA; cDNA DKFZp547J125 (fr	4.85
	416661	AA634543	Hs.79440	IGF-II mRNA-binding protein 3	4.85
	450375	AA009647		a disintegrin and metalloproteinase doma	4.85
	416201	AA467752	Hs.195161	ESTs	4.85
	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M126 (f	4.84

	423198	M81933	Hs.1634	cell division cycle 25A	4.82
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.81
	418971	AA360392	Hs.87113	ESTs	4.80
5	411571	AA122393	Hs.70811	hypothetical protein FLJ20516	4.80
	409517	X90780		troponin I, cardiac	4.80
	424322	AL157491	Hs.145211	Homo sapiens mRNA; cDNA DKFZp434K1111 (f	4.80
	443169	AI038687	Hs.133338	ESTs	4.80
	438624	AA889055	Hs.123468	ESTs	4.79
10	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	4.76
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	4.76
	443715	AI583187	Hs.9700	cyclin E1	4.76
	423123	NM_012247	Hs.124027	SELENOPHOSPHATE SYNTHETASE ; Human selen	4.75
	451105	AI761324		gb:wi60b11.x1 NCI_CGAP_Co16 Homo sapiens	4.71
15	444431	AW513324	Hs.42280	Homo sapiens, clone MGC:9010, mRNA, comp	4.71
	440591	AA431599	Hs.132799	hypothetical protein FLJ23451	4.71
	424281	AA766243		gb:oa13b11.s1 NCI_CGAP_GCB1 Homo sapiens	4.70
	447175	AI365208	Hs.293606	ESTs	4.70
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.69
20	430183	BE010038		gb:PM3-BN0176-100400-001-g04 BN0176 Homo	4.68
	416445	AL043004	Hs.79337	KIAA0135 protein	4.66
	429652	AA766810	Hs.259290	ESTs	4.65
	420054	U12431	Hs.166109	ELAV (embryonic lethal, abnormal vision,	4.65
	418618	U66097	Hs.86724	GTP cyclohydrolase 1 (dopa-responsive dy	4.64
25	445537	AJ245671	Hs.12844	EGF-like-domain, multiple 6	4.62
	427298	AA400495		ESTs	4.62
	412863	AA121673	Hs.59757	zinc finger protein 281	4.62
	446700	AW206257	Hs.156326	Human DNA sequence from clone RP11-145L2	4.61
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.60
30	446751	AA766998	Hs.79126	Human DNA sequence from clone RP11-16L21	4.60
	432656	NM_000246	Hs.3076	MHC class II transactivator	4.60
	434283	AW235341	Hs.58715	thiamine pyrophosphokinase	4.60
	437915	AI637993	Hs.202312	Homo sapiens clone N11 Ntera2D1 teratoca	4.60
	421830	AA789269	Hs.122509	ESTs, Weakly similar to dJ1018D12.3 [Hs	4.59
35	440006	AK000517	Hs.6844	NALP2 protein; PYRIN-Containing APAF1-II	4.58
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	4.58
	431721	AB032996	Hs.268044	KIAA1170 protein	4.55
	423175	W27595	Hs.347310	hypothetical protein FLJ14627	4.55
	453529	AA036729	Hs.335639	ESTs	4.55
40	416209	AA236776	Hs.79078	MAD2 (mitotic arrest deficient, yeast, h	4.55
	444386	BE065183		gb:RC1-BT0314-020200-012-c04 BT0314 Homo	4.55
	428976	AL037824	Hs.194695	ras homolog gene family, member I	4.55
	449510	AI653154	Hs.328147	ESTs	4.55
	414725	AA769791		ring finger protein 21, Interferon-respo	4.54
45	424153	AA451737	Hs.141496	MAGE-like 2	4.53
	414466	AA349211	Hs.76205	cytochrome P450, subfamily XIA (choleste	4.52
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.50
	458443	AV647010	Hs.27	glycine dehydrogenase (decarboxylating;	4.48
	453289	AI188161	Hs.144627	ESTs	4.48
50	433641	AF080229		gb:Human endogenous retrovirus K clone 1	4.45
	440196	N72847	Hs.125221	ESTs	4.45
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.45
	428855	AA435901	Hs.89563	nuclear cap binding protein subunit 1, 8	4.45
	416734	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	4.45
55	442240	AI791883	Hs.292719	ESTs	4.45
	421917	AB028943	Hs.109445	KIAA1020 protein	4.45
	420949	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	4.44
	449676	AW380579	Hs.209657	ESTs	4.43
	433183	AF231338	Hs.222024	transcription factor BMAL2	4.40
60	439314	AA382413	Hs.178144	ESTs	4.40
	425312	AA354940	Hs.145958	ESTs	4.39
	427584	BE410293	Hs.179718	v-myb avian myeloblastosis viral oncogen	4.39
	430444	AW296421	Hs.121035	ESTs	4.35
	416773	AK000340	Hs.79828	hypothetical protein FLJ20333	4.35
65	421010	AW974553	Hs.267124	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.34
	418216	AA662240	Hs.283099	AF15q14 protein	4.32
	450351	BE547267	Hs.59791	hypothetical protein MGC13183	4.32
	454073	AW206286	Hs.116727	ESTs	4.30
	417005	AW673506	Hs.80758	aspartyl-tRNA synthetase	4.30
70	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.30
	448877	AI583696	Hs.253313	ESTs	4.28
	421379	Y15221	Hs.103982	small Inducible cytokine subfamily B (Cy	4.27
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	4.25
	430292	AK000534	Hs.238270	hypothetical protein FLJ20527	4.25
75	427778	AA412323	Hs.105323	ESTs	4.25
	418768	T39310		gb:ya04a09.r2 Stratagene lung (937210) H	4.25
	409268	AA625304		ESTs	4.25
	442010	AI032680	Hs.132213	ESTs	4.24
	452807	AA028933	Hs.162434	ESTs	4.23
80	401435			C14000397::gil7499898[pil7]T33295 hypoth	4.23
	447519	U46258	Hs.339665	ESTs	4.21
	421307	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	4.21
	424590	AW966399	Hs.46821	hypothetical protein FLJ20086	4.20
	453909	AW004045	Hs.203365	ESTs	4.20

	431126	AF085243	Hs.283619	zinc finger protein 236	4.20
	429628	H09604	Hs.13268	ESTs	4.20
	415989	AI267700		ESTs	4.20
5	421373	AA808229	Hs.46677	ESTs	4.20
	433979	AA620999		gb:ag03a08.s1 Soares_testis_NHT Homo sap	4.20
	408321	AW405882	Hs.44205	cortistatin	4.19
	410193	AJ132592	Hs.59757	zinc finger protein 281	4.17
	430335	D80007	Hs.239499	KIAA0185 protein	4.17
10	408031	AA081395	Hs.42173	Homo sapiens cDNA FLJ10366 fis, clone NT	4.16
	438885	AI886558	Hs.184987	ESTs	4.15
	451578	NM_016323	Hs.26663	cyclin-E binding protein 1	4.15
	432446	AA542845	Hs.294088	GAJ protein	4.13
	445076	AI206888	Hs.154131	ESTs	4.11
	420218	AW958037		ribosomal protein L4	4.10
15	453628	AW243307	Hs.83937	hypothetical protein	4.10
	418459	R85436	Hs.268814	ESTs	4.10
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.08
	440404	AI015881	Hs.324527	mitochondrial ribosomal protein S5	4.06
	426300	U15979	Hs.169228	delta-like homolog (Drosophila)	4.06
20	446223	BE300091	Hs.119699	hypothetical protein FLJ12969	4.05
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	4.05
	449687	W68520		intermediate filament protein syncollin	4.05
	452109	AI525873	Hs.61164	hypothetical protein FLJ14909	4.05
	401464			histone deacetylase 5	4.05
25	444670	H58373	Hs.332938	hypothetical protein MGC5370	4.05
	415884	H22966	Hs.13471	ESTs	4.05
	442066	BE502147	Hs.128418	ESTs	4.04
	402098			ENSP00000217725*-Laminin alpha-1 chain p	4.02
	404287			FGENESH predicted novel CUB-domain conta	4.01
30	422756	AA441787	Hs.119689	glycoprotein hormones, alpha polypeptide	4.01
	449704	AK000733	Hs.23900	GTPase activating protein	4.00
	445685	AW779829		gb:hn88a05.x1 NCL_CGAP_Kid11 Homo sapien	4.00
	444379	N99035	Hs.30352	ESTs	4.00
35	435373	AW665538	Hs.117689	ESTs	4.00
	424557	AA343057	Hs.164588	ESTs, Moderately similar to neuronal thr	4.00
	413646	BE155042		gb:PM0-HT0349-101299-002-E04 HT0349 Homo	4.00
	418648	AW979223	Hs.292478	ESTs	4.00
	446074	AA079799	Hs.343103	hypothetical protein FLJ11896	4.00
	447353	AI375701	Hs.25884	ESTs	4.00
40	410100	AA081636	Hs.271916	ESTs, Weakly similar to S41044 chromosom	4.00
	428856	AA346735	Hs.183171	hypothetical protein FLJ22002	4.00
	445140	AI650599	Hs.197913	ESTs, Weakly similar to SCP3 MOUSE SYNAP	4.00
	406367			NM_022357:Homo sapiens putative metallo	3.99
	437834	AA769294		gb:mz38g03.s1 NCL_CGAP_GCB1 Homo sapiens	3.99
45	453985	N44545	Hs.251865	ESTs	3.98
	408446	AW450669	Hs.45068	hypothetical protein DKFZp4341143	3.97
	408562	AI436323	Hs.31141	roundabout (axon guidance receptor, Dros	3.97
	414713	BE465243	Hs.12664	ESTs	3.96
	426067	AW664691	Hs.97053	ESTs	3.96
50	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 utinu	3.96
	454679	AW813110		gb:CM4-ST0189-051099-021-405 ST0189 Homo	3.95
	451865	H43737	Hs.33186	ESTs, Weakly similar to unknown protein	3.95
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	3.95
	445730	AI624342	Hs.179082	ESTs	3.95
55	451993	AA765776	Hs.122983	ESTs	3.95
	428819	AL135623	Hs.193914	KIAA0575 gene product	3.92
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	3.91
	420812	AA715303	Hs.107369	ESTs	3.90
	423806	AA331247	Hs.85617	ESTs	3.90
60	437205	AL110232	Hs.279243	Homo sapiens mRNA; cDNA DKFZp564D2071 (T	3.90
	449211	AI922972	Hs.196073	ESTs	3.90
	409757	NM_001898	Hs.123114	cystatin SN	3.90
	436027	AI864053	Hs.39972	ESTs, Weakly similar to I38588 reverse t	3.89
	432512	NM_003284	Hs.3017	transition protein 1 (during histone lo	3.89
65	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	3.88
	449099	AI629041	Hs.46908	ESTs	3.88
	408092	NM_007057	Hs.42650	ZW10 interactor	3.85
	423909	AJ223183	Hs.135194	immunoglobulin superfamily, member 6	3.85
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.84
70	424381	AA285249	Hs.146329	protein kinase Chk2(CHEK2)	3.83
	433023	AW864793		thrombospondin 1	3.82
	452571	W31518	Hs.34665	ESTs	3.81
	421413	AI826128	Hs.55209	ESTs, Weakly similar to A49364 59 protei	3.80
	440953	AI683036	Hs.124135	Homo sapiens cDNA FLJ13051 fis, clone NT	3.80
75	420697	AA827705	Hs.26605	ESTs	3.80
	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_U14 Homo sapiens	3.80
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	3.80
	411856	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone C	3.80
	449529	AI990559	Hs.232033	ESTs	3.80
80	447444	AK000318	Hs.18616	hypothetical protein FLJ20311	3.78
	444656	AI277924	Hs.145199	ESTs	3.77
	448674	W31178	Hs.154140	ovary-specific acidic protein	3.77
	415829	AW450198	Hs.163742	ESTs	3.76

	436188	AK001049	Hs.48712	hypothetical protein FLJ20736	3.75
	402178			C19001998*:g 6453813 ref NP_008926.2 b	3.75
	418179	X51630	Hs.1145	Wilms tumor 1	3.75
5	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.75
	429063	AW363845	Hs.322903	ESTs, Weakly similar to A46010 X-linked	3.75
	437440	AA846804		ESTs	3.75
	427366	AA885108	Hs.223806	TATA box binding protein (TBP)-associate	3.74
	438456	AA913381	Hs.20594	ESTs	3.73
10	418821	AA436002	Hs.183161	ESTs	3.73
	417918	AA209205	Hs.163754	hypothetical protein FLJ12606	3.73
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.71
	423020	AA383092	Hs.1608	replication protein A3 (14kD)	3.70
	409928	AL137163	Hs.57549	hypothetical protein dJ47384	3.70
	414206	AW276887	Hs.46609	ESTs	3.70
15	427761	AA412205	Hs.140996	ESTs	3.69
	428728	NM_016625	Hs.191381	hypothetical protein	3.68
	452631	AI188658	Hs.87496	ESTs	3.68
	427719	AJ393122	Hs.134726	ESTs	3.68
20	431869	AA521136	Hs.190176	ESTs	3.67
	429830	AI537278	Hs.225841	DKFZP434D193 protein	3.67
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.66
	421972	M18185	Hs.1454	gastric inhibitory polypeptide	3.66
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.65
25	456030	AA136106	Hs.184852	KIAA1553 protein	3.65
	402408			NM_030920:Homo sapiens hypothetical pro	3.65
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	3.65
	416608	R11499	Hs.189716	ESTs	3.65
	417553	L09190		trichohyalin	3.65
30	408065	AW954272		gb:EST366342 MAGE resequences, MAGC Homo	3.65
	431077	AI669133	Hs.115660	hypothetical protein FLJ12810	3.64
	452461	N78223	Hs.108106	transcription factor	3.60
	437660	W31708	Hs.55304	ESTs	3.60
	420552	AK000492	Hs.98806	hypothetical protein	3.60
35	419926	AW900992	Hs.93796	DKFZP586D2223 protein	3.59
	420161	AI683069	Hs.120817	ESTs	3.59
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	3.59
	449571	AW016812	Hs.200266	ESTs	3.58
	424727	AW590378	Hs.152519	hypothetical protein FLJ20574	3.55
40	441820	AA969119	Hs.143502	ESTs, Weakly similar to envelope protein	3.55
	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	3.55
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.55
	437700	AA766060	Hs.301209	myeloid/lymphoid or mixed-lineage leukem	3.55
	438176	AW138970	Hs.122113	ESTs	3.55
45	453062	AW207538	Hs.61603	KIAA1677	3.55
	447054	AB002350	Hs.17262	KIAA0352 gene product	3.55
	430056	X97548	Hs.228059	KRAB-associated protein 1	3.54
	418049	AA211467		Homo sapiens, Similar to nuclear localiz	3.54
	434288	AW189075	Hs.116265	fibrillin3	3.54
50	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	3.52
	421350	AW301608	Hs.278188	ESTs, Moderately similar to I54374 gene	3.52
	413943	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	3.52
	412123	BE251328	Hs.73291	hypothetical protein FLJ10881	3.51
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.50
55	449467	AW205006	Hs.197042	ESTs	3.50
	405935			Target Exon	3.50
	429782	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain	3.50
	411027	AF072099	Hs.67846	leukocyte immunoglobulin-like receptor,	3.50
	412140	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines	3.49
60	429183	AB014604	Hs.197955	KIAA0704 protein	3.49
	428878	AA436884	Hs.48926	ESTs	3.49
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.49
	435068	H16262	Hs.31415	ESTs	3.48
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	3.48
65	451065	AW295132	Hs.222231	ESTs, Weakly similar to granule cell mar	3.48
	419741	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.48
	406542			C19000728*:g 12585552 sp Q9Y2Q1 Z257_HU	3.47
	422406	AF025441	Hs.116206	Opa-interacting protein 5	3.46
	402099			ENSP00000217725*:Laminin alpha-1 chain p	3.45
70	418826	AK000375	Hs.88820	HDCMC28P protein	3.45
	424513	BE385864	Hs.149894	mitochondrial translational initiation f	3.45
	427617	D42063	Hs.199179	RAN binding protein 2	3.45
	428361	NM_015905	Hs.183858	transcriptional intermediary factor 1	3.45
	400268			NM_003292:Homo sapiens translocated prom	3.45
75	443596	AW026048	Hs.134124	ESTs	3.45
	442875	BE623003	Hs.23625	Homo sapiens clone TCCTA00142 mRNA sequ	3.45
	416031	T30290	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	3.45
	435244	N77221	Hs.187824	ESTs	3.45
	423354	AB011130	Hs.127436	calcium channel, voltage-dependent, alph	3.45
80	453785	AI368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	3.45
	420686	AI950339	Hs.40782	ESTs	3.44
	429467	NM_004477	Hs.203772	F5HD region gene 1	3.43
	448769	N66037	Hs.38173	ESTs	3.43
	423453	AW450737	Hs.128791	CGI-09 protein	3.41

	417705	AW134952	Hs.175220	hypothetical protein FLJ14541	3.41
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	3.41
	404068			Target Exon	3.40
	401644			Target Exon	3.40
5	422364	AF087800	Hs.115515	C-type (calcium dependent, carbohydrate-	3.40
	452907	BE256966	Hs.31652	ESTs, Moderately similar to IS4374 gene	3.40
	420281	AI623693	Hs.323494	Predicted cation efflux pump	3.39
	452404	AW450675	Hs.212709	ESTs	3.39
10	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	3.39
	420892	AW975076	Hs.172589	nuclear phosphoprotein similar to S. cer	3.39
	440606	AI828751		ESTs, Weakly similar to I38022 hypothe	3.38
	425474	Z48054	Hs.158084	peroxisome receptor 1	3.37
	429714	BE561801	Hs.2484	T-cell leukemia/lymphoma 1A	3.37
15	446214	AK001322	Hs.14347	hypothetical protein FLJ10460	3.36
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.36
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	3.36
	421633	AF121860	Hs.106260	sorting nexin 10	3.36
	438192	AI859065	Hs.293807	Homo sapiens AFG3L1 isoform 1 mRNA, part	3.36
20	436511	AA721252	Hs.291502	ESTs	3.35
	402680			Target Exon	3.35
	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	3.35
	449477	AI652602	Hs.197043	ESTs	3.35
	413686	AI469213	Hs.71404	ESTs	3.35
	401091			decay accelerating factor for complement	3.35
25	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	3.35
	433220	AI076192	Hs.131933	ESTs	3.34
	453200	AA033832	Hs.212433	ESTs	3.33
	427239	BE270447		ubiquitin carrier protein	3.33
30	418355	L42563	Hs.1165	ATPase, H7 transporting, nongastric, alp	3.33
	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide syntha	3.31
	441243	AI767056	Hs.193002	ESTs	3.30
	440716	AW105245	Hs.146509	ESTs	3.30
	400587			C100006499:gi7296574 gb AA51857.1 (AE	3.30
35	401148			Target Exon	3.30
	411752	AW236047	Hs.126497	ESTs	3.30
	433252	AB040957	Hs.151343	KIAA1524 protein	3.30
	434008	AA740878	Hs.112982	ESTs	3.30
	444655	BE613126	Hs.47783	B aggressive lymphoma gene	3.30
40	458067	AA393603	Hs.36752	protein kinase anchoring protein GKAP42	3.30
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.29
	452761	BE244742	Hs.30532	CGI-77 protein	3.29
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	3.29
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.28
45	432809	AA565509	Hs.131703	ESTs	3.27
	449426	T92251	Hs.198882	ESTs	3.27
	425174	D87450	Hs.154978	KIAA0261 protein	3.25
	435159	AA668879	Hs.116649	ESTs	3.25
	446597	AK001334	Hs.15470	putative ring zinc finger protein NY-REN	3.25
50	411554	W22895	Hs.112360	prominin (mouse)-like 1	3.25
	447555	AI391662	Hs.160963	Homo sapiens, clone MGC:12318, mRNA, com	3.25
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	3.25
	445093	AI207197		ESTs	3.25
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	3.24
55	424568	AF005418	Hs.150595	cytochrome P450, subfamily XXVIA, polype	3.24
	453293	AA382267	Hs.10653	ESTs	3.24
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.23
	430552	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	3.22
	411975	AI916058	Hs.144583	ESTs	3.22
60	448140	AF146761	Hs.20450	BCM-like membrane protein precursor	3.22
	403432			NM_001622:Homo sapiens alpha-2-HS-glycop	3.21
	436515	AJ278111	Hs.195292	putative tumor antigen	3.21
	456505	AA504585		ESTs	3.21
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	3.21
65	452794	AI192444	Hs.25892	ESTs, Weakly similar to I37356 epithelia	3.20
	427314	AB033024	Hs.175475	KIAA1198 protein	3.20
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	3.20
	452028	AK001859	Hs.27595	hypothetical protein FLJ21142	3.20
	421002	AF116030	Hs.100932	transcription factor 17	3.20
70	422225	BE245652	Hs.118281	zinc finger protein 266	3.20
	437549	AA759149	Hs.128757	gb:ah70e03.s1 Soares_testis_NHT Homo sap	3.20
	418524	AA300576	Hs.85769	acidic 82 kDa protein mRNA	3.20
	427642	R40761	Hs.9834	ESTs	3.20
	442765	BE567353	Hs.99480	ESTs	3.20
75	410048	W76467	Hs.343874	proline oxidase homolog	3.20
	412008	NM_001841	Hs.73037	cannabinoid receptor 2 (macrophage)	3.20
	423675	AI990509	Hs.131342	small inducible cytokine subfamily A (Cy	3.20
	453895	AA039843	Hs.61948	Homo sapiens, clone MGC:16466, mRNA, com	3.20
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	3.19
80	428612	AA770001		ESTs	3.19
	422805	AA436989	Hs.121017	H2A histone family, member A	3.19
	444371	BE540274	Hs.239	forkhead box M1	3.18
	427528	AU077143	Hs.179585	minichromosome maintenance deficient (S.	3.17
	451684	AF216751	Hs.26813	CDA14	3.17

5	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	3.17
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	416000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H88923	Hs.270247	Homo sapiens cDNA FLJ11977 fs, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
10	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
	437642	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450405	AI694913	Hs.279637	ESTs	3.15
	414161	AA136106	Hs.184852	KIAA1553 protein	3.15
15	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
	441013	AI125252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
20	434769	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fs, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
	410704	BE076754		gb:CM1-8T0601-180200-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.98397	A kinase (PRKA) anchor protein 3	3.11
25	423419	R55335	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195631	ESTs	3.10
30	441795	NS8115	Hs.21137	AD024 protein	3.10
	456053	S57498	Hs.76252	endothelin receptor type A	3.10
	403610			C3001199:gil7494834[pir]T15308 hypothet	3.10
	421281	AI299139	Hs.17517	ESTs	3.10
	429274	AI379772	Hs.99206	ESTs	3.10
35	438243	AI581311		ESTs	3.10
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.09
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	416443	N69469	Hs.194225	ESTs	3.08
	421230	AW958439	Hs.105633	ESTs	3.07
40	427906	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76989	KIAA0097 gene product	3.06
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	AI343868	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
45	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	3.05
	438869	AF075009		gb:Homo sapiens full length insert cDNA	3.05
50	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
55	435726	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
	420596	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-ocl	3.00
	434776	AA548988		gb:ns41f11.s1 NCI_CGAP_GCB1 Homo sapiens	3.00
	414132	AI801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
65	433493	AA594915	Hs.155087	ESTs	3.00
	452606	N45202	Hs.50012	hypothetical protein FLJ23441	3.00
	453416	NM_003037	Hs.32970	signaling lymphocytic activation molecu	3.00

TABLE 53B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
432666	144_7	AA558585 AA565499 AI360576 AW204069 AA991648 AA864939
423458	30480_1	BC018070 BG702493 AI204212 AA460929 AA993606 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539 BG215094 BG198867 BG196332 BG208220 BG212418 BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922595 BE061603 AI352469 BE061601 BI062752 AW818206 BF887722 BE671981 BE503379 AI655440 AI337054 AI288920 AI242370 AI825182 AA758081 BF855141 BF091068 BC022538 AI990847 BF478249 BG217996 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092 AI623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 AI910424 AV752763 AI032142 N30308 N22181 H95390 AW675632 AW978773 AW298067 AA810101 AW194180 AA731645 AI690573
422828	227063_1	
418477	4172_1	
443068	18695_17	
436812	659779_1	

5	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892
	436899	1000797_1	AA764852 AA736937
	422689	874209_1	AW954733 AA315006 AW856655
	440968	518029_1	AI964001 AI634418 AW236545 AI824860 BF223710 AW139686 AI672051 AI655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451
10	427486	684159_1	BF510715 BE673055 BE464111 AW590620 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433
	421974	864120_1	AA301270 AA301379 AA301366
	435514	132288_1	AA683356 AW592804 AI150287
	434609	14739_1	AF147390 R76593 R76594
15	414136	30243_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI566516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566534 AA211796 BG615512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135833 AI831542 N63376 AA214392 AU154486 AW605017 AW450072 AA445459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812 BF666746 D59356 BG678312 N56640 AA166861 AA917062 AA757369 AW592218 AL105688 R23665 R26578 BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336 AA210987 D57294 AA214584 AA207006 D56572 AK025201 AA425472 AI694282 BG057305 AA907787 AI286170 AI684577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI69807 AI969353 BE552356 N66509 AA736741 AA382555 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167566 AI208445 AA889823 BF982682 N90322 BI090862 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282 AA906366 AA938956 AI910938 AW102570 AA907150 AA907120 AA737188 AI248890 AW977353 BG676155 BM009591 AI479075 AI025794 AI017967 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW989605 AI553633 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 BE072634 BE072653 AA830615 AA214736 AA331718 AA218925 AW962081 AA354237 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H59605 BE157601 AA113758 NM_000363 X54163 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI657074 C03333 AI193911 C05024 C03193 AI950215 C05070 C05613 W17389 C05351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C03114 C03103 AI369979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339 AK056685 BG399272 AA187835 BF821903 AV680550 AV660556 AV660502 BG564397 BE379584 BF446961 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI656750 AW92830 AW021142 AI472184 AW170056 AI082443 AI167921 D59940 BI492088 H74180 AW130886 AI348577 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832 BI015205 AI761324 AW680937 AW880941 AA338252 AA338213 AK055746 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF995651 AI675065 BG001051 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038 AA933717 BF061897 AW628327 AA641788 AA400495 BE065183 AI144398 BE065367 BF377924 NM_058166 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE892241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338826 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA609112 BI054316 AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AL535594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87595 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N29986 N25895 H69001 U87596 BE673974 AI797496 AI701526 AA703396 AW139734 H92278 N66048 BE219539 BE671665 AI624817 BE466611 AI206344 AA574397 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496808 AA204833 AA207155 BI004756 AA206262 AI365204 H77608 AW590511 T39328 T39310 T39303 T39284 BE893356 AA625304 AI765607 AI624898 R76060 AA069651 BG998885 R35783 BF086499 AA428755 AI245055 BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 N50454 AA620999 T16375 AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 T65754 AA229658 AA229857 AK056550 AK056356 AI928212 AI742073 AW300558 BG058755 AA058343 AI554842 AW207438 BF509981 BF444954 AW026234 AI620104 AA973460 AI370934 N63066 AA493129 AW590888 AI682952 AI167202 AA631394 AI421915 AI222883 BF477519 AI208777 AA765849 AI675076 AI370922 AI339579 AA486224 AA453524 AW771805 AI492842 H54679 AA961022 AW023555 H06192 AA910222 AI660021 AI032525 AI375480 AI361860 AI032919 AA833599 BG057928 AA553913 AW235737 AA002124 AA913636 F04607 AI867699 AA648100 BE091446 AA486378 BE002022 H84627 BI059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG290981 AW954251 AA757126 H11545 AA353384 N48448 AA379845 AA004943 AA379928 AA002123 BM470118 AL598847 AL598830 BG899239 R57470 BF939179 AI650642 AI758851 BF352505 W668422 W35297 H11435 AA937499 AI783996 R12500 AI819557 N39093 Z41619 H22849 AA004942 R09436 R02403 T90942 T85823 BG025683 AI248120 BI850480 AW779829 N22484 BE155042 BE155040 BE154987 BE155012 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749288 AW749296 AA769294 AW749297 AW749295 AW749292 BE002573 AW813110 BF771370 BF771371 AW813113 AW003381 BI862319 AA204955 BF240507 BG212143 AW205739 BI760647 BI760482 AW300025 AI288591 AW236114 AI302852 AI038548 AI797207 AA534496 BG188194 AA921877 BG191846 BG182959 BE620243 BF217428 BC009514 BM463015 AL529077 BM051874 BG773269 BM314351 BM314660 AW629666 AA316207 AI623431 AA504153 AA314700 BG195449 BG614101 BE999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968583 AA846676 AA927355 H80424 AW973295 R88209 F29868 BE928871 AA846804 AA757581 AI050950 AI092024 AA838807
20	417886	1031334_1	
	412537	14056_1	
25	440801	2635916_1	
	436909	596835_1	
	429228	215430_1	
30	451050	11847_4	
	418235	886897_1	
	418378	1227421_1	
	450375	16559_3	
35	409517	4537_1	
40	442562	39593_1	
45	451105	1145037_1	
	424281	892055_1	
	430183	17316_1	
50	427298	115241_1	
	444386	1490237_1	
	414725	19377_1	
55	433641	35983_1	
60	418768	2293204_1	
	409258	109625_1	
	415989	10194_1	
65	433979	2076469_1	
	420218	191547_1	
70	418866	245947_1	
	449687	25369_2	
75	445685	381678_1	
	413646	1525656_1	
	437834	294580_1	
80	454679	174325_1	
	440840	29686_1	
85	433023	3970_8	
90	437440	2497201_1	

5	417553	258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878 AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
	408065	101881_1	BI603077 AW954272 BI598724 AI003154 AA059300 AA046911 BI669907 BI600966 BI669987
	418049	12052_4	AJ314647 NM_052888 BI494693 AA835065 AI634477 AI336678 AI807696 BF477887 AI701147 Z39187 R38979 F02234 AA984711 BI222234
	430968	1237115_1	AV731417 R42406 HQ4996 T98498 R12489 R12577 R42405
	400268	840_4	AW972830 AA489820 AA527647 AA570362
10			U69668 AA448366 X63105 BC016514 BE694436 AI655840 AW235355 BG427984 AA612862 AA448223 BM145813 BM194565 AI870824 BE973573
			BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687
			BF908518 BF907890 R11490 AL536642 BF109180 AA953881 AI783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859
			AW167268 AI990460 AW300443 AA779660 AI620568 BF115024 BE504703 AW628332 AI922851 BE006636 AU158376 AI168279 AA809916
			AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477364 BG261301 AA326388 AU150565 AU158374 AA687967 N58510 AI650450
			AL549572 BF349280 BF349269 BM463016 AW836798 AI120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782
			AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW366516 AW391532
15	440606	10075_1	BE934857 BF925057 AW438446 R86246 AW179270 BE087782 BI832144
	427239	20459_2	BC017350 BC021031 AI220219 AI828751 AW134498 BE139642 AA894554 AI278594 AV747315 BE561749 BI085690 T80117 H69682 N70904
			AV741999 H70098
20			AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
			AJ251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839
			AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420
			AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260
			AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
			BF718773 BF716645 AW074866 BE857822
25	445093	175963_1	AI207197 BF773544 AW195462
	456505	15472_2	BC017965 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
	428612	1383189_1	AA770001 AA431112 AA432126
	437642	77594_1	AL079309 AA281819
	440129	2607882_1	AI732997 AA977633 AA865818
30	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
			AW840571
	438243	2532601_1	AI581311 AA781682 AA781678
	438869	52134_1	AF075009 R63109 R63068
35	434776	118129_1	AW974599 AA648988 R98760

TABLE 53C

40	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	NL_position:	Indicates nucleotide positions of predicted exons.

45	Pkey	Ref	Strand	NL_position
	406547	7711513	Minus	172780-174358
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	402199	8576116	Minus	84187-84744
	402145	8018280	Plus	113086-114800
50	401837	7630990	Minus	120993-121095,121660-121729
	403780	8076989	Plus	93160-93409
	402299	6693370	Plus	23367-25175
	401435	8217934	Minus	54508-55233
	401464	6682291	Minus	170688-170834
55	402098	8117697	Minus	44186-44330
	404287	2326514	Plus	53134-53281
	406367	9256126	Minus	58313-58489
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402178	8575912	Plus	391138-391711
60	403433	9719611	Minus	72225-72437
	402408	9796239	Minus	110326-110491
	405935	6758795	Minus	163112-163652
	406542	7711499	Plus	117335-118473
	402099	8117697	Plus	121553-121742,123265-123423
65	404068	3168621	Minus	18123-18766
	401644	8576138	Plus	82655-83959
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	401091	9958240	Plus	94760-94898
	400587	9887626	Plus	25435-25588,25668-25747
70	401148	2547238	Minus	22521-23053
	403432	9719611	Minus	68204-68392
	400592	9887642	Minus	24542-24815
	403610	8308266	Plus	157705-157860

TABLE 54A:

75	Pkey:	Unique Eos probeset identifier number
	ExAccon:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigene number
	Unigene Title:	Unigene gene title
80	R1:	Ratio of normal testis to normal adult tissues
	R2:	Ratio of "average" normal testis to "average" testicular cancer

Pkey	ExAccon	UnigenelD	Unigene Title	R1	R2
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	401979		C17000767:gi 11990770 emb CAC19651.1 (A	10.08	43.3	
	421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35	36.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74	32.0
5	441728	AI797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54	24.5
	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.86	22.0
	415211	R64730	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93	19.8
	418677	S83308	Hs.87224	SRV (sex determining region Y)-box 5	4.94	18.5
	449108	AI140683	Hs.98328	hypothetical protein MGC13040	7.94	17.5
10	420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75	15.6
	436532	AA724299	Hs.304020	ESTs, Weakly similar to CRTC_HUMAN CALRE	6.51	14.9
	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96	14.6
	406409			Target Exon	3.98	14.3
	427060	AW378993	Hs.90286	ESTs	3.56	14.2
15	427310	AI613480	Hs.47152	teklin 3	4.50	14.0
	427166	AA431576	Hs.99154	ESTs	4.28	13.9
	427178	AA398868	Hs.97542	Homo sapiens testis-development related	10.19	13.7
	410694	AL137538	Hs.65500	Homo sapiens mRNA; cDNA DKFPz434N2019 (f	5.76	13.4
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24	13.3
20	427441	AA412605	Hs.343879	SPANX family, member C	10.45	12.6
	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB MOUSE CORNI	18.57	12.3
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1068E13 on	5.18	12.3
	427293	AA705799	Hs.183714	ESTs	10.79	12.1
	444963	AI916973	Hs.213603	ESTs	3.18	12.1
25	428608	AI699329	Hs.99168	ESTs, Weakly similar to AF132972.1 CGI-3	15.40	11.8
	453178	AA496086	Hs.61648	ESTs	4.13	11.8
	428618	AA885360		Target CAT	7.53	11.5
	401741			Target Exon	10.41	11.5
	422086	AW182930	Hs.250182	ESTs	4.39	10.7
30	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04	10.6
	442373	AI377758	Hs.164799	testes development-related NYD-SP17	8.23	10.3
	427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax interacti	3.03	10.1
	437248	AW449340	Hs.93090	ESTs	9.06	10.1
	426608	AA444162	Hs.99344	hypothetical protein PRTD-NY3	3.68	10.0
35	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70	9.8
	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85	9.7
	451610	AW118604	Hs.207126	ESTs	5.63	9.7
	410630	BE044562	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38	9.5
	426577	AW949856	Hs.97165	ESTs	6.58	9.3
40	437558	AI126471	Hs.124112	ESTs, Moderately similar to HSJ2_HUMAN D	4.47	9.2
	423088	NM_006687	Hs.123530	actin-like 7A	15.07	8.9
	426476	NM_003296	Hs.2042	testis specific protein 1 (probe H4-1 p3	18.55	8.9
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	13.93	8.8
	429877	W37337	Hs.103014	ESTs	6.97	8.7
45	413114	AI825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78	8.6
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	22.03	8.5
	411844	AI807681	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	7.34	8.3
	436868	AA974263	Hs.120319	Homo sapiens autoimmune infertility-rela	4.16	8.2
	426599	AW183574		ESTs	6.29	8.1
50	426683	AI073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89	8.0
	426930	AA393442		ESTs	5.06	8.0
	427836	AA416642	Hs.116176	ESTs	4.79	8.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11	7.9
	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26	7.6
55	434150	BE047007	Hs.116116	testis specific, 10	4.85	7.6
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.29	7.5
	422116	H64205	Hs.111850	mitochondrial capsule selenoprotein	9.12	7.5
	433724	AI827749	Hs.144924	serine/threonine protein kinase SSTK	22.24	7.4
	410187	AA860341	Hs.104680	ESTs	3.03	7.4
60	419584	AF053356	Hs.283764	F-box only protein 24	6.43	7.4
	458182	AI147996	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90	7.3
	418665	T19204	Hs.195685	ESTs	7.14	7.3
	426646	AA382787	Hs.122713	ESTs	7.03	7.3
	420349	NM_016611	Hs.97174	potassium inwardly-rectifying channel, s	14.90	7.3
65	428624	AI125222	Hs.98712	hypothetical protein DKFPz434H0311	3.71	7.1
	420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78	7.1
	434317	AI674095		ESTs	3.98	7.1
	443432	AI056863	Hs.339871	ESTs	3.46	7.0
	425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21	7.0
70	426670	AA383047	Hs.310210	ESTs	6.92	7.0
	408613	AW242086	Hs.253967	ESTs	5.77	6.8
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23	6.7
	434133	AI655275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46	6.7
	427294	AA412594	Hs.125902	ESTs	3.44	6.7
	427262	AA448509	Hs.128652	ESTs	5.66	6.5
75	429551	AA459835	Hs.120573	hypothetical protein DKFPz434K1172	9.01	6.5
	406378			NM_021247*:Homo sapiens protamine 3 (PRM	3.96	6.4
	425865	AA393491	Hs.183740	ESTs	9.15	6.4
	428665	NM_017481	Hs.189184	ubiquitin 3	11.07	6.4
	439379	AA835002	Hs.125611	ESTs	5.06	6.3
80	427520	BE467881	Hs.97489	ESTs, Weakly similar to B28096 line-1 pr	9.29	6.2
	458940	BE149824	Hs.132888	KIAA1674	3.11	6.2
	426620	AW450252		ESTs	12.27	6.2
	429516	AI653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15	6.1

	426736	AA431615	Hs.130722	ESTs	3.58	6.1
	427843	AC005622	Hs.180943	hypothetical protein R30953_1	6.34	6.1
	426639	AI799059	Hs.112807	ESTs	6.93	6.0
5	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
	433795	AI216683	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
	441232	AI656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
	426955	AA393669	Hs.238094	ESTs	4.75	5.8
10	428918	AL036967	Hs.2324	protamine 2	38.40	5.8
	427851	AA846543	Hs.98257	ESTs	15.87	5.8
	428208	AA442327	Hs.104854	ESTs	6.34	5.7
	422207	AI828862	Hs.10964	ESTs	6.43	5.7
	431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
15	419350	AC005328		Homo sapiens chromosome 19, cosmid R2666	14.94	5.6
	427107	AA889586	Hs.180346	ESTs	6.25	5.6
	429461	AI188219	Hs.99311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
	432512	NM_003284	Hs.3017	transition protein 1 (during histone to	22.03	5.6
	434451	AW445179	Hs.121438	ESTs	7.89	5.5
20	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1126 (f	11.26	5.5
	427214	AA442240	Hs.178213	ESTs	8.41	5.5
	458658	AI301117	Hs.122055	ESTs	4.35	5.5
	457034	AA398061	Hs.296587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
	423120	AW160551	Hs.124021	soggy-1 gene	8.88	5.4
25	438983	AF085884	Hs.20029	proacrosin binding protein sp32 precursor	22.69	5.4
	426619	AI357194	Hs.119284	ESTs	7.07	5.4
	440822	AI554897		Homo sapiens clone 191B7 placenta expres	3.60	5.4
	416205	AA176396	Hs.169624	ESTs	10.26	5.4
	426712	AW173177	Hs.197755	hypothetical protein MGC5356	8.17	5.3
30	427840	AI216654	Hs.98251	ESTs	6.44	5.3
	439314	AA382413	Hs.178144	ESTs	8.35	5.3
	426943	BE551631	Hs.20969	ESTs	6.31	5.2
	409209	AA460160	Hs.73217	ESTs	7.85	5.2
	441710	AI187883	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
35	420571	AA442366	Hs.98962	Human DNA sequence from clone RP1-39G22	9.39	5.1
	428563	AA431616	Hs.98660	ESTs	14.94	5.1
	433994	AL042483	Hs.335499	ESTs	6.84	5.0
	441856	AI674774	Hs.128014	ESTs	3.74	5.0
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
40	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
	430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHUH ferti	10.66	4.9
	421850	AW274576	Hs.121021	ESTs	12.27	4.9
	449436	AA860329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
	426699	AA383337	Hs.121269	ESTs	5.67	4.9
45	426627	AF012359	Hs.195685	ESTs	20.66	4.9
	427285	AA401664	Hs.97784	ESTs	4.72	4.8
	423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
	457019	AA421844	Hs.12830	hypothetical protein	3.87	4.8
	405264			NM_030813*:Homo sapiens suppressor of po	4.48	4.8
50	450606	AI668605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
	421378	L77564	Hs.103978	serine/threonine kinase 22B (spermiogene	7.35	4.8
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
	427423	BE267041	Hs.177926	exonuclease NEF-sp	19.27	4.7
	438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
55	424197	AF095834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
	423284	AC005784	Hs.126496	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
	432117	AL036195	Hs.2909	protamine 1	55.33	4.7
	424426	AI476416	Hs.132888	KIAA1674	5.41	4.6
	437387	AI198874	Hs.28847	AD026 protein	5.04	4.6
60	420718	NM_002301	Hs.99881	lactate dehydrogenase C	9.18	4.6
	420768	AI468780	Hs.292503	ESTs, Weakly similar to T47142 hypotheti	5.70	4.6
	423677	M86808	Hs.131361	pyruvate dehydrogenase (lipoamide) alpha	10.93	4.5
	436661	AI125270	Hs.128069	ESTs, Weakly similar to T19142 hypotheti	3.82	4.5
	427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
65	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
	427877	AW138725	Hs.178057	ESTs	4.09	4.5
	426623	AA382826	Hs.132793	ESTs	26.62	4.5
	429965	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.88	4.4
70	417592	AA204664	Hs.182437	ESTs, Weakly similar to 154383 chromosom	3.46	4.4
	421938	AA405951		gb:zu66c01.r1 Soares_testis_NHT Homo sap	4.69	4.4
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
	426710	BE041517	Hs.143893	ESTs	5.57	4.4
	428710	AI890919	Hs.126780	ESTs, Weakly similar to T12519 hypotheti	11.86	4.4
75	438641	AW138484	Hs.190653	ESTs	6.19	4.4
	420614	AL110291	Hs.99364	putative transmembrane protein	6.86	4.4
	422705	NM_006686	Hs.119287	actin-like 7B	9.73	4.4
	421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610712, mRNA,	6.77	4.3
80	426738	AA421097	Hs.291902	ESTs	3.49	4.3
	440403	AW665135	Hs.130531	ESTs	6.97	4.3
	456085	AI184560	Hs.130352	ESTs, Weakly similar to A47582 B-cell gr	6.30	4.3
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
	428909	AI190714	Hs.98945	ESTs	7.79	4.3

	426735	T78716	Hs.120446	ESTs	5.10	4.3
	438653	AW188099	Hs.131813	ESTs	5.29	4.3
	443038	AI958058	Hs.209206	ESTs, Weakly similar to S38782 actin bel	7.29	4.2
5	428677	AI657119	Hs.120036	tropoin I, cardiac	10.73	4.2
	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.169222	acrosomal vesicle protein 1	4.87	4.2
	428871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTT5 protein	7.29	4.2
10	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401692			C16000122:gi5689527[dbj]BAA83047.1] (A	6.37	4.1
	403783			NM_031956:Homo sapiens NYD-SP14 protein	3.74	4.0
15	421611	AA459841	Hs.97309	ESTs	11.51	4.0
	404271			ENSP00000244792:Phosphoglycerate kinase	4.02	4.0
	441800	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RP5-660F19	4.84	4.0
20	420419	AA397796	Hs.11614	HSPC065 protein	4.07	3.9
	435897	AF269223	Hs.128322	I-complex 11 (a murine top homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400590	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRTD-NY3	10.07	3.9
25	452579	AA131657	Hs.23830	ESTs	5.24	3.9
	441443	BE465999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRIN protein	3.82	3.9
	435484	AA682756	Hs.88051	ESTs	5.10	3.9
30	425555	AA359291	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.61	3.8
	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
35	436643	AA757626	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYCI	7.69	3.8
40	437982	N93466	Hs.121764	ESTs, Weakly similar to testicular tekli	3.46	3.7
	442589	BE409869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262951	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
	440487	AI203685	Hs.135763	ESTs	5.90	3.7
45	419455	AW172570	Hs.14600	ESTs	4.23	3.7
	435588	AA759233		ESTs	5.04	3.7
	421610	AA393168	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434I099	5.17	3.6
50	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CO-	3.17	3.6
	438064	AI476330	Hs.234934	ESTs	3.56	3.6
55	426658	AA397912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
	431986	AA536130		Novel human gene mapping to chromosome 20	6.13	3.6
	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-261G23	4.04	3.6
	437896	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fis, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cyclin, basic protein of sperm head cyt	5.13	3.5
60	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
	437399	AI808626	Hs.121188	ESTs, Weakly similar to T29922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.135283	ESTs	4.47	3.5
65	423329	AF054910	Hs.127111	teklin 2 (testicular)	4.40	3.5
	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005261	Hs.98338	serine/threonine kinase 13 (aurora/IPL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-I	10.39	3.4
70	420482	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
	426988	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW628609	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
75	422782	AL133054	Hs.120369	hypothetical protein DKFZp434H2215	4.72	3.4
	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	rel finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	cofilin	6.30	3.4
	435587	AF215924	Hs.97899	putative allantoicase	3.48	3.3
80	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
	427541	AI788983	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotropin-regulated testicular RNA ha	10.76	3.3

5	412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypothel	5.27	3.3
	441579	AW468847	Hs.127194	ESTs	7.13	3.3
	420619	AF130255	Hs.99430	testis zinc finger protein	5.19	3.3
	425368	AB014595	Hs.155976	cullin 4B	3.07	3.3
	425638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
10	429938	BE296804	Hs.226377	phosphate cytidyltransferase 2, ethano	3.03	3.3
	453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
	424466	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
	442084	H81173	Hs.34596	ESTs	4.78	3.3
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
15	434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
	428093	AW594506	Hs.104830	ESTs	6.95	3.3
	433982	AA724720	Hs.112941	ESTs	5.11	3.2
	429821	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
	408415	AW418788		ESTs, Weakly similar to S43569 R01H10.6	3.49	3.2
20	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
	402857			Target Exon	3.19	3.2
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
	427748	AA421041		ESTs	4.57	3.2
25	422794	AJ011733	Hs.120857	synaptogyrin 4	4.23	3.2
	417488	AL046052	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
	440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
	437143	AW204056	Hs.8917	ESTs	4.16	3.2
	417473	M55268	Hs.82201	casein kinase 2, alpha prime polypeptide	4.02	3.2
30	426594	AA884317	Hs.97130	ESTs	3.45	3.2
	426733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
	440864	AI382142	Hs.132104	ESTs	8.48	3.2
	427141	AW628007	Hs.97643	testis-specific protein TSP-NY	5.60	3.2
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
35	438570	AI275803	Hs.123428	ESTs	4.08	3.2
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fis, clone L	4.26	3.2
	452251	R37132	Hs.65009	ESTs	4.01	3.1
	444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
	428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
40	421621	AL045589	Hs.180197	ESTs	7.09	3.1
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
	457138	AW140059	Hs.98579	ESTs	13.17	3.1
	428524	AA429772		ESTs	4.40	3.1
	428726	AA432195	Hs.98694	ESTs	6.47	3.1
45	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fis, clone TH	4.07	3.1
	428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
	424450	AL137526	Hs.147472	dynein intermediate chain 2	6.01	3.1
	433963	AI218808	Hs.187778	ESTs	5.68	3.1
50	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
	440933	AI208217		ESTs	3.44	3.1
	441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
	423313	NM_014269	Hs.126838	a disintegrin and metalloproteinase doma	6.36	3.1
	428630	AA431270	Hs.140646	ESTs	3.59	3.1
55	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R.2	5.63	3.0
	434720	AI208541	Hs.189160	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
	436328	AI201145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
	429293	AI767879	Hs.99214	ESTs	5.69	3.0
	427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
60	440713	AA904448	Hs.126368	ESTs	6.28	3.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
	423218	NM_015896	Hs.167380	BLu protein	6.68	3.0
	444644	AW070634	Hs.144794	ESTs	5.00	3.0
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
65	427829	AI188225		ESTs	7.36	3.0
	426879	AI969340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
	427362	AA625582	Hs.97752	EST	4.38	3.0
	441973	T60072	Hs.10688	ESTs, Weakly similar to RHIFB2157 [H.s	4.06	2.9
	428989	AF104260	Hs.194712	p1w1 (Drosophila)-like 1	4.45	2.9
70	438735	M76676		ESTs	3.81	2.9
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
	427586	AA609661	Hs.190592	ESTs, Moderately similar to WASP-family	6.26	2.9
	427306	AI476743	Hs.229275	ESTs	3.00	2.9
	418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
75	456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.60	2.9
	433836	AA610065	Hs.179646	ESTs	3.33	2.9
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	3.22	2.9
	437426	AW136558	Hs.125246	ESTs	4.49	2.9
80	405528			C2002647:gi4507721 ref NP_003310.1 tit	6.03	2.9
	442977	AW291731	Hs.144090	ESTs	4.23	2.9
	433330	AW207084	Hs.132816	hypothetical protein MGC14801	13.24	2.8
	424275	AW673173	Hs.144505	DKFZP566F0546 protein	5.60	2.8
	426667	AA770016	Hs.121192	ESTs	3.64	2.8
	410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
	428080	AI198656	Hs.98330	ESTs	4.09	2.8
	427252	AA400069	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

	458255	AW140126	Hs.132357	ESTs	3.23	2.8
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
	440582	AA593337	Hs.129082	ESTs	5.29	2.8
5	435566	AI457958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
	433771	AI028794	Hs.112684	ESTs	3.36	2.8
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.30	2.8
	426703	AI221893	Hs.121549	ESTs	3.93	2.8
	430251	AA609246	Hs.181451	ESTs	4.04	2.8
10	427184	AI969361	Hs.180471	ESTs	6.78	2.8
	439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
	448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 testi	3.34	2.7
	450340	AA442322	Hs.60288	ESTs	5.39	2.7
	428100	AW665592	Hs.190413	ESTs	5.32	2.7
15	449333	AI203021		ESTs	4.35	2.7
	429861	AI989571	Hs.99510	ESTs	3.28	2.7
	426622	AL044400	Hs.25371	ESTs, Weakly similar to A37232 mucin, tr	5.38	2.7
	427256	AL042436	Hs.97723	ESTs	4.08	2.7
	408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
20	403328			Target Exon	4.26	2.7
	436264	AA707457	Hs.120014	ESTs	3.58	2.7
	427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci	3.68	2.7
	426640	AI200961	Hs.98104	ESTs	4.60	2.7
	428789	AW296167	Hs.91930	ESTs	4.23	2.7
25	435274	AA887547	Hs.150905	ESTs	4.25	2.7
	426612	AA922067	Hs.184185	ESTs	7.17	2.7
	435110	N42688	Hs.81001	F-box only protein 25	4.85	2.7
	433792	AA778661		ESTs	4.06	2.7
30	423278	AL117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
	427284	AA400298	Hs.144696	ESTs	5.81	2.6
	423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.36	2.6
	422362	Z46967	Hs.115460	calcin	4.72	2.6
	439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
	409364	AI480252	Hs.137368	ESTs	7.22	2.6
35	419224	NM_012189	Hs.314452	fibrousheathin II	13.86	2.6
	428915	AI041278	Hs.87908	Snf2-related CBP activator protein	4.73	2.6
	427181	AI183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
	442122	AI932330		ESTs	3.07	2.6
	424812	AF069252	Hs.153299	DOM-3 (C. elegans) homolog Z	3.80	2.6
40	430956	AI183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
	427234	AA399667	Hs.104675	ESTs	3.43	2.6
	423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
	428214	AA936282	Hs.120397	ESTs	4.14	2.6
	452613	AA461599	Hs.23459	ESTs	7.78	2.6
45	410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
	452537	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
	401712			Target Exon	4.51	2.6
	429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
50	438124	AA778610	Hs.122045	ESTs	3.43	2.6
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
	410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
	428625	W87565	Hs.18566	ESTs	5.29	2.6
	433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.5
	433760	AW592321		ESTs	3.26	2.5
55	431219	AI190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
	453468	W00712	Hs.32590	DKFZP566F084 protein	3.56	2.5
	445158	AI992108	Hs.127206	ESTs	3.60	2.5
	440860	R10482	Hs.132876	ESTs	4.26	2.5
60	452420	BE564871	Hs.29463	centrin, EF-hand protein, 3 (CDC31 yeast	3.95	2.5
	433281	N48673	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
	429369	AI269514	Hs.129802	ESTs	3.49	2.5
	433949	AI674766	Hs.112877	ESTs	5.15	2.5
	427668	AA298760	Hs.180191	hypothetical protein FLJ14904	10.46	2.5
65	414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypotheti	3.87	2.5
	408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	6.10	2.4
	412869	AA290712	Hs.82407	CXC chemokine ligand 16	5.64	2.4
	426956	AA393673		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
	429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
70	426247	U92992	Hs.98834	ESTs	5.40	2.4
	427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
	453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
	413372	H55532		tubulin, alpha 2	9.32	2.4
75	411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
	453868	NM_014433	Hs.35984	rhabdoid tumor deletion region protein 1	3.05	2.4
	427098	AA398161	Hs.97602	ESTs	3.21	2.4
	427165	AA429709	Hs.99336	ESTs, Weakly similar to T15446 hypotheti	4.27	2.4
	425808	AA364109	Hs.177990	ESTs	7.80	2.4
80	444790	AB030506	Hs.11955	B9 protein	3.32	2.4
	426718	AA383555	Hs.126413	ESTs	4.20	2.4
	411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
	450852	AI983354	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
	427054	AA421240	Hs.97570	ESTs	3.10	2.3

	438633	AI653327	Hs.123501	ESTs	3.46	2.3
	427199	AW015836	Hs.292919	ESTs	4.31	2.3
	440182	AA868919	Hs.250110	ESTs	3.03	2.3
5	435517	AA928626	Hs.130177	ESTs	3.64	2.3
	446309	BE044261	Hs.149774	ESTs	3.52	2.3
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC:17339, mRNA, com	4.23	2.3
	433829	AI190715	Hs.102021	ESTs	6.08	2.3
	429485	AW197086	Hs.99338	ESTs	3.14	2.3
10	423058	AW964568	Hs.111591	ESTs	3.36	2.3
	433822	AI218609	Hs.112772	ESTs	3.83	2.3
	442268	BE278064	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
	434298	AA860090	Hs.116290	ESTs	3.71	2.3
	440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
	427554	AW246578	Hs.179515	hypothetical protein FLJ10058	3.39	2.3
15	414251	AL042306	Hs.97689	VASA protein	11.25	2.3
	430254	AI809520		ESTs	3.27	2.3
	437418	AI478954	Hs.59459	ESTs	3.43	2.2
	437522	AA983844	Hs.121383	ESTs	4.15	2.2
	422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
20	436695	AA725655	Hs.120480	ESTs	5.26	2.2
	422247	U18244	Hs.113602	sokute carrier family 1 (high affinity a	6.78	2.2
	421625	AA405386	Hs.178004	ESTs	3.22	2.2
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
	428174	AA913321	Hs.126778	ESTs	3.09	2.2
25	409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
	444467	AI150368		ESTs	3.81	2.2
	433832	AA918018	Hs.172516	ESTs	6.94	2.2
	440036	AW593295	Hs.210956	ESTs	5.87	2.2
	415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
30	432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
	440882	AI205777	Hs.129538	ESTs	3.83	2.1
	436605	AI187742		ESTs	3.41	2.1
	422990	AF035520	Hs.122764	BRCA1 associated protein	5.66	2.1
	432174	AW590264	Hs.132806	ESTs	3.05	2.1
35	409267	NM_012453	Hs.52515	transducin (beta)-like 2	5.46	2.1
	423021	AL036111	Hs.292767	ESTs	3.87	2.1
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
	433812	AA725026	Hs.97165	ESTs, Weakly similar to T31611 hypotheti	3.62	2.1
	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
40	437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
	426038	AA368101	Hs.99052	ESTs	3.03	2.1
	427065	AA397903	Hs.236635	gb:z189f12.r1 Soares_testis_NHT Homo sap	3.23	2.1
	428824	W23624	Hs.173059	ESTs	3.07	2.1
45	428224	X54017	Hs.183088	acrosin	3.18	2.1
	436954	AA740151	Hs.130425	ESTs	3.20	2.1
	444470	AA412195	Hs.13740	ESTs	4.27	2.1
	457579	AB030816	Hs.36761	HRAS-like suppressor	5.30	2.1
	427886	AA417083	Hs.104789	ESTs	3.49	2.1
	439273	AW139099	Hs.269701	ESTs	3.83	2.1
50	434318	AW207552	Hs.116328	ESTs, Weakly similar to A39564 transcrip	4.01	2.1
	427015	AA397520		ESTs	4.28	2.1
	421598	AW630942	Hs.106061	RD RNA-binding protein	3.30	2.1
	427236	AA399959	Hs.148271	ESTs	3.07	2.1
	434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
55	456051	T85626	Hs.76239	hypothetical protein FLJ20608	3.11	2.0
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
	451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	4.73	2.0
	420484	W32963	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
60	414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
	424558	AF038847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 64B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
70	428618	2668_1	BC017998 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI652853 AI990773 AW665193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515652 H15004 AA909115 BI465310 BI462024 BI561578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272
	426599	10110_1	BE736800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 BI830957 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203663 BE041513 AA382260 AA382261 AI554887 BE273483
75	426930	1310779_1	AI809889 AA393442 AI150574 AI200886 AI221692 AA608977 AA813213
	434317	599587_1	AI209094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW665317 AA629314 AA776691 AA906846 AA974625 AA884357 AI808590
	426620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI636668 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI139837
80	419350	13086_1	AI218809 BC014609 BG724383 AI024359 AA904573 AI138595 AA868685 AI768931 BI828436 BG717350 BG719800 AW182303 AA448181 BI826670 BI827131 BI830254 BI824155 BI831745 T19190 BI830415
	440822	532606_1	BG207562 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA906867 AI873494 AI015039
	421938	863689_1	AA412383 AA300675 BG773248 AA412243 AA405951

44258933097_2

5

4365882470836_1

43198676926_1

42043129290_1

43660110131_1

4084154581_6

10

4277481372622_1

44011534_3

4285241382184_1

440933980517_1

15

4278291373537_1

43873510316_1

44933336378_1

20

4337922204621_1

4421222684549_1

433760584982_1

426956657337_1

41337232896_1

25

43025413102_1

4444671008400_1

4366051008207_1

427015683123_1

45180717758_2

30

35

TABLE 54C

Pkey:Unique number corresponding to an Eos probeset

Ref:Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.

Strand:Indicates DNA strand from which exons were predicted.

NL_position:Indicates nucleotide positions of predicted exons.

45

4019792828778

4064099256364

4017412982169

4063789256142

4052647329374

50

4016923540172

4037838081824

4042719828129

4017986730720

4028579801639

55

4055289581957

4033288469085

4017126682593

60

TABLE 55A:

Pkey:Unique Eos probeset identifier number

ExAccn:Exemplar Accession number, Genbank accession number

UnigeneID:Unigene number

Unigene Title:Unigene gene title

RI:Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues

70

416680AW245540

423961D13666

412948BE243313

428928BE409838

424247X14008

414438AI879277

75

406658AI920965

468999NM_005397

411573AB029000

432730AI066520

418870AF147204

80

444381BE387335

446619AU076643

447526AL048753

418174L20688

416680AW245540

423961D13666

412948BE243313

428928BE409838

424247X14008

414438AI879277

406658AI920965

468999NM_005397

411573AB029000

432730AI066520

418870AF147204

444381BE387335

446619AU076643

447526AL048753

418174L20688

NM_004157 X14968 BG480488 BE409869 BG723898 BG476313 AU121626 BE386516 AI969297 AW172340 AA89668 R23436 AI015037 BE250558 BF590945 AW385993 BF983000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899095 BG827945 BE741233 AI015465 AW370169 BE297350 AA093249

AI122828 AA909991 AA759233

AL591713 BF197609 AI985094 AW448916 AI243277 AL449630 AL449629

AW241405 AW205071 AI671586 AI652354 AI638465 AW590359 AW662771 AW594067 BE502532 AI218894 BE466416 BF056295 AI247366

AI990484 AI917746 AW665925 AI216456 AW182169 AA969884 AA723888 AI018419

BI602176 BI603138 BI459895 BI755030 AW418788 AA883999 AA724858 AI480311 AW196355 AI004813 AI651117 BE814363 AW589856

AA448124 AA447982 BI461166 AA405629

AI208966 AA421041 AA815377 AA411954

BF980396 R51074 BF979883 AI539370 BI2128735 AA993397 AI611039 AW593985 R41808

AI208080 AA442862 AA429772

AI125404 AW593312 AI247364 AI208217 AA910021 AI915307

AI190292 AI188225 AA416673 AA416596 AA952888 AA972172 AA906874

M76676 NM_022571 BG772522 BF516449 AI537485 AW517245 BF762536 AA634446 AW196331 AI203035 BG72281

AK056320 AL522040 BI793043 AW071691 AI433682 AA865414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA482563

N33446 N25222 Z41110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 AI655113

AI309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA364618 AA364851 AA421448 T74231

R52350 AA482415 AI203021 T88948 AI565842

AI024286 AA769898 AA778661 AA868972 AA609524

AI932330 AI190707 AI376782 AA976847

AA609179 AW592321 AA758282 AI214437 AW072537 AA781937

BI831486 AW190479 AI472793 AA460217 AA459937 BF082576 AA393673 AA398702

NM_006001 L11645 AI205604 AI207994 AI187362 AA709190 BI462421 BG772170 BG722772 AA436991 BG771655 BI553260 BF126025

BF125857 BI462670 BG724164 BI562424 BG721652 BI559662 BG722455 BI596415 BG717561 BG722138 BG773507 BG720572 C03867 AI016802

AL042663 AA770436 AA435720 T19365 AA626698 AA759057 AI208021 BF507844 AI208058 AA412719 AA426374 AI208775 AA977217 AA758055

F34585 AA180062

BG700885 AA868017 AW341719 AA971332 AI688794 Z20462 AI808145 AW665263 AA884952 AA906136

AW663704 AI150368 AI216464

AI125340 AI125684 AI377949 AI126470 AI218351 AW665355 AI243952 AW663454 AI240603 AI187742 AA884214 AA723933

AA857437 AI968733 AI968938 AA992784 AA397520 AW235244

BM479185 AL552795 AL577722 BF038888 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522 AA993634

AI827626 AA904788

	406856	AW515335	Hs.29797	ribosomal protein L10	23.66
	414682	AL021154	Hs.76884	Inhibitor of DNA binding 3, dominant neg	23.60
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	23.60
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.35
5	417426	NM_002291	Hs.82124	laminin, beta 1	21.60
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
	439180	AJ393742	Hs.199057	v-erb-b2 avian erythroblastic leukemia v	21.50
	413787	AJ352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
10	408669	A493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
	412636	NM_004415		desmoplakin (DPI, DPII)	20.90
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	20.30
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	19.45
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	19.30
15	406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
	412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
	424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
20	415314	N88802	Hs.5422	glycoprotein M6B	16.80
	408656	M16714	Hs.85643	major histocompatibility complex, class	16.75
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.25
	406820	AJ223958	Hs.108124	ribosomal protein S4, X-linked	16.00
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
25	417088	M54915	Hs.81170	pim-1 oncogene	15.60
	449338	H73444	Hs.394	adrenomedullin	15.51
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
	414420	AA043424	Hs.76095	immediate early response 3	15.30
	425543	R23313	Hs.334895	ribosomal protein L10a	15.10
30	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
	420754	W79431	Hs.346911	ribosomal protein L22	14.92
	410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
35	405786	AW161678	Hs.111334	ferritin, light polypeptide	14.57
	422105	A1929700	Hs.111680	endosulfine alpha	14.57
	422714	AB018335	Hs.119387	KIAA0792 gene product	14.25
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
40	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
	429614	AJ371172	Hs.211539	hypothetical protein MGC4248	13.95
	410185	BE294068	Hs.737	immediate early protein	13.85
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	13.60
	410611	AW954134	Hs.20924	KIAA1628 protein	13.60
45	448588	A1970276	Hs.156905	KIAA1676	13.40
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	13.10
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.00
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
50	454413	A1653672	Hs.40092	PNAS-123	12.90
	415221	W07418	Hs.78225	annexin A1	12.89
	425535	AB007937	Hs.158287	KIAA0468 gene product	12.48
	450000	A1952797	Hs.10888	hypothetical protein FLJ21709	12.45
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
55	414799	A1752416	Hs.77326	insulin-like growth factor binding prote	12.19
	412025	A1827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	12.12
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
	408437	AW957744	Hs.278469	lacrimal protein rich protein	11.80
60	430542	AJ557486	Hs.119122	ribosomal protein L13a	11.51
	424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
	432409	AA806538	Hs.130732	KIAA1575 protein	11.50
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	11.44
	425996	W67330		hypothetical protein AL110115	11.40
65	449961	AW265634	Hs.133100	ESTs	11.40
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	11.25
	407179	AA206465		thymosin, beta 4, X chromosome	11.21
	412623	R28898	Hs.74170	metallothionein 1E (functional)	11.10
	429978	AA249027		ribosomal protein S6	11.10
70	450377	AB033091		KIAA1265 protein	11.10
	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	11.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
	451106	BE382701	Hs.25960	N-MYC oncogene	10.93
75	426552	BE297660	Hs.170328	moesin	10.91
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhotekin, clone	10.75
80	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
	435056	AW023337	Hs.5422	glycoprotein M6B	10.70
	406743	AA911568	Hs.279860	tumor protein, transcriptionally-controlle	10.70
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
	420676	AI434780	Hs.4248	vav 2 oncogene	10.60

	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
	436075	BE090176	Hs.179902	transporter-like protein	10.30
5	450139	AK001838		serum/glucocorticoid regulated kinase	10.30
	427691	AW194426	Hs.20726	ESTs	10.26
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	10.15
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
	440528	BE313555	Hs.7252	KIAA1224 protein	10.06
10	423184	NM_004428	Hs.1624	ephrin-A1	10.05
	450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
	417407	AA923278	Hs.290905	ESTs, Weakly similar to proleasin [H.sapi	9.90
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	9.90
	421395	D90084	Hs.1023	pyruvate dehydrogenase (lipoamide) alpha	9.89
15	435918	AF263538	Hs.86232	growth differentiation factor 3	9.89
	411251	R19774	Hs.22835	HHGP protein	9.80
	406791	AI220684	Hs.347939	hemoglobin, alpha 2	9.75
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
	425580	L11144	Hs.1907	galanin	9.60
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
	413813	M96956	Hs.75561	larotocarcinoma-derived growth factor 1	9.60
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.60
	417944	AU077196	Hs.82985	collagen, type V, alpha 2	9.53
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
25	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila))-like	9.42
	416926	H03109	Hs.263395	HT018 protein	9.41
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
	428065	AI634046	Hs.157313	ESTs	9.40
	441455	AJ271671	Hs.7854	zinc/ferron regulated transporter-like	9.39
30	410325	AB023154	Hs.62264	KIAA0937 protein	9.30
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	9.24
	447211	AL161961	Hs.17767	KIAA1554 protein	9.22
35	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	8.93
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	8.90
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
40	449335	AW150717	Hs.345728	STAT induced STAT inhibitor 3	8.84
	413886	AW958264	Hs.103832	similar to yeast Upt3, variant B	8.80
	447471	AF039843	Hs.18676	spouty (Drosophila) homolog 2	8.70
	426215	AW963419	Hs.155223	stanniocalcin 2	8.70
	446627	AI973016	Hs.15725	hypothetical protein SBB148	8.60
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	8.50
	445245	AB032973	Hs.12461	LCHN protein	8.50
	448776	BE302464	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
50	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
	410143	AA188169		KIAA1191 protein	8.35
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
	433208	AW002834	Hs.24095	ESTs	8.30
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.25
55	432559	AW452948	Hs.257631	ESTs	8.20
	450581	AF081513	Hs.25195	TGF-beta 4	8.10
	450157	AW961576	Hs.60178	ESTs	8.10
	444795	AI193356	Hs.160316	ESTs	8.10
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	8.05
60	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
	419970	AW612022		ESTs	8.00
	411975	AI916058	Hs.144583	ESTs	7.95
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
65	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	437103	AW139408	Hs.152940	ESTs	7.90
	432636	AA340864	Hs.278562	claudin 7	7.87
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
	419682	H13139	Hs.92282	patred-like homeodomain transcription fa	7.80
70	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	7.80
	450147	AW373713	Hs.146324	CGI-145 protein	7.75
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
	449571	AW016812	Hs.200266	ESTs	7.70
	429355	AW973253	Hs.292689	ESTs	7.70
75	446488	AB037782	Hs.15119	KIAA1361 protein	7.70
	414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
	422424	AI186431	Hs.296638	prostate differentiation factor	7.67
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
80	451812	X81889	Hs.152151	plakophilin 4	7.65
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
	422746	NM_004484	Hs.119651	glypican 3	7.60
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	7.57

5	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426589	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	7.50
10	419223	X60111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	7.40
	413686	AI469213	Hs.71404	ESTs	7.40
15	408505	AF025374	Hs.46465	T-cell, Immune regulator 1	7.40
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp66780711 (f	7.30
	444838	AV651680	Hs.208558	ESTs	7.30
	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
20	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87135	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
25	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	7.00
	449567	AI990790	Hs.188614	ESTs	7.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	7.00
30	450506	NM_004460	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464964		gb:zx80f10.s1 Soares ovary tumor NbHOT H	7.00
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
	442492	AA528489	Hs.234518	ribosomal protein L23	6.84
35	417365	D50583	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	6.80
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
	435684	NM_001290	Hs.4980	LIM domain binding 2	6.80
	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
40	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adilcan	6.76
	441565	AW953575	Hs.303125	p53-Induced protein PIGPC1	6.75
	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3577185, mRNA	6.74
	444207	AI565004		cathepsin D (lysosomal aspartyl protease	6.72
45	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	6.70
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	6.70
	429469	MG4590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.70
	430332	R51790	Hs.239483	Human clone Z3933 mRNA sequence	6.70
50	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	6.65
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
	406858	AI865720	Hs.29797	ribosomal protein L10	6.65
	435748	AA699756	Hs.117335	ESTs	6.63
55	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	6.62
	424415	NM_001975	Hs.146590	enolase 2, (gamma, neuronal)	6.61
	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	6.60
	442379	NM_004613	Hs.8265	transglutaminase 2 (C polypeptide, prote	6.55
60	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	H42587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	6.43
	402145			Target Exon	6.43
65	414682	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436860	H12751	Hs.5327	PRO1914 protein	6.40
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	6.40
	435937	AA830893	Hs.119769	ESTs	6.40
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
70	446173	BE565849	Hs.14158	copine III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242691	Hs.14947	ESTs	6.34
	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
75	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445917	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
	434423	NM_006769	Hs.3844	LIM domain only 4	6.30
	434524	AA635931	Hs.249716	ESTs	6.30
80	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	6.25
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
	407284	AI539227	Hs.214039	hypothetical protein FLJ23556	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	AI080042	Hs.180450	ribosomal protein S24	6.20

	418840	AI821614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159651	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
5	413840	AJ301558		RNA binding motif protein, X chromosome	6.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
10	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	6.10
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	6.10
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
15	432805	X94630	Hs.3107	CD97 antigen	6.06
	441283	AA927670	Hs.131704	ESTs	6.06
	417632	R20855	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0456 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
20	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo sapien	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
25	447217	BE465754	Hs.17778	neuropilin 2	5.90
	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGCA248	5.84
	427747	AW411425	Hs.180655	serine/threonine kinase 12	5.84
30	414483	R25513	Hs.10583	ESTs	5.82
	428570	AA430321	Hs.293945	ESTs	5.81
	443194	AI954968		matrix Gla protein	5.80
	429582	AI569068	Hs.22247	ESTs	5.80
	414405	AI362533		KIAA0306 protein	5.80
35	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 [H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
40	406745	AW511970	Hs.279860	tumor protein, translationally-controlled	5.70
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.68
45	444273	AI903474	Hs.230	fibromodulin	5.65
	441623	AA315805		desmoglein 2	5.63
	418300	AI433074	Hs.85682	Homo sapiens cDNA: FLJ21578 fis, clone C	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	5.60
50	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associated	5.60
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE409248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
	406699	L05605	Hs.182979	ribosomal protein L12	5.53
55	458965	AA010319	Hs.60389	ESTs	5.50
	430592	AJ224864	Hs.9688	leukocyte membrane antigen (IRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratlin	5.42
60	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
	417849	AW291587	Hs.82733	nidogen 2	5.40
	408989	AW361666	Hs.49500	KIAA0746 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
65	406819	AA908472		gb:gb82a10.s1 NCI_CGAP_Ov8 Homo sapiens	5.39
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.36
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AI857607	Hs.181301	cathepsin S	5.32
70	429307	AI076592	Hs.198951	jun B proto-oncogene	5.30
	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AI754813	Hs.146428	collagen, type V, alpha 1	5.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
75	411165	NM_000169	Hs.69089	galactosidase, alpha	5.26
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435631	BE254086	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539674		actinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
80	440703	AL137663	Hs.7378	Homo sapiens mRNA: cDNA DKFZp434G227 (tr	5.20
	403014	AA369601	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430556	AW967807	Hs.13797	ESTs	5.16
5	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.15
	454227	AW963897	Hs.44743	KIAA1435 protein	5.15
	429367	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
10	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
	442295	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23516	5.10
	421878	AA299552	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AI187945	Hs.199310	ESTs	5.10
	427641	AI270591	Hs.146116	ESTs	5.10
15	442806	AW294522	Hs.149991	ESTs	5.10
	442495	AI184717		ESTs	5.10
	439941	AI392640	Hs.18272	amino acid transporter system A1	5.10
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.09
20	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.07
	418117	AI922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE resequences, MAGL Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.06
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.03
	431805	NM_014053	Hs.270594	FLVCR protein	5.00
25	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA233439	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443634	H73972	Hs.134460	ESTs	5.00
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	5.00
30	444621	AA298085	Hs.11465	glutathione-S-transferase like; glutathi	4.97
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.95
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.94
	452063	R53185	Hs.32366	ESTs, Weakly similar to TWIST_HUMAN TWIST	4.93
35	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.93
	429558	AI391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	4.92
	433162	AI025842		ESTs	4.92
	406797	AA432224		ribosomal protein L6	4.91
40	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:rh88b01.s1 Soares placenta Nb2HP Homo	4.90
	447832	AI433357		ESTs	4.90
45	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
	413593	AA205248		gb:zq78c12.r1 Stratagene hNT neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypol	4.90
	441224	AU076964	Hs.7753	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
50	417308	H60720	Hs.81892	KIAA0101 gene product	4.90
	438763	AI583207	Hs.99029	CCAAT/enhancer binding protein (C/EBP),	4.89
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	4.89
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (elfin)	4.88
	421748	NM_014718	Hs.107809	KIAA0726 gene product	4.87
55	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.86
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.82
	406867	AA157857	Hs.182265	keratin 19	4.81
	449378	AW664026	Hs.59892	ESTs	4.81
60	427202	BE272922	Hs.173936	Interleukin 10 receptor, beta	4.80
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.80
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.79
	441321	H17182	Hs.7771	B-cell associated protein	4.75
65	448896	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	4.75
	447232	AW499834	Hs.327	Interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.73
	436372	AW972301	Hs.310286	ESTs	4.71
70	422082	AA016188	Hs.111244	hypothetical protein	4.70
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	4.70
	446659	AI335361	Hs.226376	ESTs	4.70
	414829	AA321568	Hs.77436	pleckstrin	4.70
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
75	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.70
	432407	AA221036	Hs.13273	gb:zr03f12.r1 Stratagene NT2 neuronal pr	4.69
	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
80	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.67
	406794	AI890243		ribosomal protein L6	4.66
	449475	AI348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
5	417535	AA203569	Hs.191482	ESTs	4.61
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	4.61
	408491	AI088063	Hs.7882	ESTs	4.60
	428398	AI249368	Hs.98558	ESTs	4.60
	410295	AA741357		nidogen (enactin)	4.60
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.60
10	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (I	4.60
	426141	CD5886	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
15	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108288	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
20	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	4.53
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
25	440774	AI420611	Hs.153934	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	AI638640	Hs.220624	ESTs	4.51
30	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	4.50
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothi	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
35	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myc-responsive	4.47
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.47
	408307	AI761786	Hs.204674	ESTs	4.46
40	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.46
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.45
	406870	AA075144		gb:zm86f06.s1 Stralagene ovarian cancer	4.45
	446291	BE397753	Hs.14523	interferon, gamma-inducible protein 30	4.44
45	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	4.44
	428773	BE256238	Hs.193163	bridging integrator 1	4.43
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.86154	hypothetical protein FLJ12457	4.43
50	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424868	AI568170	Hs.96886	ESTs	4.41
	408380	AF123050	Hs.44532	diubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
55	428782	X12830	Hs.193400	interleukin 6 receptor	4.40
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW891965		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
60	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypothi	4.39
	414219	W20010	Hs.75823	ALL-1-fused gene from chromosome 1q	4.39
	427779	AA906997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75260	mitogen inducible 2	4.36
	452651	AI218918	Hs.30209	KIAA0854 protein	4.35
65	453467	AI535997	Hs.30089	ESTs	4.35
	435961	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963979	Hs.24723	ESTs	4.34
	435968	AW161481	Hs.111577	integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
70	421522	R48881	Hs.102991	hypothetical protein FLJ13956	4.33
	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
75	437275	AW976035	Hs.292396	ESTs, Weakly similar to A47582 B-cell gr	4.30
	408784	AW971350	Hs.63386	ESTs	4.30
	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
80	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	408896	AI610447	Hs.48778	ribon protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

	406230		Target Exon	4.25	
	435655	AW105663	Hs.6947	HSPC069 protein	4.25
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
5	437386	W52452		ribosomal protein L10	4.24
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	4.23
	447341	AF106941	Hs.18142	arrestin, beta 2	4.22
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	4.22
	409453	AI885516	Hs.95612	ESTs	4.22
10	428453	AB011110	Hs.184367	GTPase activating protein-like	4.22
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.21
	416072	AL110370	Hs.79000	growth associated protein 43	4.20
	450937	R49131	Hs.26267	ATP-dependant interferon response proteai	4.20
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.20
15	418452	BE379749	Hs.85201	C-type (calcium dependent, carbohydrata-	4.20
	430594	AK000790	Hs.246885	hypothetical protein FLJ20783	4.20
	425259	AL049280	Hs.155397	Homo sapiens mRNA: cDNA DKFZp564K143 (fr	4.20
	431560	BE244135	Hs.260238	hypothetical protein FLJ10842	4.20
	439403	BE265745		ESTs, Weakly similar to ALUC_HUMAN !!!!!	4.20
20	409245	AA361037		IRNA isopentenylpyrophosphate transferas	4.18
	437296	AA350994	Hs.20281	KIAA1700	4.17
	406877	AA226392	Hs.179943	ribosomal protein L11	4.17
	419652	AL157485	Hs.91973	hypothetical protein	4.15
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.15
25	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	4.14
	448782	AL050295		KIAA0758 protein	4.14
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	4.14
	422960	AW890487		cadherin 13, H-cadherin (heart)	4.13
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	4.12
30	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	4.11
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.11
	419726	U50330	Hs.1274	bone morphogenetic protein 1	4.11
	426075	AW513691	Hs.270149	ESTs, Weakly similar to 2109260A B cell	4.10
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.10
35	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S	4.10
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	4.10
	457415	AK000010	Hs.258798	hypothetical protein FLJ20003	4.10
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	4.10
	427509	M62505	Hs.2161	complement component 5 receptor 1 (C5a I	4.10
40	444633	AF111713	Hs.286218	junctional adhesion molecule 1	4.10
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	4.09
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	4.09
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.08
	439815	AA206079	Hs.6693	hypothetical protein FLJ20420	4.07
45	417930	H81136	Hs.334604	Homo sapiens mRNA for KIAA1870 protein,	4.06
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.06
	424464	R68537	Hs.17962	ESTs	4.06
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.06
	412627	BE391959	Hs.74276	chloride Intracellular channel 1	4.06
50	414890	BE281095	Hs.77573	uridine phosphorylase	4.05
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.05
	450887	AA011518	Hs.271778	ESTs, Weakly similar to t38022 hypotheri	4.05
	444224	AV648599	Hs.199438	ESTs	4.05
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
55	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	4.04
	439864	AF720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.04
	408745	AW936356	Hs.300925	ESTs, Weakly similar to A46010 X-linked	4.03
	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.01
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.01
60	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	4.01
	426398	BE256390	Hs.169718	calponin 2	4.01
	417777	AI823763	Hs.7055	ESTs, Weakly similar to I78885 serine/th	4.01
	446879	AI654443	Hs.197683	ESTs	4.00
	416000	RB2342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	4.00
65	426647	AA243454	Hs.294101	pre-B-cell leukemia transcription factor	4.00
	436394	AA531187	Hs.126705	ESTs	4.00
	409956	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a	4.00
	414602	AW630088	Hs.76550	Homo sapiens mRNA: cDNA DKFZp564B1264 (f	4.00
	446013	AI360167	Hs.152774	ESTs	4.00
	452404	AW450675	Hs.212709	ESTs	4.00
70	444736	AA533491	Hs.23317	hypothetical protein FLJ14681	4.00
	438590	AA811465	Hs.123375	ESTs	4.00
	451838	AW005866	Hs.193969	ESTs	4.00
	449832	AA694264	Hs.60049	ESTs	4.00

TABLE 55B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
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413787	7612_1	BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 A1082748 A1470204 B1711078 BF350700 B1496963 A1087141 AA720684 AA862331 AA605146 BM313650 A1089749 A1359738 N69107 AW995424 A1086917 A1083995 AW340217 N99662 A1829449 A1089839 A1608761 A1342365 A1199076 AA908944 A1248943 A1160053 A1191245 A1218477 A1077943 AA864930 A1310394 AA872478 A1279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG055114 A1469689 BE464590 AW664539 H67097 AL534332 C21397 A1085941 AW028427 BG939820 A1897089 A1039008 A1125315 A1655561 AW150042 L20422 X57345 B1458375 A1142852 B1666601 BE888276 A1119302 B1603754 BG705953 B1598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127798 A124697 D54224 F08031 AA340253 BF923383 BM467808 B1546644 BG777200 BG705941 BG468577 A1272209 AW403970 B1597630 B1458091 AV689560 B1689267 BG506219 B1837163 B1667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 B1869271 BF998207 N31547 BF945817 BF947918 N90630 BG980194 AA156681 B1493502 AW273118 A1473820 AA608688 A1539337 AV712091 AA084101 BF592036 H13301 A1864305 AA505883 A1423963 AW084401 A1917740 R69858 AA033631 N79982 BE885276 A1635674 AA096126 AA700018 AV707753 A1082545 A1145681 AA629032 A1421367 AA740589 AA150830 A1248541 AA988608 AA150478 W65347 BM310234 AA262704 T28031 A1811116 BM272753 H21979 T15405 AA938406 F04963 A1188296 AW152629 AA905196 BG223058 A1831016 A1766457 A1811102 AA776573 A1922133 AA775958 A1261476 AA219489 A1688035 A1872093 BE537084 AW189078 D82630 A1123121 AL583492 BE350791 R69901 W65436 BE155392 B1089081 BE155394 AL120538 AW166100 A1359620 A1174338 N20527 W47413 AA155615 A1272249 H25293 BE614558 H69864 AW383484 H78021 H11617 R56892 H23204 N21530 R82499 AW383522 AA774536 AL534331 W94127 W46459 A1866231 AA513281 AA192465 H69844 W85827 AW383642 AW383529 AA171496 AL537424 BE814866 BF823254 R25253 A1809817 A1559406 M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 B1438324 H27408 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BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA098891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705987 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW365143 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 A1190590 A1554403 A1392926 A1158477 B1467252 A1159919 A1760816 BF082516 A1439101 AA451923 A1340326 A1590975 B1791553 A1700963 A1142882 AA039975 AA946936 AA644381 BM314884 AA702424 A147612 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW165807 A1346078 W95070 A149191 AA026864 A1830049 AW780435 A1078449 A1819984 A1858282 B1468588 A1860584 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 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AW604738 AW385757 AW580796 AW801247 BE003239 BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW866589 AW604758 N44337 AI378548 AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW861938 AW894816 AW580841 AA094372 T06399 AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW851939 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI248811 BE179917 BE002200 AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW601420 AI595314 BE083790 AW858568 AW945550 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW885979 AW794240 AW945566 AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW664582 AW877775 AW838449 BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW389211 AW604286 AW610312 AI904717 AW610318 AW996909 AW610295 AW901923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842089 AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577 AI90628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835656 AW606765 AW606770 AW835678 AW606758 AW606778 AI907484 BE172821 AW606768 AW999517 AW844165 BE171738 AW751683 AW610493 BE177484 BE177487 AA900510 AW844117 BE173357 AW999878 AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA610287 AW176676 AW607622 BE172639 AW893232 AA329629 BE089008 BE178350 BE178214 BE063291 AW820236 AW999553 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999112 BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998972 AA767189 AW044272 H50689 AA768399 AA767764 AI087688 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945 AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI681913 AI759983 N69591 N69276 BE467722 AW392780 BE172457 H92861 AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781 BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990 BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895 AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806066 AI090653 AI129205 AI248410 H72930 AW615341 BF805990 BF805982 AA993819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371 AK056692 AF086220 AI375065 AA284293 W32566 AW797961 AA960897 AA504145 AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45605 AV752798 AV657116 AA296632 AI137857 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830 AW960845 BM466252 AW958813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024 BF093291 AW021929 H22650 AA459715 BG495341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752 BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF373229 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845 AI693426 AI652147 AI435449 N47325 AA434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897 AW665247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245 AA884954 AI125702 AI382934 AA931835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667 AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 D12465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848 H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128 AB018301 AL050295 BF513128 AW385080 AL551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118768 AI453845 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039546 AI002491 AI240412 Z25099 AA995178 AW050649 AW026140 AI796309 AI584012 BE166666 AI767991 AI309041 AA724059 AI695284 AI245095 T63971 Z40627 BE166681 BG570071 BF921915 BI562702 BG506502 AV658066 R48378 AA121543 AI096938 AA618131 AI40993 R48277 AI352281 BG540263 BG538901 N95226 AI356752 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361 N73937 AA127680 AW044037 AI096437 AA384077 BF941499 T93764 BG003285 BF092049 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE070277 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE689260
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TABLE 55C

Pkey:

Ref:

Strand:

Nt_position:

Unique number corresponding to an Eos probeset
Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Indicates DNA strand from which exons were predicted.
Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401466	6682292	Plus	28748-29023
401192	9719502	Minus	69559-70101
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402145	8018280	Plus	113086-114800
406230	4760409	Plus	71716-72515

TABLE 56A:

Pkey:

ExAccn:

UnigenelD:

Unigene Title:

R1:

Unique Eos probeset identifier number
Exemplar Accession number, Genbank accession number
Unigene number
Unigene gene title
Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigenelD	Unigene Title	R1
414438	AI879277	Hs.76136	thioredoxin	47.30

	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
5	417088	M54915	Hs.81170	plm-1 oncogene	31.10
	430542	A1557486	Hs.119122	ribosomal protein L13a	29.60
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	A1223958	Hs.108124	ribosomal protein S4, X-linked	28.13
10	433800	A1034361	Hs.135150	lung type-I cell membrane-associated gly	28.10
	406658	A1920965	Hs.77961	major histocompatibility complex, class	27.85
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
15	429978	AA249027		ribosomal protein S6	25.40
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	AI371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
20	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	24.10
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	24.05
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
25	406856	AW515336	Hs.29797	ribosomal protein L10	22.77
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
	412636	NM_004415		desmoplakin (DPI, DP11)	22.40
	420676	AI434780	Hs.4248	vav 2 oncogene	22.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.40
30	446627	AI973016	Hs.15725	hypothetical protein SBBI48	21.20
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	21.10
	420754	W79431	Hs.346911	ribosomal protein L22	20.98
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.90
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	20.80
35	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.50
	422714	AB018335	Hs.119387	KIAA0792 gene product	19.15
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.00
	413787	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
40	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.50
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.00
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.90
	448588	AI970276	Hs.156905	KIAA1676	17.70
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.50
45	428782	X12830	Hs.193400	interleukin 6 receptor	17.40
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	17.20
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.15
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.10
	440528	BE313555	Hs.7252	KIAA1224 protein	17.06
50	410143	AA188169		KIAA1191 protein	17.05
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.90
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.70
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	16.60
55	449571	AW016812	Hs.200266	ESTs	16.50
	432730	AI068520	Hs.131358	ESTs	16.20
	426295	AW367283		zinc finger protein 6 (CMPX1)	16.15
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.90
60	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	15.80
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.80
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	15.50
	428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	14.90
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	14.90
65	406656	M16714	Hs.89643	major histocompatibility complex, class	14.85
	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.71
	450377	AB033091		KIAA1265 protein	14.70
	425996	W67330		hypothetical protein AL110115	14.60
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	14.60
70	427691	AW194426	Hs.20726	ESTs	14.42
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	14.35
	451106	BE382701	Hs.25960	N-MYC oncogene	14.21
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	14.13
	436860	H12751	Hs.5327	PRO1914 protein	13.90
75	446899	NM_005397	Hs.16426	podocytin-like	13.90
	450000	AI952797	Hs.10688	hypothetical protein FLJ21709	13.75
	408380	AF123050	Hs.44532	diubiquitin	13.70
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.40
	427521	AW973352		ESTs	13.30
80	410598	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	13.25
	428664	AK001666	Hs.189095	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	13.23
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.70
	426552	BE297660	Hs.170328	moesin	12.69

5	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
	436398	H87136	Hs.5174	ribosomal protein S17	12.50
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.30
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	12.30
	410275	U85658	Hs.61795	transcription factor AP-2 gamma (activat	12.28
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	12.25
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
10	419384	AA490866	Hs.39429	ESTs	12.20
	410185	BE294068	Hs.737	immediate early protein	12.15
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	12.05
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
	406743	AA911568	Hs.279860	tumor protein, translationally-controlle	11.90
15	408989	AW361666	Hs.49500	KIAA0746 protein	11.80
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.80
	410325	AB023154	Hs.62264	KIAA0937 protein	11.70
	445817	NM_003542	Hs.13340	histone acetyltransferase 1	11.70
20	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	11.61
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	11.60
	454413	AI653672	Hs.40092	PNAS-123	11.60
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	11.40
	428065	AI634046	Hs.157313	ESTs	11.40
25	432805	X94630	Hs.3107	CD97 antigen	11.36
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	11.30
	409963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	11.11
30	402474			NM_004079:Homo sapiens cathepsin S (CTSS	11.00
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.00
	406786	AW161678	Hs.111334	ferritin, light polypeptide	10.95
	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
	444656	AI277924	Hs.145199	ESTs	10.90
35	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	10.85
	440774	AI420611	Hs.153934	ESTs	10.82
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	10.80
	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
40	418509	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
	437374	AL359571	Hs.44054	ninein (GSK3B interacting protein)	10.65
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
	450719	AI096837	Hs.21349	ESTs, Weakly similar to RB8B_HUMAN RAS-R	10.43
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
45	446682	AW205632	Hs.211198	ESTs	10.40
	447211	AL161961	Hs.17767	KIAA1554 protein	10.31
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
	422105	AI929700	Hs.111680	endosulfine alpha	10.21
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	10.20
50	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
	452651	AI218918	Hs.30209	KIAA0854 protein	10.15
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
	427761	AA412205	Hs.140996	ESTs	10.10
55	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
	402145			Target Exon	9.82
	413686	AI469213	Hs.71404	ESTs	9.80
	446488	AB037782	Hs.15119	KIAA1361 protein	9.80
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
60	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
	407179	AA206465		thymosin, beta 4, X chromosome	9.72
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
	430068	AA464964		gb:zx80f10.0.1 Soares ovary tumor NbHOT H	9.70
	446795	AI797713	Hs.156471	ESTs	9.70
65	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
	451864	N20370	Hs.69547	ESTs	9.65
	419490	NM_006144	Hs.90708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
	419904	AA974411	Hs.18672	ESTs	9.60
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
70	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	9.52
	424950	AA602917	Hs.156974	ESTs	9.50
	447534	AW953935	Hs.288655	ESTs	9.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
75	422960	AW890487		cadherin 13, H-cadherin (heart)	9.33
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	9.32
	408784	AW971350	Hs.63386	ESTs	9.30
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.30
	432409	AA806538	Hs.130732	KIAA1575 protein	9.30
	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
80	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.20
	434280	BE005398		gb:CM1-BN0116-150400-189-h02 BN0116 Homo	9.20
	434524	AA635931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
5	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE:3677185, mRNA	9.03
	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypothe	8.90
10	442806	AW294522	Hs.149991	ESTs	8.90
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	408437	AW957744	Hs.278469	lacrimal proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
15	431187	AW971146	Hs.293187	ESTs	8.80
	421098	AI697901	Hs.192425	ESTs	8.70
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PKA) anchor protein 2	8.70
	401091			decay accelerating factor for complement	8.62
20	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	438089	W05391		nuclear receptor subfamily 1, group I, m	8.60
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.60
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547M072 (fr	8.59
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (ellin)	8.56
	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
25	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.50
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.45
	407833	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r	8.43
30	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.38
	425284	AF155568		NS1-associated protein 1	8.33
35	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.33
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	8.30
	453716	AA037675	Hs.152675	ESTs	8.30
	418840	AI821614	Hs.185831	ESTs	8.20
40	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
	449656	AA002008	Hs.188633	ESTs	8.20
	425535	AB007937	Hs.158287	KIAA0468 gene product	8.17
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.13
	432559	AW452948	Hs.257631	ESTs	8.10
45	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.10
	420099	D80011	Hs.95140	KIAA0189 gene product	8.01
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
50	437886	BE264111	Hs.31314	retinoblastoma-binding protein 7	8.00
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.92
	433655	AL036559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.89
	434511	R28982	Hs.18106	ESTs	7.88
55	423523	AW299828	Hs.193580	ESTs	7.86
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	7.84
	411960	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	AI381900	Hs.159212	ESTs	7.80
60	406699	L06505	Hs.182979	ribosomal protein L12	7.75
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.68
	426759	AI590401	Hs.21213	ESTs	7.66
	406776	T16206	Hs.237164	ESTs, Highly similar to LDH_HUMAN L-LAC	7.62
	422689	AW856665		gb:RC3-CT0297-290100-013-d03 CT0297 Homo	7.60
65	444795	AI193366	Hs.160316	ESTs	7.60
	406663	U24683		immunoglobulin heavy constant mu	7.59
	442821	BE391929	Hs.8752	transmembrane protein 4	7.56
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	7.52
	407252	AA659037	Hs.163780	ESTs	7.50
70	414405	AI362533		KIAA0306 protein	7.50
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	429999	AI761802	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.50
75	420943	AI718702	Hs.279930	major histocompatibility complex, class	7.46
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.43
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.42
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.41
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	7.40
80	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	7.40
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20384 fis, clone KA	7.40
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	7.40
	432598	AI341227	Hs.157106	ESTs	7.38

	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
5	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AI184717		ESTs	7.30
	445929	AI089660	Hs.323401	dpy-30-like protein	7.30
	446013	AI360167	Hs.152774	ESTs	7.30
10	436075	BE090176	Hs.179902	transporter-like protein	7.20
	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:og82a10.s1 NC1 CGAP_Ov8 Homo sapiens	7.16
	407719	AW963866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
15	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424577	U09414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
20	427307	AF117947	Hs.174795	PDZ domain-containing guanine nucleotide	7.10
	438980	AW502384		gb:UL-HF-BR0p-aka-f-12-0-UL.r1 NIH_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	7.10
	441878	AI801869	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
25	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
	417315	AI080042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12461	LCHN protein	7.00
30	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.00
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418696	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
35	418134	AA397769	Hs.86617	ESTs	6.90
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypotheti	6.89
	451838	AW005866	Hs.193969	ESTs	6.88
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	6.87
	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
45	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
	449971	AA807346	Hs.268581	Homo sapiens cDNA FLJ14296 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
50	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	6.80
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432656	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
55	425277	NM_001241	Hs.155478	cyclin T2	6.72
	425246	AI085561	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016625	Hs.191381	hypothetical protein	6.70
	430299	W28673	Hs.108747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA508955	Hs.109653	ESTs	6.70
60	430555	AW967807	Hs.13797	ESTs	6.69
	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AI922013	Hs.83496	linker for activation of T cells	6.67
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
65	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PRO0641 protein	6.60
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.57
70	415221	W07418	Hs.78225	annexin A1	6.56
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	catumenin	6.50
	443749	R38828	Hs.143463	ESTs	6.50
75	448094	H24387	Hs.32061	ESTs, Weakly similar to 138022 hypotheti	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
	421633	AF121860	Hs.106260	sorting nexin 10	6.40
80	435937	AA830893	Hs.119769	ESTs	6.40
	445612	N94126	Hs.12969	hypothetical protein	6.40
	451653	W18193		ESTs, Moderately similar to HERC2 [H.sap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlled	6.39

	434817	AA082118	Hs.102737	gofath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	6.35
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
5	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW963897	Hs.44743	KIAA1435 protein	6.30
	412220	BE350058	Hs.36787	chromodomain helicase DNA binding protei	6.30
10	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
	444933	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
15	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.27
	411975	AI916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	6.25
	433162	AI025842		ESTs	6.23
	449322	AI638616	Hs.196566	ESTs	6.22
20	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.191146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
25	427968	AI657607	Hs.181301	cathepsin S	6.18
	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.16
	418113	AI272141	Hs.83484	SRV (sex determining region Y)-box 4	6.16
	406870	AA075144		gbzm86f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
30	445493	AI915771		metallothionein 1E (functional)	6.15
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	AI269666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
35	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
	406797	AI432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	AI277367	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
40	441962	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
45	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
	412949	AA71639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AI418466	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
50	441623	AA315805		desmoglein 2	5.98
	416926	H03109	Hs.263395	HT018 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subuni	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.95
55	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
	422310	AA316622	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	408605	AF025374	Hs.46465	T-cell, immune regulator 1	5.91
	433891	AA613792		gbno97h03.s1 NCL_CGAP_Pr2 Homo sapiens	5.90
	406542			C19000728*:g[12585552]sp[Q9Y2Q1]Z257_HU	5.90
60	406858	AI665720	Hs.29797	ribosomal protein L10	5.90
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW961702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
65	441321	H17182	Hs.7771	B-cell associated protein	5.88
	429083	Y09397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW088535		ribosomal protein, large, P0	5.87
	416987	D86957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
70	428773	BE256238	Hs.193163	bridging Integrator 1	5.83
	406794	AI890243		ribosomal protein L6	5.82
	457752	AI821270	Hs.285643	Homo sapiens cDNA FLJ14364 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
75	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
	412528	AI123478	Hs.32112	ESTs	5.80
	424875	AI187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AI459554	Hs.161286	ESTs	5.80
80	449961	AW265634	Hs.133100	ESTs	5.80
	416759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137395	ESTs, Weakly similar to JCS238 galactosy	5.79
	422773	AB028962	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	5.78

	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363867	Hs.155029	ESTs	5.73
5	414890	BE281095	Hs.77573	uridine phosphorylase	5.72
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne	5.71
	435961	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	5.70
10	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
	446659	AI335361	Hs.226376	ESTs	5.70
	457250	AA811987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	AI885897	Hs.125293	ESTs	5.67
15	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
	451812	X81889	Hs.152151	plakophilin 4	5.65
	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	5.63
	424326	NM_014479	Hs.145296	ADAM-like disintegrin protease, decysin	5.60
20	431770	BE221880	Hs.268555	5'-3' exonuclease 2	5.60
	436511	AA721252	Hs.291502	ESTs	5.60
	446630	AW384793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X68392	Hs.91379	ribosomal protein L26	5.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.57
25	416047	BE439894	Hs.78991	DNA segment, numerous copies, expressed	5.56
	437296	AA350994	Hs.20281	KIAA1700	5.56
	453985	N44545	Hs.251865	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	AI583696	Hs.253313	ESTs	5.53
30	435748	AA699756	Hs.117335	ESTs	5.52
	420732	AA789133	Hs.63525	ESTs	5.51
	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	5.50
	430915	AA488953		gb:aa55e05.r1 NCI_CGAP_GCB1 Homo sapiens	5.50
	436716	AI433540		gb:ti69g05.x1 NCI_CGAP_Kid11 Homo sapien	5.50
35	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
	449625	NM_014253		od2 (odd Oz/ten-m, Drosophila) homolog 1	5.50
	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associat	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
40	427640	AF058293	Hs.180015	D-dopachrome tautomerase	5.47
	420552	AK000492	Hs.98806	hypothetical protein	5.45
	449338	H73444	Hs.394	adrenomedullin	5.42
	427176	AW381569	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
45	421568	W85858	Hs.99804	ESTs	5.40
	423961	D13666	Hs.136348	perlestin(OSF-2os)	5.40
	440719	AA150869	Hs.26267	ATP-dependant Interferon response protei	5.40
	443035	Z45822	Hs.8906	Homo sapiens clone 24889 mRNA sequence	5.40
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
50	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	5.39
	422163	AF027208	Hs.112350	prominin (mouse)-like 1	5.38
	439815	AA205079	Hs.6693	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
55	457465	AW301344	Hs.122908	DNA replication factor	5.37
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.36
	409485	S80990	Hs.252136	ficollin (collagen/fibrinogen domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
60	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
	412623	R28898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
65	419926	AW900992	Hs.93798	DKFZP586D2223 protein	5.30
	422900	AA641201	Hs.222051	ESTs	5.30
	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA278583	Hs.180737	Homo sapiens clone 23664 and 23905 mRNA	5.30
70	430177	AW969233	Hs.302746	MSTP028 protein	5.30
	430835	AI240006	Hs.192326	ESTs	5.30
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens	5.30
	439776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
75	415995	NM_004573		phospholipase C, beta 2	5.29
	424578	AK001973	Hs.150890	hypothetical protein	5.27
	441303	AW293081	Hs.241801	ESTs	5.27
	427816	AA159248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.26
80	450273	AW296454	Hs.24743	hypothetical protein FLJ20171	5.24
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl cis/trans isome	5.23
	415121	D60971	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	AI796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405086			NM_006652:Homo sapiens Snt2-related CBP	5.20

	413401	AI361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0061 protein	5.20
5	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp564F133 (fr	5.20
	434372	AA631373		gb:ncp86c01.s1 NCL_CGAP_Thy1 Homo sapiens	5.20
	436812	AW298067		gb:U1-H-BW0-ajp-g-09-0-U1.s1 NCL_CGAP_Su	5.20
	441390	AJ692560	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
10	453127	AI696671	Hs.294110	ESTs	5.20
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.20
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	5.19
	451814	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	5.18
15	406799	AA908548		gb:og83g12.s1 NCL_CGAP_Ov8 Homo sapiens	5.16
	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.15
	422293	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	5.14
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
20	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.12
	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.186704	ESTs	5.11
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
25	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
	428403	AI393048	Hs.326159	leucine rich repeat (in FLII) interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	5.10
	436137	AI056769	Hs.133512	ESTs	5.10
30	440948	AW188311	Hs.128619	ESTs	5.10
	448497	BE613269	Hs.21893	hypothetical protein DKFZp761N0624	5.09
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.09
	424868	AI568170	Hs.96886	ESTs	5.08
35	418905	BE539674		actinin, alpha 4	5.08
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.07
	442618	R56222	Hs.26514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
40	406813	AW276131		ribosomal protein L13a	5.06
	454128	AL031259	Hs.41639	programmed cell death 2	5.05
	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.05
45	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.04
	418876	AA740616		gb:my97111.s1 NCL_CGAP_GCB1 Homo sapiens	5.03
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	AI133096	Hs.64593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
50	431451	AA761378	Hs.192013	ESTs	5.00
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
	435655	AW105663	Hs.6947	HSPC069 protein	5.00
	435919	AI052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
55	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	5.00
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	H58373	Hs.332938	hypothetical protein MGC5370	5.00
60	447197	R36075		gb:yh88b01.s1 Soares placenta Nb2HP Homo	5.00
	450113	AI683098	Hs.200866	ESTs, Moderately similar to ALU7_HUMAN A	5.00
	450511	R07423	Hs.85092	thyroid hormone receptor interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to t38022 hypotheti	5.00
	452056	AW955065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	5.00
65	457068	X69391		ribosomal protein L6	5.00
	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.97
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	4.95
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.94
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.92
70	400281			Eos Control	4.91
	414420	AA043424	Hs.76095	immediate early response 3	4.90
	415799	AA653718	Hs.225841	OKFZP434D193 protein	4.90
	434666	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
75	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
	451598	N29102	Hs.118078	ESTs	4.90
	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.88
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.85
80	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.86
	418458	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.85
	437186	AA338305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

	406781	AA639388		gb:nq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
	449810	AB006681	Hs.23994	activin A receptor, type IIB	4.82
	410323	AI241708	Hs.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
	444652	BE513613	Hs.11538	actin related protein 2/3 complex, subun	4.81
5	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.81
	400424	AJ276316	Hs.287374	zinc finger protein 304	4.80
	411573	AB029000	Hs.70823	KIAA1077 protein	4.80
	421045	BE144608	Hs.55533	ESTs	4.80
10	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.80
	438590	AA811465	Hs.123375	ESTs	4.80
	442071	BE048433	Hs.276043	ESTs	4.80
	449567	AI930790	Hs.188614	ESTs	4.80
15	453213	AA082650	Hs.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
	437802	AI475995	Hs.122910	ESTs	4.77
	409461	AA382169	Hs.54483	N-myc (and STAT) interactor	4.77
	421932	W51778	Hs.323949	kangal 1 (suppression of tumorigenicity	4.74
20	428453	AB011110	Hs.184367	GTPase activating protein-like	4.74
	413441	AI929374	Hs.75367	Src-like-adaptor	4.74
	446560	AK001567	Hs.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
	435541	AA687361	Hs.221318	ESTs	4.71
	410557	AA085803	Hs.192997	ESTs, Moderately similar to I78885 serin	4.70
25	412766	BE544475	Hs.54347	ESTs	4.70
	415526	N76536	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
	418973	AA233056	Hs.191518	ESTs	4.70
	421433	AI829192	Hs.22380	ESTs	4.70
	432925	AA878324	Hs.264750	ESTs	4.70
30	438869	AF075009		gb:Homo sapiens full length insert cDNA	4.70
	442233	AW967149	Hs.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
	447198	D61523	Hs.283435	ESTs	4.70
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	4.70
	444681	AJ243937	Hs.288316	chromosome 6 open reading frame 9	4.66
35	414598	AI094221	Hs.135150	lung type-I cell membrane-associated gly	4.66
	447817	BE620775	Hs.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
	416062	AA724811	Hs.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
	406661	X66975	Hs.172550	polypyrimidine tract binding protein (he	4.64
	424582	AF026849	Hs.150922	BCS1 (yeast homolog)-like	4.64
40	411165	NM_000169	Hs.69089	galactosidase, alpha	4.63
	435905	AW997484	Hs.5003	KIAA0456 protein	4.63
	445776	NM_001310	Hs.13313	cAMP responsive element binding protein-	4.62
	424730	NM_003358	Hs.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
	414747	U30872	Hs.77204	centromere protein F (350/400kD, mitotin	4.62
45	410668	BE379794	Hs.159651	hypothetical protein	4.61
	406774	AW518383	Hs.177592	ribosomal protein, large, P1	4.60
	406648	AA563730	Hs.277477	major histocompatibility complex, class	4.60
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	4.60
	415682	AI347128	Hs.191870	ESTs	4.60
50	417621	AV654694	Hs.82316	interferon-induced, hepatitis C-associat	4.60
	419970	AW612022		ESTs	4.60
	420012	AW957965	Hs.99014	Homo sapiens, clone IMAGE:3632168, mRNA	4.60
	431574	AW572659	Hs.261373	hypothetical protein dJ434014.3	4.60
	432586	AA568548		ESTs	4.60
55	437438	AL358620	Hs.14217	hypothetical protein DKFZp762P2111	4.60
	441355	AI822034	Hs.137097	ESTs	4.60
	444539	AI955765	Hs.146907	ESTs, Weakly similar to 2004399A chromos	4.60
	458965	AA010319	Hs.60389	ESTs	4.60
	406655	M21533	Hs.277477	major histocompatibility complex, class	4.60
60	414915	NM_002462	Hs.76391	myxovirus (influenza) resistance 1, homo	4.60
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.59
	423766	AA303799	Hs.300141	ribosomal protein L39	4.59
	451351	AW058261	Hs.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	450043	AA885699	Hs.24332	CGT-26 protein	4.56
65	447742	AF113925	Hs.19405	caspase recruitment domain 4	4.54
	433339	AF019226	Hs.8036	glioblastoma overexpressed	4.54
	426395	BE151985		hypothetical protein FLJ23316	4.53
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
	423799	AW026300	Hs.132906	19A24 protein	4.53
70	445093	AI207197		ESTs	4.52
	428044	AA093322	Hs.301404	RNA binding motif protein 3	4.52
	453968	AA847843	Hs.62711	High mobility group (nonhistone chromoso	4.51
	414194	BE175494	Hs.75811	N-acetylserine amidohydrolase (acid c	4.50
	427747	AW411425	Hs.180655	serine/threonine kinase 12	4.50
75	406745	AW511970	Hs.279860	tumor protein, translationally-controlled	4.50
	407013	U35637	Hs.83870	gb:Human nebulin mRNA, partial cds	4.50
	407198	H91679		gb:yyv04a07.s1 Soares fetal liver spleen	4.50
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	4.50
	429687	AI675749	Hs.211608	nucleoporin 153kD	4.50
80	436566	BE545588	Hs.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
	437634	AW293046	Hs.255158	ESTs	4.50
	439971	W32474	Hs.301746	RAP2A, member of RAS oncogene family	4.50
	442485	BE092285	Hs.29724	hypothetical protein FLJ13187	4.50
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	4.50

	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447667	AL117611	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
5	413856	D13639	Hs.75586	cyclin D2	4.49
	419556	U29615	Hs.91093	chitinase 1 (chitinotrioidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
10	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protel	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
15	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
	436623	AI417073	Hs.107265	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypotheti	4.41
20	436671	AW137159	Hs.183291	ESTs	4.40
	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, non	4.40
25	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	4.40
	430280	AA361258	Hs.237868	interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens	4.40
	444794	AI419991	Hs.145225	ESTs	4.40
30	445100	AW188205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
35	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
	441607	NM_005010	Hs.7912	neuronal cell adhesion molecule	4.37
	406742	AI468091	Hs.279860	tumor protein, translationally-controlled	4.35
	425095	AW014160	Hs.182585	KIAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity I, rec	4.34
40	442333	AI650877	Hs.129302	ESTs	4.33
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp66780711 (f	4.30
45	408875	NM_015434	Hs.48604	DKFZP434B168 protein	4.30
	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
50	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432290	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
55	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regl	4.30
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	4.30
	452994	AW962597	Hs.31305	KIAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.30
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
60	440910	H97875	Hs.117974	ESTs	4.29
	406853	AA614553	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
	413518	BE149455	Hs.75415	beta-2-microglobulin	4.28
65	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
	406746	AA580395	Hs.279860	tumor protein, translationally-controlled	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.26
	450201	T97838	Hs.25722	ESTs	4.25
70	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
	404854			Target Exon	4.21
75	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N57334	Hs.50158	ESTs	4.20
	418304	AA215702		gb:zr97g10.r1 NCI_CGAP_GCB1 Homo sapiens	4.20
80	423180	AF068302	Hs.125031	choline/ethanolaminephosphotransferase	4.20
	424684	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_005235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW946871		gb:RC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

5	451952	AL120173	Hs.301663	ESTs	4.20
	455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
	453247	T80198	Hs.111806	ESTs	4.19
	430451	AA836472	Hs.297939	cathepsin B	4.19
	414283	AW960011	Hs.154993	ESTs	4.18
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
	450746	D82673	Hs.278589	general transcription factor II, I	4.16
10	444797	AB018333	Hs.12002	KIAA0790 protein	4.16
	445718	H79791	Hs.15227	ESTs	4.15
	425783	AJ026740	Hs.1948	ribosomal protein S21	4.15
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
	406710	AJ708347	Hs.184014	ribosomal protein L31	4.15
	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
15	422343	AI628633	Hs.346823	gb:ty77d05.x1 NCL CGAP_Kd11 Homo sapien	4.13
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
	406724	C14071	Hs.234518	ribosomal protein L23	4.12
	449475	AJ348027	Hs.108557	hypothetical protein PP1057	4.12
	413828	L19067		v-rel avian reticuloendotheliosis viral	4.11
20	416819	U77735	Hs.80205	plm-2 oncogene	4.11
	436674	AA725002	Hs.272018	low molecular mass ubiquitinone-binding pr	4.11
	405266			Target Exon	4.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
25	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.10
	423096	AA732684	Hs.278428	progesterone induced protein	4.10
	428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypotheti	4.10
	429355	AW973253	Hs.292689	ESTs	4.10
30	433308	AA582718	Hs.291650	ESTs	4.10
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
	450850	AA648886	Hs.151999	ESTs	4.10
	453785	AJ368236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
	406854	AA613705	Hs.252259	ribosomal protein S3	4.10
35	410768	AF038185	Hs.66187	Homo sapiens clone 23700 mRNA sequence	4.09
	419612	AI498287	Hs.110613	KIAA0421 protein	4.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
	441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	4.08
40	443415	AI056523	Hs.133472	ESTs	4.08
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
	422306	AI928242	Hs.293438	ESTs, Highly similar to AF198488 1 trans	4.07
	400233			Eos Control	4.06
	421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
45	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	4.06
	424795	AW102850	Hs.153177	ribosomal protein S28	4.05
	446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	4.05
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	4.05
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfamily	4.05
50	409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fis, clone C	4.03
	413891	BE271020		tumor suppressor deleted in oral cancer-	4.03
	414004	AA737033	Hs.7155	ESTs, Moderately similar to 2115357A TYK	4.02
	417035	AA192455	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	4.02
	410584	AB011112		KIAA0540 protein	4.01
55	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
	423645	AI215632	Hs.147487	ESTs	4.00
	430048	T65054	Hs.73605	ESTs	4.00
	431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
	434170	AA626509	Hs.122329	ESTs	4.00
60	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12607 fis, clone NT	4.00
	435391	AA704588	Hs.58934	ESTs	4.00
	448768	AV660305	Hs.110286	ESTs	4.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
	451831	NM_001674	Hs.460	activating transcription factor 3	4.00

TABLE 56B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358689 AW938841 BF438147 WD5391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 AI923886 AA947932 AI276125 AI185720 AW510698 AA987230 BE467708 AW896628 AW898544 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813854 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI555133 AA845571 AW898622 BF110144 AW513280 AI061126 BF362770 AI268939 AI435818 BF475318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 AI922204 AW898625 BE699458 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 BI003244 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552

5 429978 35194_2
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 55 410143 MH1244_8
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 70 450377 12109_1
 75 425996 138046_1
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 444060 6315_1

BF999056 R83430 Z29922 T85791 W03942 H63289 AI091537 BF086583 AA345570 H48870 H80720 T83523 BK039626 BI037700 R00353
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 AI191529 AW273168 AI168451 AW073812 AW090611 AW003593 AI215845 AI799616 AW474940 AA954927 BM193740 AW562704 AW090127

			AA969444 AI080438 AA552500 AW237538 AA481060 AI246378 AA565227 AA398921 AA207051 AA721378 BF438608 AI085295 AI886630 AA904112 AI864588 AW271985 AW078868 AA725342 BF326598 AA843572 AI082536 AA766654 AI453279 AA435673 AI619515 AA879080 AA234592 AA890223 AA766824 BI259822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05809 N41323 T87376 R68544 H88711 BI087136
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	430068	1177709_2	AA947566
	409208	10117_2	AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946
10	422960	11862_2	BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260
	434280	1474904_1	BE005398 AA628622 AA994155
	434442	111738_1	AA662701 AA633929 AA737415
	410730	114639_1	BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823
15	438089	22448_4	BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N59114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671764 AW897824 AI811204 AA344646 BE009121 BG899664 H91240 R60548 N41701
	425284	3834_5	BM476120 BE672181 AI697653 AA938187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917 AW771624 AA663041 AI991576 AI160622 AA717633 BE089784 BE089788 AI222942 AW418516 AA329211 AI095736 BE550294 AA738345 BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634
20	422689	874209_1	AW954733 AA315006 AW856665
	414405	112689_1	AL047596 AA393792 AI670731 AI037957 AW874364 AI038137 N62286 AI241379 BE501096 AW090596 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183289 AA477717 AI076122 AA635190 AA700984 AA781508 C81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545
25	442495	928718_1	AI184717 AW518883 AF121173
	450139	34017_1	AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW856145 AU117599 AU135386 BG254665 AA166919 BG483981 AW809606 BG494194 AA622811 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588818 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI886459 AU155873 H04255 AW243966 AA557749 AI286227 R68691 R33453 AW388097
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40	451653	MH115364_1	BG119563 AW975776 BG498478 BE245304 AW450934 BF508792 AA599489 AA599477 AI805268 AA055489 AI128758 AA761425 AA731858 AI302271 BE219432 AA687294 AA018972 AW629429 Z45675 AW961626 T30940 R34554 T84712 BG986694
	433162	2167905_1	AI742311 AI025842 AA578843
	406870	0_0	AA075144
45	445493	423456_1	AV711317 AI809938 AI808768 AI240593 AI915771
	406797	0_0	AI432224 AW276890 AI499346 AA937014 AA653573 AI318525 AI246219 AA961591 AI270640
	441623	3362_1	BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA893325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BC496559 BF248373 BG494800
50	430504	5477_6	BE219720 BF475241 AI571723 BE219848 BI789268 AI224899 AA724864 AW771467 AA480255 AW845616 AI440295 H52800 BE218790 AI681575 AW300064 AW262133 H21568 AI363015 AI884914 H86948
55	433891	647290_1	AW182329 AA613792 T05304 AW858385
	455263	26143_1	BG216963 BG164885 BG213710 BG204771 BG193014 BG197556 BG217481 BG198185 BG183594 BI596425 AA115605 AI589156 BF439839 BG188832 AI359615 BG190473 AI024233 BF439574 AW118065 AI672797 AA610042 BG212008 AI204382 R70913 AA033534 AA781036 AI627278 AA307285 AA034218 BG482749 AW162429 BI602460 AA721969 AA476516 AA476416 AA903019 BF110864 AA307286 AA115471 AW964555 AA423826 AA115129 AI419107
60	406806	0_0	AW088535 AI889321 AA954221 AI337552 R42581 AW194670 AA064862 AW001147 AA864374 AA630699 AW276176 AA676615 AA875965 AI625428 AA580792 AA582038 AA581668 AA658065 AA828156 AA857160 AA936103 AI149335 AA936925 AA581684 AA954198 AW238461 AI281504 AI265812 AA583267 AW236162 AA876535 AW304286 AW474334 AI559415 AI589241 AI660952 AA641137 AI431696 AI688844 AA552513 AA564954 AW090553 AI205612 AI245753 AA954883 AA947909 AI866014
65	406794	0_0	AI890243
	431155	1235742_1	AW971213 AA493925 AA493567 AA876839 AA934462
	414150	2305332_1	T40644 AA136139 AA136026
	430915	197844_1	BG425760 BF997600 N48516 W73454 BF816344 BF997601 AA488953
	436716	2472838_1	AI433540 AA804981 AA728984
70	449625	249224_1	BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35350
	430283	1418_1	BC013728 BI084032 BF090365 BE410706 N36391 W80436 BF813124 R90857 R62778 H00591 H02329 AA355285 AK000826 BC008721 BG744004 BG479141 BG823656 BG479061 AU121103 AU138176 BG702567 BI599840 BG422775 BG700944 BE280747 AU138529 BE269929 BG704110 AU123329 AU122058 AU138135 BG723106 BG722291 BG831041 BG705239 BE740517 BE207133 BE252867 AI139772 BG714385 BF568538 BE304393 BF971755 BE267965 BE272012 AU135396 AU124535 BI551682 BG700612 AI815488 BG475195 BE388273 BE391517 BM148991 BF929247 AV653435 AW250299 AW249189 BF093150 BF093173 AW205325 BF057101 BF000551 AI341108 AI162009 AK026136 BE907957 W73238 BI711467 BG926027 AI816428 AA837518 AI754405 BG179142 AA481485 AW023435 BE855747 AI885101 N52163 AI016096 AI090204 BE677045 AI523320 AI126855 N26501 AA043680 AA976459 AI039590 AI937917 AI361000 W94866 AI375797 AI079801 AI168236 AA599882 AA084368 AI342635 AI190294 N26093 AI085234 AI298169 BF939715 AI223164 H98704 BE218925 N29394 AI918735 N41520 AI147784 AI918796 AA854317 N22193 AA199850 AI149728 AA121263 AI051074 AA565116 AI087349 N22209 AA552917 N33151 D52422 BF47483 AA476599 AA525787 AI279198 D53353 AA738083 AA558406 BI496334 AA999948 AA425847 BI496335 AA909624 BF197591 AW023259 AI652819 T31424 AA088213 T31115 AI206650 AA976796 AI948989 AW248762 AA449265 AA290687 AI682521 AA310227 Z38743 AA935369 AW119141 BF941087 AI470657 AI349451 AW079338 D45665 N21640 T30071 AI446705 R60220 BE833481 R49680 R70049 R41223 R32402 R69984 R70111 BM476906 BE293615 BE382443 BF155692 BE720638 BE931983 BE720594 BF085890 AA336953 BF081638 AA359915 AA384116 AA360142

5			BI667664 BG823235 BE315559 BE301958 BE891114 BG826267 BE253680 BG979094 AV722757 N67629 BG997927 BI915769 BG680692 R62777 BE251116 H56358 AW369586 BG677759 B1044604 R75787 BE770960 H69529 R69983 AA259238 R97827 AA310379 W01103 AI873384 AL554578 BF038102 H87182 H87517 H01574 T5273 N28881 AA301397 T92375 R68401 AW800466 AI268172 BE876949 D54019 AI909769 AW798415 B1222383 AI393171 C15260 N26959 H17129 T53095 T52494 R68602 AI364765 BF687869 AI817035 AW105354 BE293820 H14206 BI093066 C14063 AL534349 BE255883 BE254088 AA428399 AW579360 AW579381 N53144 D60748 D54020 BG292106 H96705 D52423 T36174 D54161 R73016 D55021 BI857200 H83444 B1016954 D54163 R15563 BI818664 BE152207 B1048502 BF885667 BE613212 BE165773 BF149332 AW607045 BE305200
10	409019	32320_4	BM480413 N28908 H39792 BE240826 BE882093 BE240827 AW868637 BF739795 AA700834 AA769597 AA489668 AW968806 AW085195 AI093280 AI218457 AA063138 AI632958 AW515005 AI570530 Z41724 AA748789 AI696584 AA062544 AA773643 AA490285 AA761668 AA573621 R09670 R92814 M95678 NM_004573 AL530754 AI439623 AW374413 BF898880 AW630959 BF875526 AW02206 BF818690 BF893068 AW504110 AW408049 BG002913 AL530753 AI524064 AW769231 AA464970 AA293723 AI095051 AI953375 AI982938 BM146050 AW575804 AA962489 AI655426 BM146046 T28538 BE241935 T89023 BI910963 AI416986 AI767111 AI422290 AW468260 BE676853 AI656771 AI961755 F04675 AA582826 AA737606 BM194382 AA912021 AW183098 BE876682 AI962227 AI591366 AA621765 AA293724 R51642 F10194 BI909727 BF892632 AW950600 AW950138 BG258587 BF892649 AI000647 BF892710 AA353176 BF894726 AA465038 BI040869 BI837749 BE244320 H18054 T74300 AW797026 AA926790 F32814 AW751282 AI933994 AA578823 T78372 BF899896 BF882808 BF974969 BG622121 AA631424 AA988296 AA631373 AW978773 AW298067 AA810101 AW194180 AA731645 AI690673 AA906548 AW972830 AA489820 AA527647 AA570362 BM469076 AA533027 AI127512 AI368802 AA533141 AA700560 AW576028 AI610851 AI435361 BM129172 AW474544 BM128899 AI814292 AW502039 AA531243 BF941858 AW502037 AA702337 AI419854 AA662755 AA934364 AI300510 AI291136 AA505263 AI144527 AI076919 AI633534 AI242473 AA938561 BG055372 AA512894 AI671356 AA962403 BF080810 AA663911 AA847056 AA513301 AA369069 AA377265 BG291206 AA402298 AA885766 AW801002 AA302290 AI305842 AW800873 AA302492 AA478427 AI817291 AW801104 AW801028 AA865744 BF155979 AI374743 AA478431 AI159846 AI369757 AI800672 BF435788 AA255451 AI937707 AW006198 AI280363 BF062434 AW801115 AI919181 F28413 WD4214 AW152380 AW901567 AW901570 AA886371 AA384251 AI302846 BE701902 AA931606 H42673 R33703 AW901556 AA009816 AW901568 AW352200 AA256558 H15928 BI087170 AW800530 AA369068 N98562 H28652 N34644 H97650 H00956 W70039 AI142831 AA009817 F37136 N70289 AA531347 R72374 H27488 R66605 AW276131 AA740616 AA654854 AA229923 R36075 R36167 AI366546 BC022444 BC004138 NM_000970 BC020679 X69391 D17554 BC013863 BG779630 BG574189 BG571986 BG494603 BG575713 AV702244 AU145720 AI568177 BE350654 BG943995 AA730918 AA634024 AV744673 AI611573 AI613381 AI613403 AI250148 AW301759 AI312307 AI376488 BE139682 AV743357 AI371951 AI613376 AI613570 AI345719 AI312458 AI612697 AI334453 AW268747 AW268318 AI343026 AI335454 AI313096 AI308011 AW075176 AI348782 AI334479 AW268332 AI611433 AI371906 AI312459 AI371647 AI370051 AI335217 AI312262 AI610971 AI348798 AI613378 AI612698 AI348772 AI345434 AI345283 AI312292 AA775853 AI611363 AI345286 AI318305 BF054854 AI613384 AI348808 AI802857 AI609452 AI583301 AI349258 AI345645 AI345011 AI340442 AI335410 AI310907 BF055880 BF055774 BF055754 BF054712 AI583261 AI309664 BF054905 AI370092 AI349212 AI345583 AI345554 AI312242 BF055856 AI612686 AI611382 AI610952 AI345301 AI312235 AI610936 AI609836 AI340650 AI312472 BF054840 AI802838 AI345448 AI336508 AI313098 AI312293 AI312277 AI254912 AW302091 AW074788 AI611968 AI611948 AI583362 AI583284 AI583245 AI379398 AI371935 AI340564 AW301840 AI862239 AI612025 AI611869 AI609852 AI345449 AI312375 AI312318 AI311993 AI310895 BF057960 BE178604 AI802860 AI612115 AI611886 AI370059 AI313286 AI802856 AI611438 AI311987 AI802821 AI312997 BF054711 AI611889 AI376483 AI252445 AI611577 AI349139 BF054925 AI802840 AI583286 AI340739 AI612041 AI345196 BF054833 AI308909 AI611883 AI313275 BF477097 AI609466 AI348792 AI340468 BG944254 BG941457 AW302007 BG944413 BG941475 D58042 AA328428 BG429596 BE395392 BM424161 BF663310 AV727364 BM473884 BG531178 AA307591 BF965435 BG009500 AI376551 AA897445 T87714 BE564506 Z47727 BF028489 BI597545 AA152273 AA730753 W07504 AA406507 AA316220 AA424683 N35844 N72473 AA442109 W01788 AA747605 AA235894 N41438 AA382786 AI906934 AI906935 BF091197 N85572 N75678 AV758098 BE719745 BE719744 BE719735 AA639388 AA584945 AA776364 AA776365 AA855528 AI732997 AA977633 AA855818 AF075009 R63109 R63068 AK055270 BE348291 AI190289 AW612022 AI269506 AI266578 AI269675 AW271406 BE879851 BF574163 BI497126 AW903775 BI917368 AW150900 BF244813 H79201 BC022881 AU150944 BG750783 AW54175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548 AK057067 BF111915 AW249706 AI222199 AI887251 AI818753 AI244687 AW135782 BF476693 BF060935 AI197928 AW251092 AI685636 AI685630 BE673458 AA932894 AW205200 AA720784 BG236866 AI583152 BE677464 AW149338 AI926439 BG031285 BF915924 BG982583 BI060025 BG991393 BE830027 BE151985 BE152208 BE152002 BE818337 BE717581 BE818354 BE830030 AA377477 T51255 BF920761 BG170636 N90052 AI207197 BF773544 AW195452 AI207343 BF813684 BF928775 AA828585 AF070570 BF439282 BF109960 AI480268 AI038060 AW082339 BF516290 BE218214 AI469956 AA039955 BE644674 AI861871 AA766231 AA845840 W85716 AA676253 AI087188 AA022908 AW953178 T33195 BF594711 AA488699 R55652 D81245 D80778 D81560 AW960933 BF930897 BE698103 AA040024 BF515960 BE168475 AA453247 AI267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109 AA004849 H41952 W88634 BF031932 BM423354 AL041825 H29654 AI908178 W85754 AI905762 AA309860 C04540 AA340246 H84669 BM476605 BI545004 BI834636 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AI734997 AA931168 AA429766 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI889031 N98464 AI820039 AI459034 AV652512 AA622990 BE857200 AA932998 AA740573 AI826264 AA865683 AI344550 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895 AA535689 BF806025 BF806061 BF805985 BF746099 BF746097 AI309259 AI597603 BF806068 AI090653 AI129205 AI248410 H72993 AW615341 BF805990 BF805982 AA953819 T34373 T35604 H56242 AA648145 T35907 BF808691 N94015 AV703438 BG774276 H82341 R76371 T65754 AA229658 AA229857 X79449 BC017853 AL121035 BF196384 AW119044 AI028023 AW451110 AI971911 AW015069 AI079170 AI376367 AI264113 AA829646 AA737579 AA449679 AA740864 NM_001111 U18121 AI567297 BG773801 BF973874 AV687104 AA527579 AA843525 BE706355 AI074589 AI523475 BE890249 AW406263 BE074258 AV729485 BF809510 BG056619 AA677244 BE179838 AA622264 AI460106 AA740411 AI499168 AI078223 AI682923 BE696559 AW375385 AA788739 BG984978 Z40874 T17054 F05696 AW844043 U10439 BI711870 AW245957 AU158557 AA679305 AA679316 W72510 AI346029 BG059762 AW251062 AA132373 AI925621 AI860230 AI340172 AW192891 AI079980 AI094937 AI042115 AI200901 BE328452 AA644678 AA551209 BE351065 AA970761 N68609 AW002028 AA160826 AI422774 AW873114 AW073597 AW664483 AI218710 AW020550 AW190607 AI984545 AI871921 AI333970 AI452887 AI818335 AA398655 AI554424 AI274187 BE465703 AW512940 AW241365 AI923954 AA576649 AW168294 AA813181 AA912168 AI049738 AW514073 AA548255 AI569630 BE710031 AA241182 AI341697 AA563904 AI537990 AW517908 AW172943 Z39498 AI750294 AW150414 AI253293 BE825720 T31860 AW150775 D20310 AA150892 AU133933 BE781148 AL038957 BF910979 AA352297 BG988142 AW372175 BF229106 AW865705 BE093482 BG990396 AI499917 AA054452 H05484 AI828502 BM467331 AU140570 AL135417 BF947202 AW391926 BE813418 BF998473 T92021 BI021048 BM048783 AW501366 AW501342 AW501549 BE939021 BE707147 BE160974 BE305207 N49011 AA947119 AA678801 BE536876 AW897428 BG329648 BG818540 BE542344 BI919250 BI253018 AW130996 BE074249 BE895428 BI034862 BE083277 BF952166 BE883520 BI057842 AA215702 AA215703 AA368006 BE005876 BE066555
65	437386	5541_2	
70	418866 400244	245947_1 12188_1	
75			
80	418304	1093209_1	

438141	1173217_1	AA778849 AW946871 AW946782 AW946955
455397	1163608_1	AW936332 AW936341
413828	9453_1	BC011603 BG479117 AU124990 BG829759 AU143705 BG701663 BG699781 AU131718 BE515064 AU121812 BG898850 AL558461 BM151887
5		AU128758 BM263692 AU099013 AI241350 U88316 AW058398 AW469340 BF683967 AI470140 AU150993 AA633376 AW150821 AA536142
		AU148749 AI520647 AU151769 AU153404 AW070666 AA57758 AU153077 N99966 AW050940 BG055674 AA506657 AW301529 AI918646
		AI511235 AI266081 AI334542 AW071277 AI312434 AW303114 AI436544 AI436466 R22972 AI472987 N77886 AW072883 AA318683 D19761
		AW050566 AI312433 AA328444 R72435 AA430721 AI142599 AA582290 AU148896 AA721233 AW628132 R93935 AA100710 BI520773 AI934172
		BG222461 H85359 AW074639 AA017117 BI026412 AL582142 AA443547 AA588793 AA777535 AA693844 AI018661 AA577422 AA522800
		BF054818 AA102378 AA757993 AA687769 R55540 AA505784 BI820705 BI767939
10	410704	1054673_1
		AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
		BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166866 BE166913 BE166919 AW877456 AW877537 BE076866
		AW840571
	400233	11259_1
15		BC004324 NM_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 BI826914 BE440007 BI260656 BE395117 BE389334
		BE255792 BI194169 BI668218 BI194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM24171 BI828267 AW958606 BG831252
		BE392943 BE394033 BI858915 BI668334 BE621019 BG706995 BE791985 BF967484 BI193635 BG761859 BM466537 BG747165 BG827488
		AI133550 BM011511 BI227282 BG489212 BG478388 BE727789 BI160880 BG831707 BG324692 BM470427 BI083889 BG831605 BG754114
		BG420536 BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 BI193807 BI159866 BG473786 BG397178
		BI194428 BI117210 BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145
		BM017978 BI193934 BI160764 BI160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 BI192794 BG831002 BG830459
20		BG764737 BG761808 BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762
		BG480900 BG419627 BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI161360 BG822729
		BG110091 BG106500 BI258369 BG831982 BM458301 BM019513 BI161350 BI114178 BG481969 BG474870 BF974048 BF971122 BE741405
		BE395269 BG832027 BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 BI258301
		BI160946 BG105893 BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG760618 BE743865 BM465145
25		BG831227 BG774290 BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336
		AW328235 BG339458 BF972634 BE909808 BI160988 BI160251 BG828764 BG826860 BG768360 BF568228 BI18282 BI457127 BG2831491
		BG759864 AI830010 BF568381 BE907238 BI161172 BI16773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564
		BM045000 BG339617 BG828794 BG335767 BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919
		BG480626 AW196817 BG336261 BE906157 BE395717 BE391427 BI192954 BG829757 BG476379 BE301538 BE394727 BE257695 BE905344
30		AI433577 BE894416 BE886992 BE409223 BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 AI871751 BE744523 BI192663
		BG831669 AI000225 BE743836 BE272515 AA628078 BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297
		BE391448 BE390780 BE388821 BE258477 BE905970 BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542
		BE744156 BE394125 BE742207 BE395265 BE392942 BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753
		BE272370 BE907458 BE612801 BE392484 BE907636 BE907353 BE910491 BE909796 BE905331 AW248173 AI683576 BE908826 BE620180
35		BF037570 BE908312 BE615015 BE256977 BE746875 BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825
		BE906472 BE906509 BE906017 BE910442 BE514657 BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298
		AW327827 BE394422 BF569178 BE263240 AI700512 BG830290 BF569308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674
		AA136372 BE279892 AA442822 BE384898 AA313519 AI878866 AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063
40	413891	823_1
		F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW04280 AA379888 F29022 BF089981 F31013 F24305
		BE271020 AI925430 AI806151 AW129911 AA828002 AW003539 BE042625 AI287859 AW778973 AI621173 AI991000 AA846016 AW150029
		AW169748 AA649945 AI358496 AI470921 BF434211 AW513748 AW451232 AI953738 AI249448 AI045080 AI655280 AI637976 AW194345
		AW511997 AI367197 BF064039 F29558 AI537342 BF593207 AW879538 AA973211 AI674328 AW879559 BF061961 AA481914 AA426532
		AA426653 AA480106 AW243290 BF513102 BF346057 AI763358 AW003726 AI139045 AI570748 AW237602 T57492 BE887212 AI969311
		AA133045 F23464 AA576416 T15590 AI650891 AI950958 AI983931 AW515101 AI650820 H81989 AA508473
45	410584	35319_1
		BF828833 AI968217 AI651409 AI760574 AI147562 AW001418 AI146791 AI650589 AI952939 AI432373 AI964094 AI963870 AI20438 AI336803
		AA809634 BF590826 AA741075 BI712639 AL134637 BM264338 AA527993 AI867208 AI439038 AI684987 AI531696 AI587126 AI637622 AI651931
		AI867525 AI783674 AI638281 AI825752 AI339197 AI653411 AI341372 AI673213 AI673191 AW779768 AI627934 AI921835 AI741634 AI382284
		AI741624 AI401569 AW190430 AW196390 AI829182 AI523816 AI760522 BE505014 AI917343 BG818909 AW009307 AA927544 AA825621
		AA829400 AA527307 AI887999 AI865022 AA885063 AA653458 AA483816 AA836167 AA505879 AA421004 AA252626 AI380678 AW196980
50		AA649133 AI742276 AW015700 AA595019 AA877835 AI701658 AA729793 AA535004 AA926792 AA505113 AA603726 W68390 N90130 AA489461
		AA830462

55	TABLE 56C
	Pkey: Unique number corresponding to an Eos probe set
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand: Indicates DNA strand from which exons were predicted.
60	NT_position: Indicates nucleotide positions of predicted exons.

	Pkey	Ref	Strand	NT_position
	402474	7547175	Minus	53526-53628,55755-55920,57530-57757
	402145	8018280	Plus	113086-114800
	401091	9958240	Plus	94760-94898
65	401466	6682292	Plus	28748-29023
	401113	9966541	Minus	19419-19959
	406542	7711499	Plus	117335-118473
	405086	8072509	Plus	73664-73841,74081-74217,74610-74779,7492
70	401846	7712190	Minus	82775-82823,82912-83022
	404854	7143420	Plus	14260-14537
	405266	4156171	Minus	63337-63552

75 TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

80 Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
5	Pred.ProT.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
	UniGene Title:	UniGene gene title
	R1	95th percentile of testicular cancer Als divided by the 50th percentile of normal tissues Als, where the 10th percentile of all normal tissue Als was subtracted from both the numerator and denominator
10	Pkey; ExAccn; UniGeneID; UniGene Title; Pred.ProT.Domains; R1	
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23
		440119; AA865455; Hs.125331; ESTs, Moderately similar to unknown [H.sapiens]; ESTs, Moderately similar to unknown [H.s; 27.37
15		421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89
		431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription factor; 25.03
		435918; AF263538; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88
		432666; AW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product [H.sapiens]; ESTs, Weakly similar to unnamed protein ; 17.74
		419556; U29615; Hs.91093; chitinase 1 (chitotriosidase); chitinase 1 (chitotriosidase); 17.64
20		452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in melanoma; 17.06
		417886; AA214584; ; ESTs; ESTs; 15.95
		412265; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93
		425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcri; 15.82
		423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11
25		419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08
		427584; BE410293; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogen; 14.17
		418696; AW959433; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58
		416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20
		414034; U89277; Hs.305985; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog o; 12.93
30		454077; AC005952; Hs.37062; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90
		432730; AI066520; Hs.131358; ESTs; ESTs; 12.84
		446293; AI420213; Hs.149722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74
		423354; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; calcium channel, voltage-dependent, alph; 12.46
		450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42
35		450719; AI096837; Hs.21349; ESTs, Weakly similar to R888_HUMAN RAS-RELATED PROTEIN RAB-8B [H.sapiens]; ESTs, Weakly similar to R888_HUMAN RAS-R; 12.26
		431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96
		431354; BE046956; Hs.251673; DNA (cytosine-5)-methyltransferase 3 beta; DNA (cytosine-5)-methyltransferase 3 be; 11.91
		402199; ; Target Exon; Target Exon; 11.85
		424578; AK001973; Hs.150890; hypothetical protein; hypothetical protein; 11.81
40		416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67
		439979; AW600291; Hs.6823; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57
		410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42
		442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42
		414812; X72755; Hs.77367; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38
		421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15
45		440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; NALP2 protein; PYRIN-Containing APAF1-li; 10.92
		414683; S78296; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91
		423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage ; 10.74
		433800; AI034361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68
		429120; AK001673; Hs.196530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48
50		444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46
		441553; AA281219; Hs.121296; ESTs; ESTs; 10.37
		426534; U58096; Hs.2051; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28
		441878; AI801869; Hs.127982; ESTs; ESTs; 10.06
		432117; AL036195; Hs.2909; prolamine 1; prolamine 1; 10.01
55		425427; AI852662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97
		416201; AA467752; Hs.195161; ESTs; ESTs; 9.97
		410929; H47233; Hs.30643; ESTs; ESTs; 9.91
		427486; AA974433; Hs.362432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81
60		427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68
		402680; ; Target Exon; Target Exon; 9.68
		409208; Y00093; Hs.172631; Integrin, alpha X (antigen CD11C (p150), alpha polypeptide); integrin, alpha X (antigen CD11C (p150); 9.46
		443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42
		440207; AI371976; Hs.128326; ESTs; ESTs; 9.41
		433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41
65		447534; AW953935; Hs.288655; ESTs; ESTs; 9.33
		442333; AI650877; Hs.129302; ESTs; ESTs; 9.28
		421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425); Homo sapiens mRNA; cDNA DKFZp434B0425 (f; 9.24
		423458; AI204212; Hs.351113; ESTs; ESTs; 9.23
70		431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta; 9.23
		422938; NM_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21
		411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 9.21
		425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18
		428664; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17
75		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3 (RAIG1); metabo; 9.11
		447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11
		422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10
		449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86
		441560; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 8.86
80		440983; M20681; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86
		409342; AU077058; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83
		420367; AA259090; Hs.257028; ESTs; ESTs; 8.82
		415947; U04045; Hs.78934; muls (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); muls (E. coli) homolog 2 (colon cancer, ; 8.73
		418613; AA744529; Hs.86575; mitogen-activated protein kinase kinase kinase 1; mitogen-activated protein kinase kinase ; 8.71

- 417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapi]; 8.64
 407239; AA076350; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 8.58
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkines); 8.52
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 8.51
 424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45
 447188; H65423; Hs.17631; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45
 430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); midkine (neurite growth-promoting factor); 8.40
 430676; AF084866; Hs.372585; gb:Homo sapiens envelope protein RIC-3 (env) gene, complete cd; gb:Homo sapiens envelope protein RIC-3 (; 8.38
 420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.38
 406621; X57809; Hs.181125; immunoglobulin lambda locus; immunoglobulin lambda locus; 8.37
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25
 423198; M81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19
 418299; AA279530; Hs.83958; integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 (p95), ly; 8.17
 453968; AA847843; Hs.62711; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromoso; 8.16
 453985; N44545; Hs.251865; ESTs; ESTs; 8.14
 451106; BE382701; Hs.25960; N-MYC oncogene; N-MYC oncogene; 8.10
 420347; AL033539; Hs.97124; Human DNA sequence from clone RP1-309H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, STSs, GSSs and a CpG Is; Human DNA sequence from clone RP1-309H15; 8.03
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fis, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fis, clone HE; 8.02
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90
 421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobul; 7.89
 432407; AA221036; ; gb:zr03f12.1 Stralagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN ; mRNA sequence; gb:zr03f12.1 Stralagene NT2 neuronal pr; 7.83
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80
 433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73
 446528; AL076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71
 447350; AJ375572; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 7.71
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked moi; 7.71
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70
 444784; D12485; Hs.11951; ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1); ectonucleotide pyrophosphatase/phosphodi; 7.62
 443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; interferon, gamma-inducible protein 30; 7.55
 410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (eta, 116kD); eukaryotic translation initiation factor; 7.53
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein; ; 7.52
 411975; AJ916058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like ; 7.50
 439864; AJ720076; Hs.21997; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 7.47
 440773; AA352702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4669, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47
 407710; AW022727; Hs.23616; ESTs; ESTs; 7.45
 445093; AJ207197; Hs.374149; ESTs; ESTs; 7.41
 418113; AJ272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39
 417900; BE250127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37
 429469; M64590; Hs.111801; glycine dehydrogenase (decarboxylating; glycine decarboxylase, glycine cleavage system protein P); glycine dehydrogenase (decarboxylating; ; 7.33
 422726; U11690; Hs.1572; faciogenital dysplasia (Aarskog-Scott syndrome); faciogenital dysplasia (Aarskog-Scott sy; 7.33
 430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32
 448981; AJ968719; Hs.195387; ESTs; ESTs; 7.28
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26
 435092; AK000703; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121 (; 7.25
 434414; AJ798376; ; gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens cDNA clone 3' similar to TR:O15475 O15475 UNNAMED HERV-H PROTEIN ; mRNA sequence; gb:tr34b07.x1 NCL_CGAP_Ov23 Homo sapiens; 7.24
 428977; AK001404; Hs.194698; cyclin B2; cyclin B2; 7.19
 434274; AA628539; Hs.57783; ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1_HUMAN A; 7.19
 446700; AW206257; Hs.156326; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L2; 7.16
 420524; AB010575; Hs.98547; amiloride-sensitive cation channel 3, testis; amiloride-sensitive cation channel 3, te; 7.15
 439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14
 445076; AJ206888; Hs.154131; ESTs; ESTs; 7.14
 448588; AJ970276; Hs.156905; KIAA1676; KIAA1676; 7.13
 429486; AF155827; Hs.203963; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10
 441352; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E. coli RecA homolog); RAD51 (S. cerevisiae) homolog (E. coli Re; 7.04
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; interferon-stimulated protein, 15 kDa; 7.02
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA; 6.96
 416658; U03272; Hs.79432; fibrillin 2 (congenital contractural arachnodactyly); fibrillin 2 (congenital contractural ara; 6.92
 438450; AJ050866; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90
 444381; BE387335; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89
 447582; BE233520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89
 424779; AL046851; Hs.153053; CD37 antigen; CD37 antigen; 6.89
 443907; AU076484; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pro; 6.84
 427298; AA400495; ; ESTs; ESTs; 6.82
 414732; AW410976; Hs.77152; minichromosome maintenance deficient (S. cerevisiae) 7; minichromosome maintenance deficient (S.; 6.81
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81
 428866; U02330; Hs.172816; neuregulin 1; neuregulin 1; 6.80
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80
 427521; AW973352; ; ESTs; ESTs; 6.75
 430397; AI924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein ; 6.75
 427719; AI393122; Hs.134726; ESTs; ESTs; 6.74

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein, ; 6.70
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63
 441031; A1110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59
 424381; AA285249; Hs.145329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55
 425769; U72513; Hs.159488; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete ; 6.55
 452363; A1852743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:17279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51
 409893; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mitotin); minichromosome maintenance deficient (S.; 6.50
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A; 6.44
 427747; AW411425; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43
 409142; A136877; Hs.50758; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42
 430280; AA361256; Hs.237868; Interleukin 7 receptor; Interleukin 7 receptor; 6.42
 432938; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42
 422809; AK001379; Hs.121028; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40
 427578; A1591305; Hs.169084; ESTs, Highly similar to TUL3_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3_HUMAN TUBBY; 6.40
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (Cy; 6.39
 441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34
 451999; AW178401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; 6.31
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright ; 6.31
 425274; BE281191; Hs.155452; minichromosome maintenance deficient (mif5, S. pombe) 6; minichromosome maintenance deficient (mif; 6.31
 434649; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30
 415829; AW450198; Hs.163742; ESTs; ESTs; 6.28
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26
 446839; BE091926; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25
 428918; AL036957; Hs.2324; protamine 2; protamine 2; 6.24
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19
 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19
 407245; X90568; Hs.172004; titin; titin; 6.18
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18
 421379; Y15221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (Cy; 6.16
 435059; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino ; 6.09
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA, transcribed (FBL), mRNA; NM_001436; Homo sapiens fibrillarin (FBL); 6.09
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); interferon, alpha-inducible protein (clo; 6.04
 402678; ; Target Exon; Target Exon; 6.03
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01
 420596; NM_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01
 420676; A1434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95
 417777; A1823763; Hs.7055; ESTs, Weakly similar to I78885 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78885 serine/th; 5.94
 449569; A1656634; Hs.195389; ESTs; ESTs; 5.92
 436576; A1458213; Hs.77542; ESTs; ESTs; 5.90
 438746; A1885815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89
 420005; AW271106; Hs.133294; ESTs; ESTs; 5.89
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88
 403171; ; C2001472; gij5809678[gb]AAB41848.2 (U64675) sperm membrane protein BS-63 [Homo sapiens]; C2001472; gij5809678[gb]AAB41848.2 (U64; 5.87
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA, VERSION NM_000178.1 GI; NM_000179; Homo sapiens mutS (E. coli) h; 5.85
 423787; A1295745; Hs.235204; nuclear pore complex protein; nuclear pore complex protein; 5.85
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84
 452786; AB011100; Hs.30656; KIAA0528 gene product; KIAA0528 gene product; 5.84
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80
 447359; NM_012093; Hs.18268; adenylate kinase 5; adenylate kinase 5; 5.79
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78
 420297; A1628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1_HUMAN ALU S; 5.75
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5_HUMAN LEUKE; 5.74
436251; BE515065; Hs.296585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73
421535; AB002355; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69
425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspart; 5.69
401704; ; NM_021195; Homo sapiens claudin 6 (CLDN6), mRNA, VERSION NM_020982.1 GI; NM_021195; Homo sapiens claudin 6 (CLDN6); 5.66
425358; AL079658; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin assoc; 5.65
402677; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.64
409264; NM_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63
432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63
409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63
430252; AI638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61
419359; AL043202; Hs.90073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61
452816; AA131789; Hs.61509; ESTs; ESTs; 5.60
402679; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA, alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.59
414291; AI289619; Hs.13040; G protein-coupled receptor 86; G protein-coupled receptor 86; 5.58
453028; AB006532; Hs.31442; RecQ protein-like 4; RecQ protein-like 4; 5.58
453905; NM_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-associ; 5.55
419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino ; 5.55
446979; AI654443; Hs.197683; ESTs; ESTs; 5.54
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kin; 5.53
418962; AA714835; Hs.271863; ESTs; ESTs; 5.53
447388; AW630534; Hs.76277; Homo sapiens, clone MGC-9381, mRNA, complete cds; Homo sapiens, clone MGC-9381, mRNA, comp; 5.52
427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); integrin, alpha L (antigen CD11A (p180)); 5.52
449322; AI638616; Hs.196566; ESTs; ESTs; 5.51
428450; NM_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51
415141; AA169099; Hs.268171; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7_HUMAN ALU S; 5.48
454048; H05626; Hs.6921; ESTs; ESTs; 5.46
417079; U65590; Hs.81134; interleukin 1 receptor antagonist; interleukin 1 receptor antagonist; 5.45
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11980 fis, clone HEMBB1001304; Homo sapiens cDNA FLJ11980 fis, clone HE; 5.44
414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44
452291; AF015592; Hs.29853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisi; 5.44
438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class ; 5.44
427658; AA298760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43
449437; AI702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 5.41
453633; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40
450746; D82673; Hs.278589; general transcription factor II, I; general transcription factor II, I; 5.40
425966; NM_001761; Hs.1973; cyclin F; cyclin F; 5.39
418134; AA397769; Hs.86617; ESTs; ESTs; 5.38
432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37
417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, m; 5.36
428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.; 5.35
406811; U82979; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, ; 5.34
415819; AU077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII); 5.33
448133; AA723157; Hs.73769; folate receptor 1 (adult); folate receptor 1 (adult); 5.33
424762; AL119442; Hs.183684; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor; 5.32
421959; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 5.32
429271; AF039850; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32
456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A; 5.30
414907; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30
422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29
440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosop; 5.28
418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26
416178; AI808527; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer anti; 5.21
450377; AB033091; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20
409670; AJ368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20
429083; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20
408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 76kD); lymphocyte cytosolic protein 2 (SH2 doma; 5.19
438089; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, m; 5.16
437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-asso; 5.15
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15
436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor t; 5.14
426752; X69490; Hs.172004; titin; titin; 5.13
415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2 ; 5.13
400263; ; Hs.75309; Eos Control; Eos Control; 5.13
437099; M77793; Hs.48659; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin a; 5.12
427209; H06509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10
407347; AA829847; ; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens; 5.10
458933; AI638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10
450431; AW136797; Hs.268041; ESTs; ESTs; 5.09
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08
410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-recept; 5.08
417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05
412723; AA648459; Hs.335951; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog) ; 5.02
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha 2 (RAG cohort 1, importin); 5.00
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99
 402145; ; Target Exon; Target Exon; 4.99
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99
 408279; AF216965; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, contig; 4.98
 419525; T79257; Hs.1259; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97
 424439; AA579635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96
 448589; BE382657; Hs.21486; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94
 426427; M86699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91
 440129; AA865818; Hs.369523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-like; 4.91
 453922; AF053306; Hs.36706; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1; 4.90
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89
 452698; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88
 445333; BE557641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88
 437162; AW005505; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIG51) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIG); 4.87
 421350; AW301608; Hs.278188; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene; 4.87
 409093; BE243834; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86
 424304; NM_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86
 437696; Z83844; Hs.5790; hypothetical protein dJ37E16.5; hypothetical protein dJ37E16.5; 4.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase transporters), member 1; solute carrier family 23 (nucleobase tra; 4.84
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83
 448939; BE267795; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81
 412276; BE262621; Hs.73798; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor ; 4.81
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80
 409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79
 447250; AJ878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78
 448950; AF288687; Hs.9275; CGI-152 protein; CGI-152 protein; 4.78
 412926; AJ879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C; 4.78
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms); 4.76
 421905; AJ600247; Hs.32699; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H]; 4.75
 413880; AJ600842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74
 418355; I42563; Hs.1165; ATPase, H7 transporting, nongastric, alpha polypeptide; ATPase, H7 transporting, nongastric, alp; 4.74
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74
 428024; Z29067; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74
 421845; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bamacan); chondroitin sulfate proteoglycan 6 (bamac; 4.70
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69
 449475; AJ348027; Hs.129826; hypothetical protein PP1057; hypothetical protein PP1057; 4.69
 420062; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2, TGF(beta)-induced transcription factor 2; 4.69
 429336; AB005038; Hs.199270; cytochrome P450, subfamily XXVIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIB (25-hy; 4.69
 436856; AI469355; Hs.127310; ESTs; ESTs; 4.68
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67
 411295; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67
 426726; AA488915; Hs.171955; trophinin associated protein (tastin); trophinin associated protein (tastin); 4.67
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66
 431681; AK000378; Hs.267566; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.65
 443623; AA345519; Hs.9541; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent; 4.65
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63
 435045; BE297155; Hs.143698; ESTs; ESTs; 4.62
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62
 414972; BE263782; Hs.77695; KIAA0008 gene product; KIAA0008 gene product; 4.62
 436685; W28661; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62
 449515; AI653378; Hs.302012; ESTs; ESTs; 4.61
 425998; AU076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61
 420027; AF009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61
 438469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61
 413441; AI929374; Hs.75367; Src-like adapter; Src-like adapter; 4.60
 455847; AJ360456; Hs.86088; ESTs; ESTs; 4.58
 421506; BE302796; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57
 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L OR; 4.55

- 443068; AI188710; Hs.374480; ESTs; ESTs; 4.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54
 453227; AW135862; Hs.243991; ESTs; ESTs; 4.52
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51
 422565; BE259035; Hs.118400; singed (Drosophila)-like (sea urchin fascic homolog like); singed (Drosophila)-like (sea urchin fas; 4.51
 453613; F06838; Hs.374476; ESTs; ESTs; 4.50
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H; 4.50
 412507; L36645; Hs.73964; EphA4; EphA4; 4.50
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo; 4.49
 406547; ; Target Exon; Target Exon; 4.49
 443216; W80487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47
 448595; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46
 446236; NM_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46
 420340; NM_000734; Hs.97087; CD3Z antigen, zeta polypeptide (TIT3 complex); CD3Z antigen, zeta polypeptide (TIT3 com; 4.46
 413426; U68837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt; 4.44
 421819; NM_013403; Hs.108665; zinedin; zinedin; 4.44
 409512; AW979187; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, D; 4.43
 434551; BE387162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 [H.sapiens]; ESTs, Highly similar to A35661 DNA excis; 4.43
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42
 413186; AU077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic; 4.42
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40
 424078; AB006625; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39
 448153; Y10805; Hs.20621; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35
 400440; X83957; Hs.83870; nebulin; nebulin; 4.35
 437218; AL117497; Hs.58185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifera; 4.34
 430478; NM_014349; Hs.241535; apolipoprotein L 3; apolipoprotein L 3; 4.34
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfam; 4.29
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, receptor for (CD16); Fc fragment of IgG, low affinity IIb, r; 4.29
 434828; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29
 412314; AA825247; Hs.356084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled receptor; 4.28
 447827; U73727; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28
 426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component; 4.27
 437908; AI082424; Hs.351043; ESTs; ESTs; 4.27
 444664; N26362; Hs.11615; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26
 439334; AI148976; Hs.112062; ESTs; ESTs; 4.26
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25
 413869; NM_000878; Hs.75596; Interleukin 2 receptor, beta; interleukin 2 receptor, beta; 4.25
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24
 447200; BE543146; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24
 447528; AI612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22
 449810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22
 416714; AF283770; Hs.79630; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22
 425356; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21
 444535; AF011468; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21
 417088; M54915; Hs.81170; p1m-1 oncogene; p1m-1 oncogene; 4.20
 421707; NM_014921; Hs.107054; lectomedin-2; lectomedin-2; 4.20
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19
 419452; U33635; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18
 418755; Y14443; Hs.88219; zinc finger protein 200; zinc finger protein 200; 4.18
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17
 413686; AI469213; Hs.71404; ESTs; ESTs; 4.17
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fusin); chemokine (C-X-C motif), receptor 4 (fus; 4.16
 408482; NM_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15
 409421; AA199883; Hs.67624; ESTs; ESTs; 4.15
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

- 428479; Y00272; Hs.334552; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to M; 4.13
- 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbonate; 4.13
- 433435; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitochondrial; 4.13
- 420253; A656055; Hs.96200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 9; 4.12
- 5 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12
- 400205; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA. (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM_006265; Homo sapiens RAD21 (S. pombe); 4.12
- 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11
- 10 419607; R52557; Hs.91579; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10
- 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - *Caenorhabditis elegans* [C.elegans]; ESTs, Weakly similar to T31611 hypothetical; 4.10
- 432512; NM_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to protamine replacement); 4.10
- 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09
- 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); interferon-stimulated transcription factor 3, gamma; 4.09
- 15 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09
- 442091; AW770493; Hs.182874; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G protein) alpha 12; 4.09
- 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2; 4.08
- 421859; AA356620; Hs.108947; KIAA0050 gene product; KIAA0050 gene product; 4.08
- 20 432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-receptor type 12; 4.08
- 452069; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08
- 425069; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker-related; 4.07
- 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic acid transporters), member 3; 4.07
- 424517; AI539443; Hs.137447; Homo sapiens cDNA FLJ12169 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12169 fis, clone MA; 4.07
- 25 434224; AA380731; Hs.84; Interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe combined immunodeficiency); 4.06
- 446791; AI632278; Hs.195922; ESTs; ESTs; 4.06
- 432065; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), catalytic; 4.06
- 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta 3; 4.06
- 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory subunit, polypeptide 3; 4.06
- 30 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, delta; 4.05
- 408692; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04
- 446272; BE269912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrate 1; 4.04
- 439176; AI464444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 protein; 4.04
- 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule 1); 4.04
- 35 410068; AI633888; Hs.58435; FYN-binding protein (FYN-120/130); FYN-binding protein (FYN-120/130); 4.03
- 410639; BE269047; Hs.65234; hypothetical protein FLJ20596; hypothetical protein FLJ20596; 4.03
- 427716; L38951; Hs.180446; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03
- 451050; AW937420; Hs.351869; ESTs; ESTs; 4.02
- 449667; AB023227; Hs.23880; KIAA1010 protein; KIAA1010 protein; 4.02
- 40 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01
- 437527; AI241019; Hs.145644; ESTs; ESTs; 4.01
- 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase (NAD dependent); methylene tetrahydrofolate dehydrogenase; 4.00
- 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF1210; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00
- 412939; AW411491; Hs.75089; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor 1 gamma; 4.00
- 408581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99
- 433577; AW007080; Hs.284192; ESTs; ESTs; 3.99
- 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD); platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit; 3.99
- 418629; BE247550; Hs.86859; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99
- 50 448633; AA311426; Hs.21635; tubulin, gamma 1; tubulin, gamma 1; 3.98
- 402398; ; C19000263; gi|3108023|gb|AAC15755.1| (AC004659) BC62940.2 [Homo sapiens] [J166335; C19000263; gi|3108023|gb|AAC15755.1| (AC004659) BC62940.2 [Homo sapiens]; 3.97
- 408414; AI114688; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell; 3.97
- 415012; NM_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97
- 416084; L16991; Hs.79008; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kinase); 3.95
- 55 422051; AV327548; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; 3.95
- 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine protease; 3.95
- 430770; AA765694; Hs.123296; ESTs; ESTs; 3.94
- 442994; AI026718; Hs.16954; ESTs; ESTs; 3.94
- 420333; AJ001383; Hs.97084; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor, NK-p46); lymphocyte antigen 94 (mouse) homolog (activating NK-receptor, NK-p46); 3.94
- 60 438456; AA913381; Hs.279763; ESTs; ESTs; 3.94
- 422599; BE387202; Hs.118633; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A); 3.93
- 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93
- 424829; NM_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR superfamily, member 16); 3.93
- 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93
- 65 425797; AF002986; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93
- 421910; NM_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associated kinase; 3.92
- 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenase 1; 3.92
- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92
- 400262; ; Hs.75309; Eos Control; Eos Control; 3.90
- 424977; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90
- 70 409799; D11928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90
- 435206; AI432364; Hs.160594; ESTs; ESTs; 3.90
- 439863; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90
- 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90
- 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89
- 75 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89
- 407013; U35637; Hs.83870; gb:Human nebulin mRNA, partial cds; gb:Human nebulin mRNA, partial cds; 3.89
- 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88
- 400261; ; Hs.1802; Eos Control; Eos Control; 3.88
- 80 450447; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88
- 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); 3.87
- 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87
- 417767; BE242241; Hs.82542; acylxyacyl hydrolase (neutrophil); acylxyacyl hydrolase (neutrophil); 3.87
- 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor, beta; 3.87

- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86
 419596; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86
 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pteifler syndrome); fibroblast growth factor receptor 1 (fms; 3.85
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85
 418978; T85295; Hs.268606; ESTs; ESTs; 3.84
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84
 442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84
 447232; AW498834; Hs.327; interleukin 10 receptor, alpha; interleukin 10 receptor, alpha; 3.84
 434689; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyma; 3.83
 432539; AL138169; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83
 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82
 449433; A1672096; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80
 443402; U77846; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis ; 3.80
 422753; A1928995; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79
 421508; NM_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79
 421654; AW163267; Hs.106469; suppressor of var1 (S.cerevisiae) 3-like 1; suppressor of var1 (S.cerevisiae) 3-like; 3.79
 439668; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; frizzled (Drosophila) homolog 8; 3.79
 411125; AA156147; Hs.68877; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78
 425354; A62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78
 423909; AJ223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78
 429687; A1675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77
 414177; A1351355; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repair; 3.76
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase 2; 3.76
 400288; X06256; Hs.149609; Integrin, alpha 5 (fibronectin receptor, alpha polypeptide); integrin, alpha 5 (fibronectin receptor;; 3.75
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75
 405484; ; C3002124; gi|12737280|ref|XP_006682.2| keratin 18 [Homo sapiens]; gi|12737280|ref|XP_006682.2| k; 3.75
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75
 432460; H12912; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74
 431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 to ALU8_HUMAN ALU S; 3.74
 453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell ; 3.74
 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glur; 3.74
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74
 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73
 442233; AW997149; Hs.28439; ESTs, Weakly similar to 138022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to 138022 hypothet; 3.73
 451295; A1557212; Hs.17132; ESTs, Moderately similar to 154374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to 154374 gene ; 3.73
 410772; BE275297; Hs.194685; Homo sapiens clone 24675 mRNA sequence; Homo sapiens clone 24675 mRNA sequence; 3.73
 426251; H24283; Hs.168363; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpo; 3.71
 423523; AW299828; Hs.193580; ESTs; ESTs; 3.71
 413407; A1356293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like ; 3.71
 448336; R53848; Hs.44976; ESTs; ESTs; 3.70
 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70
 416087; AF045184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70
 442200; AW590572; Hs.235768; ESTs; ESTs; 3.70
 414280; BE410769; Hs.75873; zyxin; zyxin; 3.69
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69
 415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69
 439659; AW970780; Hs.59483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69
 446522; NM_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.69
 422785; A1824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68
 401083; ; NM_016582; Homo sapiens peptide transporter 3 (LOC51296), mRNA. VERSION NM_016579.1 GI; NM_016582; Homo sapiens peptide transpor; 3.68
 413048; M53221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68
 452690; A1536070; Hs.15085; ESTs; ESTs; 3.68
 428981; BE313077; Hs.63135; ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 to ALU2_HUMAN ALU S; 3.68
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68
 428579; NM_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68
 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.66
 442013; AA506476; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG Islands. Contains the NIFS gene for
 cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66
 416602; NM_001519; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0610012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;
 3.65
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65
 429303; AW137635; Hs.44238; ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to S65657 alpha-1C; 3.65
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GCN20), member 2; ATP-binding cassette, sub-family F (GCN2; 3.65

- 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65
 450295; AL041949; Hs.24758; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyros; 3.64
 437669; A1358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA657999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep); 3.64
 444388; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63
 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63
 447495; AW401864; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc; 3.62
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62
 411165; NM_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62
 453020; AL162039; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61
 438795; AA825792; Hs.377119; gb:od84b11.s1 NCI_CGAP_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCI_CGAP_Ov2 Homo sapiens ; 3.61
 445515; BE388665; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61
 407797; AK000524; Hs.39350; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60
 423217; NM_000094; Hs.1640; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60
 444985; A1677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60
 437764; AW753676; Hs.39982; zinc finger protein RINZF (NM_023929); zinc finger protein RINZF (NM_023929); 3.59
 427857; AL113017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59
 415020; BE249915; Hs.293533; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STSs, GSSs and CpG islands. Contains the gene for a novel
 glutathione-S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57
 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57
 423576; NM_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57
 440270; NM_015986; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57
 404976; ; NM_014323; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM_014323; Homo sapiens zinc finger prot; 3.57
 449655; AA002008; Hs.188633; ESTs; ESTs; 3.56
 413795; AL040178; Hs.142003; ESTs; ESTs; 3.56
 406859; A1581134; Hs.181357; laminin receptor 1 (67kD, ribosomal protein SA); laminin receptor 1 (67kD, ribosomal prot; 3.56
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56
 447079; AA280057; Hs.105280; ESTs, Weakly similar to DJ963K23.2 [H.sapiens]; ESTs, Weakly similar to DJ963K23.2 [H.sapiens]; 3.56
 424263; M77640; Hs.1757; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high affi; 3.55
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; inducible Ik; 3.55
 426746; J033626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55
 450931; N25156; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55
 425836; AW955696; Hs.90960; ESTs; ESTs; 3.54
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54
 440592; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53
 449027; AJ271216; Hs.22680; dipeptidylpeptidase II; dipeptidylpeptidase II; 3.53
 421662; NM_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53
 422732; AA577455; Hs.24937; transformer-2 alpha (hra-2 alpha); transformer-2 alpha (hra-2 alpha); 3.53
 424870; T15545; Hs.244624; ESTs; ESTs; 3.52
 442794; A1744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51
 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51
 421921; H83363; Hs.355993; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenit; 3.50
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50
 429592; AB029041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49
 430647; AC003682; Hs.127988; ESTs, Weakly similar to Z211_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211_HUMAN ZINC ; 3.47
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77
 430439; AL133561; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76
 435897; AF269223; Hs.128322; t-complex 11 (a murine tcp homolog); t-complex 11 (a murine tcp homolog); 2.53
 417592; AA204664; Hs.182437; ESTs, Weakly similar to I54383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to I54383 chromosom; 2.46
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33
 426627; AF012359; Hs.195685; ESTs; ESTs; 2.12
 438983; AF085884; Hs.20029; proacrosin binding protein sp32 precursor; proacrosin binding protein sp32 precursor; 2.07
 425709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99
 433724; A182749; Hs.144924; serine/threonine protein kinase SSTR; serine/threonine protein kinase SSTR; 1.68
 420710; NM_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

417886 1031334_1 AA210987 D57294 AA214584 AA207006 D56572
 432407 MH1429_12 BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
 AW847519 AA059426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 A1732411 BG778834 BG283641 BE748279
 BE748870 BG319540 BE748864 BF739224 BG986155 AK057283 B1861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
 AA584918 BG959570 BF773485 AL041698 BF959013 R87170 C16859 BF770411 BF771298 A1075321 L13823 AA216700 BF771864 AW861859
 BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
 AW861687 AW821826 B1055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA055592
 AF134164 BF809407 AA218567 BF842863 A1267168 BF876178 BG999253 AW861851 AW858362 A1817548 BF771300 AA113928 AA223422
 AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871084 BE001132 BF826831 AW754298
 AA223267 BG997895 BG997897 AW991957 AA534354 BG319501 BF736309 A1694265 AA045564 BG950256 A1829309 BG987850 BE093175
 BF854337
 427298 115241_1 AA933717 BF061897 AW628327 AA641788 AA400495
 427521 513212_1 AW973352 BF222929 AW016853 BF059130 A1651829 BE551767 AA558414 A1339359 BF059601 A1961162 A1341422 A1206248 A1205165
 AA548736 AA768578 A1539081 AW025957 AA736837 N79575 AW594357 AA480892
 407347 810943_1 T23514 A1655785
 430439 6750_2 AL133561 AL117481 AL122069 AW439292 A1968826 AL041090

TABLE 57C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768, 139702-139893, 140475-14059
402260	3399665	Minus	113765-113910, 115653-115765, 116808-11694
402678	8113438	Plus	37395-37514, 37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3097841	Plus	24712-25374
402677	8113438	Plus	22135-22309, 23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4092817	Minus	24019-24973
405484	5922025	Plus	199214-199579, 199672-199920, 200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix HuD3 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar accession number, GenBank accession number
 UniGeneID: UniGene number
 Pred.ProL.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
 UniGene Title: UniGene gene title
 R1 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.ProL.Domains; R1

430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 35.25
 422282; AF019225; Hs.114309; apolipoprotein L; MolA_ExcB;TM=Y;SS=M; 33.25
 414555; N98569; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 31.68
 415192; D17793; Hs.78183; aldo-keto reductase family 1, member C3 ; aldo_ket_red;TM=M; 31.04
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazaro; none,none; 28.50
 439180; A1393742; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,kinase,Recep_L_domain,Furin-like,kinase,Recep_L_domain,Peptidase_M24; 27.43
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 25.98
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT,none; 25.38
 418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT,none; 25.28
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyraseB,DNA_topoisolV,HATPase_c;SS=M; 23.58
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (ach; ig,kinase;TM=Y;SS=M; 21.24
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 20.45
 447343; AA256641; Hs.236894; ESTs, Highly similar to S02392 alpha-2-m; none,none; 19.78
 408243; Y00787; Hs.624; interleukin 8; HLHPAS;ILB;TM=M; 18.90
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; kinase;TM=M; 18.75
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 18.63
 444381; BE387335; Hs.283713; ESTs, Weakly similar to S64054 hypothet; Collagen;TM=M;SS=M; 18.60
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; ig,Rhbd_glycop;TM=Y;SS=M; 18.55
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M; 18.25

- 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependent, catalytic); PKI;SS=M; 17.73
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIIb, r; Ig;TM=Y;SS=M; 17.68
 450746; D82673; Hs.278589; general transcription factor II, i; none;SH3,PX; 17.12
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 16.88
 420981; A40904; Hs.100724; peroxisome proliferative activated recep; hormone_rec,zf-C4;TM=M; 16.78
 439941; A1392640; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y; 16.75
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 16.56
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys.ig,FAD_Synth,ldh,ldh_C,phkinase;SS=M; 16.43
 414883; AA926560; CDC28 protein kinase 1; CKS; 16.20
 438091; AW373062; nuclear receptor subfamily 1, group I, m; hormone_rec,zf-C4,none; 15.80
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase; PAF-AH,lb,Lipase_GDSL;TM=M; 15.70
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,phkinase;TM=M; 15.63
 422278; AF072873; Hs.114218; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 15.45
 434293; NM_004445; Hs.3796; EphB6; EPH,ld,fn3,phkinase,SAM;TM=Y;SS=M; 15.43
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF,lectin_c,sushi;TM=M;SS=M; 15.28
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 15.10
 416305; AU076628; Hs.79187; coxsackie virus and adenovirus receptor; ig;TM=Y;SS=M; 14.90
 432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib); CBM_21;TM=M; 14.80
 413076; U10564; Hs.75188; wee1 (S. pombe) homolog; phkinase;TM=M; 14.73
 429345; R11141; Hs.199695; hypothetical protein; K,letra,SAM; 14.58
 449230; BE613348; Hs.211579; melanoma cell adhesion molecule; ig,ldh,Ribosomal_L6,F-box;TM=Y;SS=M; 14.55
 421508; NM_004833; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M; 14.53
 446006; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35
 429566; AW139399; Hs.98983; ESTs; none;TM=M; 14.18
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; efhand;SS=M; 14.13
 429673; AA884407; Hs.211595; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;SS=M; 13.90
 426657; NM_015865; Hs.171731; solute carrier family 14 (urea transport); UT;TM=Y; 13.83
 428157; A1738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80
 400843; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 13.78
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,CoaE;TM=M; 13.38
 432314; AA533447; Hs.312989; ESTs; Xlink,none; 13.25
 413109; AW389845; Hs.110855; ESTs; PHO4,none; 13.15
 424490; AJ278016; Hs.55565; ankyrin repeat domain 3; ank,phkinase;TM=M; 13.13
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M; 12.93
 426158; NM_001982; Hs.199087; v-erb-b2 avian erythroblastic leukemia v; Furin-like,phkinase,Recep_L_domain,Furin-like,phkinase,Recep_L_domain,Peptidase_M24; 12.43
 440249; AJ245590; Hs.249175; ESTs; TaD_DNase,phkinase,death,none; 12.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38
 404942; U30825; ; splicing factor, arginine/serine-rich 9; CD38;TM=Y;SS=M; 12.03
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_c6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 11.93
 431395; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT; Aa_trans,none; 11.88
 408000; L11890; Hs.198689; bullous pemphigoid antigen 1 (230/240kD); efhand,spectrin,GAS2,SH3,Plactin,RA_Xylose_isom,Flid,bZIP,Tropomyosin,Myc-LZ,MJdh,C,CH,AlP3;TM=M; 11.88
 412182; AA205588; Hs.155160; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr; 11.85
 433470; AW960564; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_C,THF_DHG_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,M,xan_ur_permease,HCO3_cotransp;TM=M; 11.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus); 7tm_1,7tm_2;TM=Y;SS=M; 11.50
 426761; A1015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586i2022 (f, none;TM=Y;SS=M; 11.48
 439750; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDN; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricin_B,lectin; 11.38
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23
 438729; BE621807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18
 409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate_kin;TM=M; 10.78
 417821; BE245149; Hs.82643; protein tyrosine kinase 9; cofilin_ADF;SS=M; 10.63
 427654; AA410183; Hs.137475; ESTs; ion_trans,vwc,IGFBP,isp_1; 10.58
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member ; aldedh;TM=M;SS=M; 10.53
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor (SH3,PH,RhoGEF;TM=M; 10.53
 449437; A1702038; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone K; none,none; 10.52
 436856; A469355; Hs.127310; ESTs; phkinase,rrm;TM=M; 10.48
 451035; AU076785; Hs.430; plasmin 1 (i isoform); efhand,CH,Adaptin_N;SS=M; 10.38
 418299; AA279530; Hs.83968; Integrin, beta 2 (antigen CD18 (p95), ly; integrin_B,EGF,PSI;TM=Y;SS=M; 10.35
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,integrin_A,FG-GAP;TM=Y;SS=M; 10.34
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN,NA;NA; 10.25
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 10.18
 437852; BE001838; Hs.256897; ESTs, Weakly similar to dJ365012.1 [H.s.]; GPS,7tm_2;TM=Y; 10.13
 400752; ; NM_003105; Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 10.08
 427700; AA262294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPC;TM=M; 10.05
 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,ig,phkinase,PH,spectrin,RhoGEF;TM=M; 10.05
 400496; ; ENSP00000224716; GTP-binding protein SAR; none;TM=Y; 10.01
 413899; AF083892; Hs.75608; tight junction protein 2 (zona occludens); SH3,PDZ,Guanylate_kin;TM=M; 10.00
 404568; ; NM_022071; Homo sapiens hypothetical pro; SH2;TM=M; 10.00
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 9.93
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; efhand,kazal,arf,ras,7tm_1;TM=M; 9.90
 413441; A1929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 9.90
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,IRK;TM=M; 9.88
 452269; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; phkinase;TM=M; 9.85
 439223; AW238299; Hs.250818; UL16 binding protein 2; ldl_recept_a,PKD,MHC_1;TM=M;SS=Y; 9.83
 429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y_phosphatase;TM=Y;SS=M; 9.80
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; Rhodanese,DSPC,Y_phosphatase;TM=M; 9.73
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPC;TM=M; 9.72
 403912; ; C5000394; gij12737280[re]XP_006682.2; k; none;TM=M; 9.70
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f, none,spectrin,SH3,PH,CH; 9.70

- 428428; AL037544; Hs.184298; cyclin-dependent kinase 7 (homolog of Xc; pkinase; TM=M; 9.68
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3_Y_phosphatase; TM=M; 9.63
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 9.63
 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic; PI3_P14_kinase, FAT, FATC; TM=M; 9.55
 430259; BE550182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3_RA_RasGEF; TM=M; SS=M; 9.50
 428520; AA331901; Hs.184736; hypothetical protein FLJ10097; none; TM=M; 9.50
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; 9.50
 448913; AA194422; Hs.22564; myosin VI; mm.zf-RanBP, pkinase, GST_C, Ets, SAM_PNT, ABC2_membrane, myosin_head, IQ, Myosin_N, bZIP, zf-C2H2, PHD, BTB, TFIIS, AT_hock, SAM; TM=M; 9.50
 414911; NM_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40, homeobox, LIM; TM=M; 9.48
 451295; AI557212; Hs.17132; ESTs, Moderately similar to I54374 gene; pkinase, DAG_PE-bind, pkinase_C, OPR, none; 9.45
 402328; ; Target Exon; pkinase; TM=M; 9.44
 443710; AI928135; Hs.9691; Homo sapiens cDNA: FLJ23249 fis, clone C; G-alpha; none; 9.42
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; 9.42
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfurylase, PRK, Thymidylate_kin, SS=M; 9.40
 418827; BE327311; Hs.47166; HT021; none; TM=M; 9.40
 440675; AW005054; Hs.47883; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase; none; 9.35
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; SS=M; 9.28
 410668; BE379794; Hs.65403; hypothetical protein; death, TNFR_c6; TM=Y; SS=M; 9.25
 430024; AI808780; Hs.227730; integrin, alpha 6; integrin_A, FG-GAP; TM=Y; SS=M; 9.23
 452696; AI826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate_kin, PDZ, SH3; 9.13
 434263; N34895; Hs.44648; ESTs; Ig; none; 9.13
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal_S14, ank, pkinase, death; none; 9.10
 429332; AF030403; Hs.199263; Ste-20 related kinase; pkinase, melalithio; TM=M; SS=M; 9.08
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, integrin_B; SS=M; 9.08
 443951; F13272; Hs.111334; ferritin, light polypeptide; PMP22, Claudin; none; 9.07
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK, CoaE; 8.98
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3; TM=M; 8.93
 438000; AI825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none; TM=M; 8.90
 446620; AA128808; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 8.90
 436075; BE090176; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 8.88
 437056; AI147061; ; gbok33a11.s1 Soares_NSF_F8_9W_OT_PA_P_S; none, spectrin, SH3, PH, CH; 8.78
 445496; AB007860; Hs.12802; development and differentiation enhancer; SH3, ank, PH, ArfGap; TM=M; 8.78
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75
 434608; AA805443; Hs.179909; hypothetical protein FLJ22995; none; TM=M; 8.70
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.68
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none; TM=M; SS=M; 8.65
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept Y_phosphatase; SS=M; 8.65
 430397; AI924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp; TM=Y; 8.64
 448888; AW196663; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 8.60
 442994; AI026718; Hs.16954; ESTs; ank, pkinase, death, Ribosomal_S14; 8.60
 429109; AL008637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3, OPR, PX; TM=M; 8.60
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8_HUMAN ALU S; none, 7tm_1; 8.55
 437763; AA469369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP, pkinase, DAG_PE-bind, RBD; 8.43
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE:451939, mRNA se; none, none; 8.40
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 8.39
 448209; AW160489; Hs.20709; tetraspan 5; transmembrane4; TM=Y; SS=M; 8.33
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none, none; 8.33
 445350; AF052112; Hs.12540; lysophospholipase 1; abhydrolase_2; TM=M; 8.31
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7tm_1; TM=Y; SS=M; 8.30
 445633; AI453388; Hs.17287; ESTs, Weakly similar to S26689 hypotheti; IRK; none; 8.28
 446719; W39500; Hs.301872; hypothetical protein MGC4840; AAA, SKI; TM=M; 8.23
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none, none; 8.20
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, fo; Ig, pkinase; TM=Y; SS=M; 8.18
 416094; AW595512; Hs.225977; nuclear receptor coactivator 3; none, none; 8.15
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zf-C2H2, SET; 8.15
 417366; AL037228; Hs.82043; D123 gene product; NUDIX, secY, E1_dehydrog, transket_pyr; TM=Y; SS=M; 8.13
 431236; AV656840; Hs.285115; Interleukin 13 receptor, alpha 1; fn3; TM=Y; SS=M; 8.10
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none; TM=M; SS=M; 8.09
 425424; NM_004954; Hs.157199; ELK1 motif kinase; pkinase, UBA, KA1; TM=M; 8.08
 422573; AW297985; Hs.295726; integrin, alpha V (vitronectin receptor, FG-GAP, integrin_A, none; 8.05
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg; TM=M; SS=M; 8.03
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase; SS=M; 8.03
 404891; ; Target Exon; none, none; 7.95
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none, none; 7.93
 452888; AW955454; Hs.30942; ephrin-B2; Ephrin, fn2; TM=Y; SS=M; 7.93
 433211; H11850; Hs.12808; MARK; pkinase, UBA, KA1; SS=M; 7.91
 438485; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase, ABC1; none; 7.90
 413219; AA878200; Hs.118727; Homo sapiens cDNA FLJ13692 fis, clone PL; HLH, death, TNFR_c6, Acyl-CoA_hydro; 7.90
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan_ur_permease, RA; 7.88
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like, pkinase, Recep_L_domain, YLP; TM=Y; SS=M; 7.86
 405036; ; NM_021628; Homo sapiens arachidonate lip; lipoxigenase, complex1_49kD, PLAT; TM=M; 7.83
 418529; AW005695; Hs.250697; TRK-fused gene; Band_41, ERM, pkinase, LRR, LRRCT, MAM, Nucleoplasmin, Tropomyosin, OPR, filament, bZIP, G-gamma, M, DUF164; TM=M; 7.83
 431912; AI660552; Hs.76549; ESTs, Weakly similar to A58154 Abl subst; none, Acyl-CoA_dh, Acyl-CoA_dh_N; 7.80
 432981; NM_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS, Aa_trans; TM=M; 7.78
 422940; BE077458; ; gb:RC1-BT0606-090500-015-b04 BT0606 Homo; Sec7, PH, ANF_receptor, lig_chan, WD40, IRK; 7.78
 446636; AC002563; Hs.15767; ciron (rho-interacting, serine/threonin; CNH, DAG_PE-bind, PH, Involucrin, M; TM=M; 7.78
 431183; NM_006855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 7.78
 400845; ; NM_003105; Homo sapiens soritin-related; EGF, fn3, Idl_recept_a, Idl_recept_b, granulin, BNR; TM=Y; SS=M; 7.73
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromoso; ABC_tran, M, SMC_N, SMC_C, DUF164, none; 7.73
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ_con_Y_phosphatase, SH2; 7.70
 403212; ; NM_019595; Homo sapiens intersectin 2 (IT; SH3, ehfand, C2, PH, RhoGEF; TM=M; 7.70
 441190; H09073; Hs.25046; ESTs; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase, none; 7.68

- 409745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7m_1,zf-C3HC4,ln3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 7.68
 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,pkinase;SS=M; 7.65
 447898; AW969638; Hs.112318; 6.2 kd protein; none;none; 7.65
 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 7.63
 401927; ; C17000914;gij8394367/refNP_058549.1|s; none; 7.60
 407347; AA829847; ; gb:od40d07.s1 NCI_CGAP_GCB1 Homo sapiens; RhoGAP,SH2,pkinase,POLO_box;none; 7.58
 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fis, clone H; SH3;none; 7.57
 429952; AF080158; Hs.226573; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 7.55
 445800; AA126419; Hs.32944; inositol polyphosphate 4-phosphatase, ty; none;none; 7.55
 421489; AJ922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylate kinase,SRP54;TM=M; 7.50
 430570; AI417881; Hs.292464; ESTs; 7m_2,Fz,Fritzled,none; 7.50
 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
 420676; AI434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind,none; 7.48
 444252; R21135; Hs.54985; ESTs; none;none; 7.47
 414914; U49844; Hs.77613; alaxia telangiectasia and Rad3 related; FAT,FATC,PI3_P14_kinase;TM=M; 7.47
 443426; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
 418546; AA224827; ; gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens ; vwa,Integrin_A,FG-GAP,none; 7.45
 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fis, clone L; none;NA;NA; 7.43
 452007; AA426234; Hs.34906; ESTs, Weakly similar to T17210 hypotheit; none,pkinase; 7.40
 432407; AA221036; ; gb:zr03f12.r1 Stralagene NT2 neuronal pr; DEAD,helicase_C,rm,Ndr,Cys_knot,TIL,vwa,vwc,vwd,IQ,Rlla,abhydrolase,TGF-beta,DUF139,TPR,OSPc,tsp_1,Ribosomal_S21,rvp;TM=M; 7.40
 424943; AU077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,dENN,vDENN;TM=M; 7.40
 421423; NM_014922; Hs.104305; death effector filament-forming Ced-4-lf; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
 417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 7.38
 430016; NM_004738; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
 422813; AV656571; Hs.121058; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFp761G18121 (; none,spectrin,SH3,PH,CH; 7.25
 409213; U61412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M; 7.24
 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 7.19
 407591; NM_000910; Hs.37125; neuropeptide Y receptor Y2; 7m_1;TM=Y; 7.18
 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
 450285; AW383256; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
 403344; ; NM_000341;Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage_CLC;TM=Y; 7.14
 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 7.14
 404875; ; NM_022819;Homo sapiens phospholipase A2; phoslip;SS=M; 7.11
 433618; AA602539; Hs.345494; ESTs; G-alpha_A_deaminase; 7.10
 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fis, clone C; Sulfate_trans,STAS,HMG_box; 7.08
 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05
 426655; AL049589; Hs.171723; neuronal cell death-related protein; TRFD-31;TM=M; 7.05
 423387; AJ012074; ; vasoactive intestinal peptide receptor 1; 7m_2,HRM,CSD;TM=Y;SS=M; 7.03
 400211; ; NM_003899;Homo sapiens PAK-interacting ; SH3,PH,RhoGEF, Terpene_synth;TM=M; 7.03
 438150; AA037534; Hs.342874; transforming growth factor, beta receptor; zona_pellucida;none; 6.93
 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M; 6.93
 405275; AB028969; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
 415392; Z44067; Hs.10957; ESTs; PIP5K;none; 6.89
 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadiillo_seg;none; 6.88
 429663; M68874; Hs.211587; phospholipase A2, group IVA (cytosolic, ; C2,PLA2_B;TM=M; 6.85
 427832; AF038362; Hs.180930; TBP-associated factor 172; SNF2_N,helicase_C,Armadiillo_seg,HEAT;TM=M; 6.83
 447887; AA114050; Hs.19949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M; 6.80
 400158; ; ENSP00000244302;CDNA FLJ11591 fis, clone; Sm;SS=M; 6.78
 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,lon_trans,PAC,PAS;none; 6.78
 400844; ; NM_003105;Homo sapiens sortilin-related; EGF,ln3,ld_recept_a,ld_recept_b,granulin,BNR;TM=Y;SS=M; 6.73
 457238; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase; 6.73
 404440; ; NM_021048;Homo sapiens melanoma antigen; , MAGE;TM=M; 6.73
 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Ets,SAM_PNT;TM=M; 6.70
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotat; Pribosyltran,OMPdecase;TM=M; 6.70
 429429; AA829725; Hs.334437; hypothetical protein MGC4246; none,transmembrane4; 6.65
 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;SS=M; 6.64
 408638; AW451353; Hs.173328; ESTs; B56;none; 6.63
 408056; AA312329; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
 401057; BE563195; ; eukaryotic translation elongation factor; lon_trans,IQ;TM=Y; 6.60
 446526; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fis, clone PL; none;none; 6.60
 400528; ; NM_020975;Homo sapiens ret proto-oncoge; cadherin,pkinase;TM=Y;SS=M; 6.58
 418562; R60669; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
 453826; AL138129; ; gb:DKFp547F152_r1 547 (synonym: hfbt1) ; PK,PK_C;none; 6.55
 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFp547C136 (fr,ABC_tran,GTP_EFTU,ABC_membrane;none; 6.54
 415088; AI077288; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 6.50
 453489; AA300067; Hs.33032; hypothetical protein DKFp434N185; F5_F8_type_C,pkinase,Ets,F5_F8_type_C,pkinase,Ets; 6.47
 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rrm,NTF2;TM=M; 6.46
 456376; AA663904; Hs.89862; TNFRSF1A-associated via death domain; death;TM=M; 6.46
 441712; AW391927; Hs.7946; KIAA1288 protein; AIP3;TM=M; 6.44
 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7m_1; 6.43
 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 6.43
 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
 438941; AF075047; Hs.31864; ESTs; Ca_channel_B,SH3,arf;none; 6.40
 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB;none; 6.33
 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypotheit; lipoxigenase,PLAT;none; 6.33
 433255; AI274270; Hs.96840; KIAA1527 protein; MHCK_EF2_kinase;TM=M;SS=M; 6.33
 427801; AW979155; Hs.298275; amino acid transporter 2; Aa_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubiquitin, BAG, Tropomyosin; 6.30
 438454; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none, none; 6.30
 453977; AA886006; Hs.250427; ESTs; pkinase, P2X_receptor, E1-E2_ATPase, Hydrolase; 6.30
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras, arf, PP2C; TM=M; 6.30
 15 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA_gyraseB, DNA_topoisolV, HATPase_c, DNA_gyraseB, DNA_topoisolV, HATPase_c; 6.29
 404342; ; C7002192; gij7299207[gibAAAF54404.1] (AE0; none; TM=M; 6.27
 409274; NM_003930; Hs.52644; SKAP55 homologue; SH3, PH, SS=M; 6.25
 419593; AA133749; Hs.301350; FYD domain-containing ion transport reg; ATP1G1, PLM_MAT8; TM=Y; SS=M; 6.23
 405429; ; Target Exon; Y_phosphatase, none; 6.23
 10 404975; AL042279; ; uncharacterized hypothalamus protein HT0; kringle; TM=Y; SS=M; 6.20
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin, EGF, ig, Neuregulin, EGF, ig; 6.18
 446863; AW452756; Hs.16354; hypothetical protein FLJ10955; DEAD, helicase_C, rrm, Ndr, Cys_knot, TIL, vwa, vwc, vwd, IQ, Rla, abhydrolase, TGF-beta, DUF139, TPR, DSPc, lrp_1, Ribosomal_S21, vrp; TM=M; 6.18
 15 433233; AB040927; Hs.301804; KIAA1494 protein; SH3, z-C3HC4; TM=M; 6.15
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none; TM=Y; 6.15
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none, none; 6.14
 447727; AI421079; ; tumor necrosis factor receptor superfamily; none, synaptobrevin; 6.13
 401536; ; NM_002530; Homo sapiens neurotrophic tyrosine kinase, LRR, LRRNT, LRRCT; TM=M; SS=M; 6.11
 20 444317; A140566; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H.; PAN, kringle, trypsin, PI-PLC-X, C2, SH2, PH, SH3, PI-PLC-Y, PAN; 6.10
 427557; NM_002659; Hs.179657; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; SS=M; 6.08
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; 6.08
 450107; AI873287; Hs.257812; ESTs; ICE_p20, DED; TM=M; 6.05
 418175; AW967054; Hs.205312; ESTs, Weakly similar to I38022 hypothet; z-C2H2, BTB, K_tetra, Syntaxin, none; 6.05
 25 408983; NM_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC_tran, ABC_membrane, PRK, Bac_expor_3; TM=Y; 6.05
 438738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, integrin_B; TM=Y; 6.03
 427625; AF008216; Hs.285013; putative human HLA class II associated p; none, none; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine-serine-rich 5; DSPc, Rhodanese, none; 6.03
 446650; AB016525; Hs.15813; solute carrier family 22 (organic cation; sugar_tr; TM=Y; SS=M; 6.03
 30 405102; ; C15001220; gij4469558[gibAAD21311.1] (AF; DAG_PE-bind, PH, RhoGEF, DC1; SS=M; 6.03
 400121; ; Eos Control; SH3, PH, RhoGEF, Terpene_synth; TM=M; 6.03
 415327; H22769; ; gb:ym54602.r1 Soares infant brain 1N1B H; SH3, PDZ, Guanylate_kin; SS=M; 6.03
 404148; ; NM_002944; Homo sapiens v-ros avian UR2; ; fn3, pkinase, DUF139; TM=Y; SS=M; 6.03
 405531; ; Target Exon; PDZ, CARD, Guanylate_kin; TM=M; 6.00
 35 433363; AA584829; Hs.275153; non-metastatic cells 2, protein (NM23B); NDK, none; 6.00
 427270; H47921; Hs.174139; chloride channel 3; voltage_CLC, CBS, none; 5.99
 423774; L39064; Hs.1702; interleukin 9 receptor; none; TM=M; SS=M; 5.98
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked; pkinase, TBC; 5.98
 411040; AF007393; Hs.177574; protein-kinase, Interferon-inducible dour; HLH; TM=M; 5.95
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer, 7tm_1, none; 5.88
 40 453902; BE502341; Hs.3402; ESTs; none, none; 5.88
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans; TM=Y; 5.86
 436154; AA764950; Hs.119898; ESTs; ethand, DAG_PE-bind, DAGKa, PHD, DAGKc, PSI, none; 5.85
 455358; AW902641; ; gb:QV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase, Somatomedin_B, Phosphodiesterase; 5.83
 414108; AI267592; Hs.75761; SFRS protein kinase 1; ank, PH, Oxysterol_BP, pkinase; TM=M; 5.82
 45 452547; AA335295; Hs.74120; adipose specific 2; LEA; TM=M; 5.82
 415204; T27434; ; gb:hbc2294 Human pancreatic islet Homo s; Na_Ca_Ex, Calx-beta, none; 5.80
 435563; AF210317; Hs.95497; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; 5.78
 456097; C15702; Hs.288028; ESTs, Moderately similar to 154374 gene; dsrm, FKBP; 5.78
 422445; M23114; Hs.1526; ATPase, Ca transporting, cardiac muscle; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; TM=Y; 5.77
 50 436246; AW450963; Hs.119991; ESTs; none, DNA_gyraseB, DNA_topoisolV, HATPase_c; 5.75
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC_tran, PRK; TM=Y; SS=M; 5.75
 425854; AA749190; ; ESTs; RhoGAP, SH2, pkinase, POLO_box, none; 5.74
 424160; T74062; ; gb:yc8f101.r1 Soares infant brain 1N1B H; ROK, none; 5.70
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor; PTN_MK; TM=M; SS=Y; 5.69
 55 437613; R19892; Hs.10267; MIL1 protein; none, none; 5.68
 410820; BE391493; Hs.16475; Human DNA sequence from clone RP5-852M4; TBC; SS=M; 5.68
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pkinase, PBD; TM=M; 5.66
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; 5.63
 406930; U04691; ; gb:Human olfactory receptor (OR17-219) g; none; TM=Y; SS=M; 5.60
 60 401044; ; Target Exon; none, ICE_p20, ICE_p10, CARD, Peptidase_M1; 5.56
 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; pkinase, ICE_p10, ICE_p20; TM=M; SS=M; 5.55
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RP; aa_permeases, pyridoxal_deC, bromodomain, PHD, MBD, AT_hook, DDT, PI3_PI4_kinase, FAT, FATC, BoA, RUN; TM=M; 5.53
 65 426248; T18988; Hs.293658; ESTs; pkinase, none; 5.50
 418426; NM_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pkinase, death; TM=M; 5.43
 417086; AA194446; ; ESTs, Weakly similar to S55024 nebulin; ; ank, death, ZU5, EGF, kringle, trypsin, Nebulin, LIM; SS=M; 5.43
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled; 7tm_1, SH2; TM=Y; SS=M; 5.40
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF; SS=M; 5.40
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC:16169, mRNA, cont; pkinase, TBC, Rhodanese; TM=M; 5.38
 70 419355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 5.35
 411188; BE161168; ; gb:PMO-HT0425-170100-002-a10 HT0425 Homo; adenylatekinase, none; 5.35
 422461; NM_003417; Hs.117077; zinc finger protein 264; z-C2H2, KRAB, TFIIS; TM=M; 5.28
 426348; BE466586; Hs.17433; hypothetical protein FLJ20967; none, none; 5.25
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPc, Y_phosphatase, Ribosomal_S3_N; TM=M; 5.23
 75 429592; AB029041; Hs.209846; KIAA1118 protein; Troponin, Exo_endo_phos, IQ; TM=M; 5.22
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER_lumen_recept, Ribosomal_L11, Ribosomal_L11_N; TM=Y; SS=M; 5.21
 434368; AW519020; Hs.73893; dopamine receptor D2; pkinase, SH3, none; 5.15
 405586; ; NM_000299; Homo sapiens plakophilin 1 (ec; Armadillo_seg; TM=M; 5.13
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylatekinase, none; 5.12
 80 407443; AF227138; ; gb:Homo sapiens candidate taste receptor; none; TM=Y; SS=M; 5.11
 416817; AA398045; Hs.104679; ESTs; Furin-like, pkinase, Recep_L_domain, fn3, none; 5.10
 401886; ; NM_021783; Homo sapiens XEDAR (XEDAR), mR; TNFR_c6; TM=M; SS=M; 5.08
 410314; AW860708; Hs.18851; hypothetical protein FLJ10875; myb_DNA-binding, PAH, BAH, bromodomain, PHD, SET; TM=M; 5.08

- 401579; AL031447; Homo sapiens, clone IMAGE:4053044, mRNA; Neur_chan_LBD, Neur_chan_memb, none; 5.05
- 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-; PABP, rm, pkinase, 14-3-3; 5.05
- 417529; AA203634; gb:zx58b09.r1 Soares_fetal_liver_spleen; pkinase, UBA, KA1, none; 5.03
- 417527; AA203524; gb:zx56e10.r1 Soares_fetal_liver_spleen; SH3; SS=M; 4.98
- 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; pkb; TM=M; 4.96
- 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid_phosphat, none; 4.93
- 404298; C6001238; gi|121715|sp|P26697|GTA3_CHICK; none, GST_C, GST_N, pkinase; 4.85
- 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; none; TM=M; 4.82
- 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran, ABC_membrane; TM=Y; 4.73
- 422366; TB3882; Hs.97927; ESTs; pkinase, none; 4.64
- 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; 4.48
- 426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fis, clone H; Esterase, enolase, Peptidase_S9; TM=M; 4.45
- 439605; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 4.40
- 400749; NM_003105; Homo sapiens sorfilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.38
- 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4; TM=Y; SS=M; 4.33
- 444006; BE395085; Hs.10086; type I transmembrane protein Fn14; ldl_recept_a, PKD, MHC_I; TM=M; SS=Y; 4.31
- 400751; NM_003105; Homo sapiens sorfilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.18
- 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; SS=M; 3.90
- 422152; AA90227; Hs.112282; solute carrier family 30 (zinc transport; none, none; 3.88
- 458760; AA98631; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3_cotransp, SH3, RhoGAP, xan_ur_permease, FCH; SS=M; 3.85
- 441218; BE327561; Hs.202345; ESTs; none, WD40, E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; 3.78
- 419073; AW972170; Hs.183918; Homo sapiens cDNA FLJ12797 fis, clone NT; death, ZU5; SS=M; 3.76
- 451385; AA017656; gb:zx39h01.r1 Soares retina N2b4HR Homo; Alrophin-1, enolase, Alrophin-1_Y_phosphatase, SH2, fibrinogen_C, TIM; 3.60
- 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase, DAG_PE-bind, pkinase_C, OPR; TM=M; 3.30
- 409582; R27430; Hs.271565; ESTs; none, Neur_chan_LBD, Neur_chan_memb; 3.28
- 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1_LC3; SS=M; 3.23
- 436740; AW975133; gb:EST387239 MAGE resequences, MAGN Homo; none, EPH_Ibd, fn3, pkinase, SAM; 3.20
- 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked; none, IRK; 3.20
- 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none, NA; NA; 3.13
- 418764; N30531; Hs.42215; protein phosphatase 1, regulatory subunit; none, none; 3.10
- 400846; sorfilin-related receptor, L(DLR class); EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 3.09
- 422005; BE266556; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (f; none, Na_H_Exchange; 3.03
- 426440; BE382756; Hs.169902; solute carrier family 2 (facilitated glu; sugar_tr; TM=Y; SS=M; 3.02
- 424187; AA336561; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK, none; 2.98
- 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member, death, TNFR_c6; TM=Y; SS=M; 2.93
- 401279; C13000351; gi|2494033|sp|Q64398|KGDG_MES; none, none; 2.88
- 406671; AA129543; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema, pkinase, TIG, PSI; none; 2.83
- 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK; TM=Y; 2.80
- 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase; TM=M; 2.75
- 441699; AW511126; Hs.127572; ESTs; none, Aa_trans; 2.73
- 458781; AJ444821; Hs.63085; ESTs, Weakly similar to MPP3_HUMAN MAGUK; SH3, PDZ, Guanylate_kin, L27; TM=M; 2.73
- 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4; TM=Y; SS=M; 2.70
- 453487; R31770; Hs.56562; ESTs; 7tm_1, none; 2.68
- 421279; AW664878; Hs.106645; ESTs; pkinase, none; 2.68
- 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none, none; 2.65
- 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc; TM=M; 2.63
- 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF; TM=Y; 2.62
- 425212; AW962253; Hs.171618; ESTs; pkinase, none; 2.60
- 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 2.58
- 423629; AW021173; Hs.18612; Homo sapiens cDNA: FLJ21909 fis, clone H; voltage_CLC, CBS, none; 2.55
- 456737; BE247203; Hs.124831; CGI-67 protein; abhydrolase_2; TM=M; SS=M; 2.53
- 421585; U95626; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1; TM=Y; SS=M; 2.53
- 424028; AF055084; Hs.153692; Homo sapiens cDNA FLJ14354 fis, clone Y7; none, none; 2.50
- 448324; AJ571356; Hs.34174; ESTs, Moderately similar to ALU8_HUMAN A; ICE_p20, CARD, ICE_p10, none; 2.50
- 402256; Target Exon; pkinase, UBA, none; 2.43
- 452256; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fis, clone HE; GDI, 7tm_1, none; 2.40
- 419169; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothet; none, spectrin, SH3, PH, CH; 2.40
- 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP_binding, ion_trans; TM=Y; 2.35
- 419630; W57756; gb:zd20g10.r1 Soares_fetal_heart_NbHH19V; zf-C3HC4, none; 2.35
- 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 2.35
- 400704; Target Exon; lig_chan, SBP_bac_3, ANF_receptor; TM=Y; SS=M; 2.33
- 400149; Eos Control; acid_phosphat; TM=Y; SS=M; 2.30
- 459327; AW149706; Hs.7859; gb:zx41d02.x1 NCI_CGAP_Bm50 Homo sapien; PHD, PWWP, SET, pkinase, ig; 2.30
- 452220; BE158006; Hs.212296; ESTs; Integrin_AFG-GAP, none; 2.25
- 416690; H84078; Hs.108551; ESTs; pkinase, none; 2.23
- 408354; AJ382803; Hs.159235; ESTs; none, none; 2.23
- 452203; X57522; transporter 1, ATP-binding cassette, sub; ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 2.21
- 405093; C12001101; gi|7522643|pir|T32733 AMPA g; none, none; 2.20
- 412723; AA648459; Hs.335951; hypothetical protein AF301222; none; TM=M; 2.20
- 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 2.18
- 417185; NM_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; ParA, fer4_NiH, ArsA_ATPase; TM=M; 2.18
- 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 2.18
- 413627; BE182082; Hs.246973; ESTs; Armadillo_seg, IBB; TM=M; 2.18
- 407415; AF073328; gb: Homo sapiens tetracycline transporter; none, none; 2.15
- 450592; AJ701555; Hs.202562; ESTs; pkinase, none; 2.15
- 428767; AJ421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1; none, pkinase, ig; 2.15
- 429012; AW629596; Hs.194726; BCL2-associated atazanone 4; Sm, BAG; SS=M; 2.15
- 419122; AJ401360; Hs.44410; ESTs; ABC_tran, ABC_membrane, none; 2.10
- 446420; AW015693; Hs.135614; ESTs; ion_trans, none; 2.05
- 420076; AA827860; Hs.293717; ESTs; DUF59, pkinase; 2.05
- 409416; AW388359; Hs.10667; ESTs; transmembrane4; TM=Y; SS=M; 2.03
- 428766; AA477989; Hs.98800; ESTs; TPR, 7tm_1; 2.03
- 427001; NM_006482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; TM=M; 2.03

453709; AL119133; ; protein kinase C substrate 80K-H; none,histone; 2.03
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00
 456772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; Ig;TM=Y;SS=M; 1.88
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7tm_1; 1.65
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; Ig;TM=Y;SS=M; 1.00
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 58B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
414883	8371_2	AF274943 BG494894 A1719075 AA908783 A1935150 A1422691 AA910644 AA583187 BM272167 A1828996 AA527373 AW972459 A1831360 AA772418 A1033892 AA100926 AU154749 A1459432 A1423513 A1094597 AA740817 A1991988 A1090262 A1312104 B1256707 AA459522 AA416871 A1075239 A1339996 AA701623 A1139549 A1336880 AA633648 A1989380 A1362835 AA399239 A1146955 BF514270 N92892 A1348243 A1278887 AA459292 A1494230 BF507531 A1492600 AA962596 AW613002 AA293140 AA235549 BF108854 AA954344 A49682 A1457100 AW589407 AW300758 BE220715 BE220698 BE568091 BM009647 BF000351 A1537692 A1033723 A1857576 AA584410 AW371667 BM172363
438091	22448_1	AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646184 AV646179 AW880409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 A1681352 AA358689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646384 AV687497 BF155183 AV646370 AW797876 A1906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709126 BE673807 A1923886 AA947932 A1276125 A1185720 AW510698 AA987230 BE467708 AW898628 AW898544 A1146984 AW043642 A1288245 A1186932 A1635262 A1139455 A1298739 A1813854 A1024768 BE699445 BE699444 A107807 D52654 A124518 A1004723 A1698085 AW087420 A1565133 AA845571 AW898622 BF110144 AW513280 A1061126 BF362770 A1268939 A1435818 BF475318 A1024767 BE174213 AA757598 AA513019 AA902959 A1860794 A1334784 BF108411 BM310532 AW513771 A1951391 A1337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 A1922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699456 D52477 D55017 BF955933 BG623563 AV646254 AA463522 B1003244 A1299190 W040186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 R83430 Z29922 T85791 W03942 H63289 A1091537 BF086583 AA345570 H48870 H80720 T83523 B1039626 B1037700 R00353 BF155184 N98343 N79072 H01812 T55581 X75584 AL573167 A1445461 A1453743 A1983655 A1564644 AA977180 A1694111 A1591358 AW071625 A1678712 A1720939 A1927769 BE439796 A1963432 AA292956 AW192593 A1865838 A1696905 A1424384 A1161312 A1911921 A1597801 B1494959 A1240988 A1492554 AW262737 BE040433 AW008570 AW629505 B1494958 AA088439 AA705057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 A1799814 AA129575 A1671727 A1470033 BE646195 AW779725 AA903050 AA147228 AA404570 A1075878 W38161 A1972739 AW673152 AA723200 C06123 BF057147 AA527686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 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45	453826 447727 400121	366136_1 10123_14 3532_1	
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65	424160 417086	5320_3 1154_2	
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 R58506

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9673-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36481
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84974-85125
405036	7543748	Minus	121957-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos HuO3
 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 8.2. The "average" prostate cancer level was set to the
 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50th percentile amongst non-malignant tissues. In order to remove gene-specific
 background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the
 ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 UnigenTitle: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigen ID	Unigen Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420923	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
416854	H40164	Hs.80296	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	AI093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microseminoprotein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nel (chicken)-like 2	54.6
428398	AI249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (lazarol	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7

	437145	AF007216	Hs.5462	solute carrier family 4, sodium bicarbon	49.6
	446057	AJ420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
5	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	415314	N88802	Hs.5422	glycoprotein M6B	43.2
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
	416585	X54162	Hs.79386	telomodin 1 (smooth muscle)	39.0
15	447726	AL137638	Hs.19368	matrilin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, lodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.5
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
20	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	35.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	35.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
25	415539	AI733881	Hs.72472	BMP-R1B	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
30	452114	N22687	Hs.8236	ESTs	34.0
	426990	AL044315	Hs.173094	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297435	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AI918950	Hs.123642	EphA3	32.7
35	427358	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HM409 unknown mRNA	32.4
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
40	408380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	31.4
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	31.2
	408001	AA046458	Hs.95296	ESTs	30.8
45	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442993	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N46243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HT021	29.0
	410330	AW023630	Hs.46786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
55	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
60	409361	NM_005982	Hs.54416	sinu oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
65	403047			NM_005656:Homo sapiens transmembrane pr	27.2
	407709	AA458135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415989	AI267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
70	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278595	Homo sapiens protein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer antig	26.4
	426457	AW894667	Hs.169965	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
	400292	AA250737	Hs.72472	BMP-R1B	26.0
75	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448106	AI800470	Hs.171941	ESTs	25.5
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
80	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	418961	AW967646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheti	24.5
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	24.4
5	418396	AI765805	Hs.26691	ESTs	24.1
	412088	AI689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abt-interacting protein ArgBP2	24.0
	409619	AK001015	Hs.55220	BCL2-associated atlanogene 2	23.9
10	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SW/SNF related, matrix associated, acti	22.9
	440260	AI972867	Hs.7130	copline IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 [Alport syndr	22.0
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
20	450642	R39773	Hs.7130	copline IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	21.6
	408000	L11690	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
	416655	AW988613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
40	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157646	Hs.153506	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420611	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049176	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
50	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78885 serine/th	20.5
	424897	D63216	Hs.153684	frizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263*:HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14529	20.3
	429918	AW873986	Hs.119383	ESTs	20.2
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
65	441690	R81733	Hs.33106	ESTs	19.9
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PN0099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431556	AF016028	Hs.183428	sarcomspan (Kras oncogene-associated gene	19.6
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibito	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	LM domain only 4	19.2
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
80	409062	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latexin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001529	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

	445929	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
5	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407690	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	18.7
	418819	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443966	Hs.31595	ESTs	18.4
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
20	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439569	AW602166	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424682	AW604804	Hs.151717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	17.8
30	431121	AW971157		gb:EST383245 MAGE resequences, MAGL Homo	17.8
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
40	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447809	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
45	421823	N40850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp564B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp564O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.159983	ESTs	16.9
	432966	AA650114	Hs.325198	ESTs	16.9
55	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603306		gb:np12d11.s1 NCL_CGAP_Py3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF085833	Hs.135624	ESTs	16.8
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
60	442064	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zm61g01.r1 Stralagene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	16.4
	443801	AW206942	Hs.253594	ESTs	16.3
	437536	X91221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	16.2
70	409060	AI815867	Hs.50130	necdin (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30088	ESTs	16.0
75	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	426501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	15.6
15	434988	AI418055	Hs.161160	ESTs	15.6
	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.5
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AI935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens prostate mRNA, complete cds	15.4
	443574	AI081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418693	AI750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AI963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligas	15.1
	427707	NM_005578	Hs.180398	LM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AI557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.184780	ESTs	15.0
	410297	AA148710	Hs.79914	lumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AI699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	426044	AA502490	Hs.336695	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.181326	KIAA1073 protein	14.7
	407634	AW016589	Hs.136414	UDP-GlcNAc6betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simi	14.7
	433226	AW503733	Hs.9414	KIAA1488 protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCLE_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0966 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proli	14.5
75	410339	AI916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.146858	protocadherin 10	14.5
	431933	AI187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413786	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
5	416836	D54745	Hs.80247	cholecystokinin	14.4
	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
10	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133396	Hs.74621	prion protein (p27-30) (Creutzfeld-Jakob)	14.2
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
15	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl)	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA453276	Hs.288906	WW Domain-Containing Gene	14.1
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
20	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170055	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	13.9
	418848	AI820961	Hs.193465	ESTs	13.9
25	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
	439518	W76326		gb:zd60d04.r1 Scores_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153026	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
30	447384	AI377221	Hs.40528	ESTs	13.9
	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI278802	Hs.25561	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
35	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
40	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	13.8
	407939	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	13.7
	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96667	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
50	452260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
55	449474	AA019344	Hs.2035	ubiquitin-activating enzyme E1 (A1S9T an	13.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
60	410001	AB041036	Hs.57771	kallikrein 11	13.6
	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021955*:Homo sapiens phosphoglucomuta	13.6
	428648	AF052728	Hs.188021	potassium voltage-gated channel, subfam	13.6
65	414279	AW021691	Hs.101067	GCN5 (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	13.5
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
70	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
75	447082	T85314	Hs.42644	thioredoxin-like	13.5
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypotheti	13.3
80	433617	AW022133	Hs.189638	ESTs	13.3
	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371145	Hs.226627	leptin receptor	13.2
5	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
	407938	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
10	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.156880	ESTs	13.2
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
15	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68796	Hs.237731	ESTs	13.1
	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428839	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D66957	Hs.80712	KIAA0202 protein	13.0
20	453006	AI362575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
25	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
30	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
	417315	AI080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW296451	Hs.24605	ESTs	12.8
35	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA992480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
40	459513	AI032946		gb:ox06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
45	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AB040928	Hs.65366	KIAA1495 protein	12.6
	453830	AA534296	Hs.20953	ESTs	12.6
50	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI568801	Hs.71721	ESTs	12.6
	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
55	450253	AL133047	Hs.24715	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
	427078	AI676062	Hs.111802	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
60	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
65	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
	432205	AI806583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
70	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965*-Homo sapiens phosphoglucomuta	12.4
	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
75	448072	AI459306	Hs.24908	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
80	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165590	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-protei	12.2
	400880			NM_000611*:Homo sapiens CD59 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449625	NM_014253	Hs.23796	odz (odd Oz/ten-m, Drosophila) homolog 1	12.1
15	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	12.0
	443646	AJ085198	Hs.164226	ESTs	12.0
	448874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AJ984625	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730045	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206088	ESTs, Moderately similar to ALU8_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42683	ESTs	11.8
35	431645	AF078849	Hs.266483	dynein light chain-A	11.8
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	426981	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AJ472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AJ039316		gb:ox48c08.x1 Soares_tota_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AJ674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopotei	11.4
	456804	AJ421645	Hs.139851	caveolin 2	11.4
75	422546	AB007969	Hs.301478	KIAA0500 protein	11.4
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AJ633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEFS_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	448766	AJ473827	Hs.31793	ESTs	11.3

	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	11.3
5	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476:gij12737279[refXP_012163.1]	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
10	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.116410	ESTs	11.2
15	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	423342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW365224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
20	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T86534	Hs.14372	ESTs	11.1
	414341	D80004	Hs.75909	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
25	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68547	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270266	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
30	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
	412622	AW664708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
35	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
40	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
	417169	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104596	KIAA1324 protein	10.9
45	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAPI1_HUMAN DEATH	10.9
	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.156110	immunoglobulin kappa constant	10.9
	428384	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
50	441540	C01367	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI623752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcospan (Kras oncogene-associated gene	10.8
55	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	H22953	Hs.137551	ESTs	10.8
	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447595	AW379130	Hs.18953	phosphodiesterase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
60	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
65	450206	AI796450	Hs.201600	ESTs	10.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
	421977	W94197	Hs.110165	ribosomal protein L26 homolog	10.8
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 8	10.8
70	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410505	Hs.27973	KIAA0874 protein	10.8
75	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW975944	Hs.237396	ESTs	10.7
	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
80	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA: cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

	433923	AI823453	Hs.146625	ESTs	10.7
	418196	AI745649	Hs.26549	KIAA1708 protein	10.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	10.7
5	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	AI754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmegin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)-like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	AI801098	Hs.151500	ESTs	10.6
	449685	AW296669	Hs.66095	ESTs	10.6
	441111	AI806867	Hs.126594	ESTs	10.6
15	436671	AW137159	Hs.146151	ESTs	10.6
	447974	R76886		gb:yi64b03.s1 Soares placenta Nb2HP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CAMP-static aci	10.6
	424562	AI420859	Hs.150557	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965058	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	AI694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
25	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW996096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	451900	AB023199	Hs.27207	KIAA0082 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037766	Hs.146085	KIAA1345 protein	10.5
35	402076			C5002020:gi1082876 pir S55457 tropomy	10.5
	413866	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64183	Hs.282982	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (tr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	AI380429	Hs.172445	ESTs	10.5
	443684	AI681307	Hs.55098	ESTs	10.5
45	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cyclin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182982	golgin-67	10.5
	416182	NM_004354	Hs.79069	cyclin G2	10.4
	418365	AW014345	Hs.161690	ESTs	10.4
	452286	AI358570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	AI033965	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436675	Hs.16602	ESTs	10.4
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	409151	AA306105	Hs.50765	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293798	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW579960	Hs.135150	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB036063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26406	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homo sapiens cDNA FLJ11344 fis, clone PL	10.3
	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
75	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	10.3
	451593	AF151879	Hs.26706	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174600 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:U3-CT0214-291299-052-A12 CT0214 Homo	10.2
5	446553	AB021179	Hs.15299	HMB4-inducible	10.2
	418278	AI089489	Hs.83937	hypothetical protein	10.2
	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	10.2
10	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
	457498	AI732230	Hs.191737	ESTs	10.2
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
15	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	10.2
	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.646	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
20	414888	AI039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444618	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
25	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	10.1
30	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423681	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
35	446035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
	432589	AL135725	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419672	AA465113	Hs.23853	ESTs, Weakly similar to A34615 profilagg	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
40	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	10.0
	451424	AI862026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
45	425683	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.0
	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA053564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
50	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	9.9
55	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
60	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
	441054	AA913591	Hs.126480	ESTs	9.9
	415875	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
65	453078	AF053551	Hs.31584	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI858732	Hs.30443	senrin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
70	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
75	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
80	451957	AI796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179982	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
5	404571			NM_015902: Homo sapiens progesteron induce	9.7
	444427	H25094	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278626	Arg/Abi-Interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	9.7
15	417171	BE613486	Hs.81412	lipin 1	9.7
	421709	AA159394	Hs.107056	CED-6 protein	9.7
	415155	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409190	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523839	Hs.165258	ESTs	9.6
	409752	AW953990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
35	412766	BE544475	Hs.54347	ESTs	9.6
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AI280341	Hs.166571	ESTs	9.6
	424534	D87682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447889	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	9.5
	408915	NM_016651	Hs.48950	hepaticellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AI376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H46008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	436497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AI636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	reticulon 1	9.4
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-erk avian sarcoma virus CT10 oncogene	9.4
	425657	T89939	Hs.119471	ESTs	9.4
	428250	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10653	ESTs	9.4
65	412446	AI768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncollin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW298235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95665	hypothetical protein	9.4
	420061	AW024937	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419926	AW900992	Hs.93796	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
	429786	AL080232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
80	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
5	445704	AI493742	Hs.165210	ESTs, Moderately similar to I38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
	428455	AW970976	Hs.293653	ESTs	9.3
	422564	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
10	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
	433862	D85960	Hs.3610	KIAA0205 gene product	9.2
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558			ENSP00000220478*:SECRETORANIN III.	9.2
15	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA829860	Hs.122834	ESTs	9.2
	416653	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450606	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
20	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102506	eukaryotic translation initiation factor	9.1
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
25	448822	BE149845	Hs.289038	hypothetical protein MGC4126	9.1
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	9.1
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (9.1
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	9.1
30	434361	AF129755	Hs.117772	ESTs	9.1
	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cala	9.1
	448704	AW080932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500542	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
35	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
	427213	AW007211	Hs.16131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.96423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
40	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
45	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884186	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
50	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope [Hsapi	9.0
	405523			C8001409*:gll7441226[ptr]S31212 collage	9.0
	416662	T25853	Hs.7538	ESTs	9.0
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
55	445183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	8.9
60	414917	C04863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
65	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	8.9
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
70	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502663	Hs.145037	ESTs	8.9
	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
75	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sen1rin)	8.9
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
80	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny97f11.s1 NCL_CGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417355	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN IIII	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428647	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activa)	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	AI743880	Hs.12876	ESTs	8.8
	459324	AW080953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008798	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypotheti	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270858	ESTs, Moderately similar to ALU4_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA564489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32990	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452206	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251594	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gb:d77e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypotheti	8.7
40	410442	X73424	Hs.63788	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50785	SEC22, vesicle trafficking protein (S. c	8.7
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	klotho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419547	AA348947	Hs.91816	hypothetical protein	8.6
60	425907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119563	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434851	AA806164	Hs.116502	ESTs	8.6
	420608	BE548277	Hs.103104	ESTs	8.6
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135146	hypothetical protein FLJ13984	8.5
	435614	R09718	Hs.20403	ESTs	8.5
	446595	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.5071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416206	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

	434747	AA837085	Hs.220585	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	8.5
	450813	AI739625	Hs.203376	ESTs	8.5
5	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW529666	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	8.5
	407891	AA486620	Hs.411135	endomucin-2	8.5
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
10	432620	AA777749	Hs.5978	UM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE266026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pr3 Homo sapiens	8.4
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
25	421622	AB037748	Hs.105204	KIAA1327 protein	8.4
	431160	AW971174	Hs.324330	ESTs	8.4
	449567	AI990790	Hs.188614	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	VW domain binding protein 4 (formin bind	8.3
30	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	tol-like receptor 5	8.3
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433615	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	AI799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450:Homo sapiens four and a half L	8.3
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.3
	453121	AI968264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434O0921 (f	8.3
50	426101	AL049987	Hs.166361	Homo sapiens mRNA; cDNA DKFZp564F112 (fr	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	8.2
	432695	D63480	Hs.276634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stratagene HeLa cell s3 93	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN IIII	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypotheti	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	AI824719	Hs.328700	ESTs	8.2
75	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 598

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

409752	115301_1	AW963990 AA078196 AW749482 AA077468 BE151571 AA376917
411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161005 BE162499
418866	179788_1	T65754 AA229857 AA229658
418876	179960_1	AA740616 AA654854 AA229923
419536	185688_1	AA603305 AA244095 AA244183
419544	185760_2	AI909154 AA526337 AA244193 AI909153
423800	232161_1	AA331156 AA331157 AA331155
426413	266650_1	AA377823 AW954494 AI022688
429163	300543_1	AA884766 AW974271 AA592975 AA447312
430848	324621_1	AW021726 AA487752 AA488085
431121	328275_1	AW971157 AA492575 AA492520
432189	342819_1	AA527941 AI810608 AI620190 AA635266
432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
434415	385931_1	BE177494 AW276909 AA632849
434579	38916_1	T56958 T57205 AF147346
439518	47334_1	W76326 AF086341 W72300
443161	561305_1	AI038316 AI344631 AI261653
447974	745643_1	R76886 AI453674 R77049

TABLE 59C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400860	9757499	Minus	151830-152104,152649-152744
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
401747	9789672	Minus	118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
401785	7249190	Minus	165776-165995,166189-166314,166408-166569,167112-167268,167387-167469,168634-168942
402076	8117410	Plus	128316-128627
402812	6010110	Plus	25026-25091,25844-25920
402855	9662953	Minus	59763-59909
403047	3540153	Minus	59793-59958
403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
403149	9799833	Plus	25034-25185
403362	8571772	Plus	64099-64260
404210	5006246	Plus	169926-170121
404571	7249169	Minus	112450-112648
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of prostate tumor to normal adult body tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	56.6
419526	AI821895	Hs.193481	ESTs	56.2
420154	AI093155	Hs.95420	JM27 protein	44.0
432441	AW292425	Hs.163484	ESTs	41.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothe	37.9
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	36.0
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	32.9
425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	30.0
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	AI918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_001172:Homo sapiens arginase, type II	24.5
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
15	407709	AA456135	Hs.23023	ESTs	20.0
	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125885	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428336	AA503115	Hs.183752	microseminoprotein, beta-	18.7
20	410929	H47233	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418961	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603367	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	AI972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	429220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW450461	Hs.203965	ESTs	14.4
40	431548	AI834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	14.3
	430187	AI799909	Hs.158989	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970872	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432966	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.159425	ESTs	13.4
50	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	12.5
55	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249368	Hs.98558	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	12.2
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	436032	AA150797	Hs.109276	latexin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW175665	Hs.278695	Homo sapiens prostein mRNA, complete cds	11.9
70	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462O23.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	11.6
75	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218886	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	11.5
80	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN !!!	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd60d04.r1 Soares_fatal_heart_NbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415283	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
15	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416795	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193465	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW628686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021965*-Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV Integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	ALD49610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI085198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid	8.2
65	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	8.2
	428829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157920	ESTs	8.1
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453160	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
5	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AI750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
20	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI088489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homeo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AU077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
50	439492	AF086310	Hs.103159	ESTs	6.8
	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI732230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
60	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.7
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB039670	Hs.9728	ALEX1 protein	6.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250619	phorbol-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AA861697	Hs.120591	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystokinin	6.6
70	447033	AI357412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCL_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	6.4
75	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
80	421077	AK000061	Hs.101590	hypothetical protein	6.4
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoeiti	6.3
	453390	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.3
	433610	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AI922183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
	425465	L18964	Hs.1904	protein kinase C, Iota	6.2
15	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AI800470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
20	427078	AI676062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	6.2
	449907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282906	ESTs	6.1
25	437323	AA371145	Hs.194397	leptin receptor	6.1
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	ALU076674	Hs.198999	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.260024	ESTs	6.0
30	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1: cell surface	6.0
	408968	AI652235	Hs.49376	hypothetical protein FLJ20644	6.0
	409047	AW961434	Hs.31539	ESTs	6.0
	418601	AA279490	Hs.86368	calmegin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	H40873	Hs.175971	ESTs	6.0
	450295	AI766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AI852026	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Belt1 (S. cerevisiae) homolog	5.9
	405523			C8001409:gi7441226 pir J531212 collage	5.9
50	448807	AI571940	Hs.7549	ESTs	5.8
	404642			NM_021965:Homo sapiens phosphoglucomuta	5.8
	452598	AI831594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414528	AA148950	Hs.188836	ESTs	5.7
	432712	AB016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AI041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fis, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AI739825	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970976	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	AI241733	Hs.43871	ESTs	5.4
	424084	AI940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AI459306	Hs.24908	ESTs	5.4
15	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
20	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
25	412677	AW029608	Hs.17384	ESTs	5.3
	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	AI829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 feni	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Narrie disease (pseudoglioma)	5.3
	433409	AI278802	Hs.25661	ESTs	5.3
	441102	AA973905		intermediate filament protein syncoilin	5.3
35	453387	AI990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	AI823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.2
	447574	AF162666	Hs.18895	tousled-like kinase 1	5.2
40	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	E74-like factor 1 (ets domain transcript	5.2
	429467	NM_004477	Hs.203772	FSHD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	toll-like receptor 5	5.2
	453942	AW190920	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452588	AA889120	Hs.110637	homeo box A10	5.2
55	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446795	AI797713	Hs.156471	ESTs	5.1
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.1
60	432340	AA534222		gb:n121d02.s1 NCI_CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	5.1
	453293	AA382267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409643	AW450866	Hs.257359	ESTs	5.1
65	427723	AI355260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432251	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425643	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068558	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218366	kalikrein 4 (prostase, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015156	Hs.78398	KIAA0071 protein	5.1
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	5.0
	433023	AW864793	Hs.87409	thrombospondin 1	5.0
80	433662	D86960	Hs.3610	KIAA0205 gene product	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	AT734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	O13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW391569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439899	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445866	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	4.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	4.9
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496: Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
20	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225706	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	f-box and leucine-rich repeat protein 4	4.8
	416030	H15261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	4.8
	423749	U09848	Hs.132390	zinc finger protein 36 (KIX 18)	4.8
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	4.7
50	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415621	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphatase cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA453208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RP5-978E18 from 7	4.7
	418836	AI655499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478: SECRETORANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H	4.7
	443881	R64512	Hs.237146	hypothetical protein FLJ12752	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	OC-specific transmembrane protein	4.7
70	444951	AI783767	Hs.148635	ESTs, Moderately similar to ALUB_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	419005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403046			NM_005656: Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF129533		gb: Homo sapiens F-box protein Fbl3b (FBL	4.6
	426011	AW995096	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
80	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861896	Hs.304505	ESTs	4.6

	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
5	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
	432093	H28383		gb:Y52c03.r1 Soares breast 3NbH8st Homo	4.6
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
10	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
	434423	NM_006769	Hs.3844	LIM domain only 4	4.5
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
15	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
	446720	AI439136	Hs.140546	ESTs	4.5
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
20	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
	423782	AA72209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
25	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW293716	Hs.53126	ESTs	4.5
	429857	AF089897	Hs.294030	topoisomerase-related function protein 4	4.5
	459561	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
30	414272	AI651603	Hs.46988	ESTs	4.5
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	4.5
35	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476:gil12737279[ref]XP_012163.1]	4.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417051	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
40	418858	AW961805	Hs.21145	hypothetical protein RG083M05.2	4.4
	433517	AW022133	Hs.189838	ESTs	4.4
	429559	AI985345	Hs.26425	ESTs	4.4
	452338	AW608920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
45	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
50	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI167877	Hs.143716	ESTs	4.4
	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	diubiquitin	4.4
55	448766	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.4
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
60	434022	R18374	Hs.117956	ESTs	4.4
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	4.4
	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-li	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
65	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
	448550	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82719	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
70	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	4.3
	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
75	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb:wd73f12.x1 NCL_CGAP_Lu24 Homo sapiens	4.3
	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
	420405	AA743396	Hs.189023	ESTs	4.3
80	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26535	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155694	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
5	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629666		ESTs, Weakly similar to S64054 hypothe	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
10	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulin 3	4.2
	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
15	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN !!!	4.2
	450546	AA010200	Hs.175551	ESTs	4.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
20	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.2
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449685	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
25	450377	AB033091	Hs.74313	KIAA1265 protein	4.2
	419647	AA348947	Hs.91816	hypothetical protein	4.2
	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW969657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
30	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	4.1
	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447659	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
35	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	4.1
	447752	M73700	Hs.105938	lactoferrin	4.1
	402855			NM_001839*-Homo sapiens calponin 3, acid	4.1
	443161	AJ038316		gb:ox48c08.x1 Soares_tota fetal liver spleen	4.1
	415827	H17462	Hs.23079	ESTs	4.1
40	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161650	ESTs	4.1
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AJ335191	Hs.260702	ESTs, Weakly similar to 2109260A B cell	4.1
45	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239499	KIAA0185 protein	4.1
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
50	410763	AF279145	Hs.8965	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.1
	428634	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
55	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	4.0
	443273	AJ042063	Hs.132156	ESTs	4.0
	428055	AA420564	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AJ457338	Hs.29894	ESTs	4.0
60	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.0
65	409705	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
	418594	AJ732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
70	416288	H51299		gb:yp07c06.s1 Soares breast 3NbHBst Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
75	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW277121	Hs.254881	ESTs	4.0
	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451051	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
80	400695			C11002514*gi11280151 pir E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [H.s]	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fis, clone L	3.9

	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
5	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445798	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0982 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	3.9
	442320	AI287817	Hs.129636	ESTs	3.9
15	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
	444636	T96667	Hs.17677	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412576	AA447718	Hs.107057	ESTs	3.9
	423952	AW877787	Hs.136102	KIAA0853 protein	3.9
20	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.9
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	N40087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, Xenopus laevis-like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:aa80h07.s1 NCI_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280699	ESTs	3.8
	444534	AW271626	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
35	443484	AI091458	Hs.134559	ESTs	3.8
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA: cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283631	hypothetical protein DKFZp547G183	3.8
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427635	BE397988	Hs.179982	tumor protein p53-binding protein	3.8
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453698	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B168 protein	3.8
50	431197	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177502	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW105663	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
65	448207	AI475490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
70	447608	AW205042	Hs.18955	Homo sapiens cDNA FLJ20667 fis, clone KA	3.7
	408312	AF263613	Hs.44198	intracellular membrane-associated calciu	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	3.7
	424882	AI379461	Hs.153636	far upstream element (FUSE) binding prot	3.7
75	425898	AA365649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
80	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AJ831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.7
	445941	AJ267371	Hs.172636	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.6
10	412533	AA679863	Hs.69606	ESTs	3.6
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	3.6
	442710	AI015631	Hs.23210	ESTs	3.6
	448212	AA75858		gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
	453038	AW292415	Hs.20509	HBV pX associated protein-8	3.6
15	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	3.6
	406815	AA833930	Hs.288036	tRNA isopentenylpyrophosphate transferas	3.6
20	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN IIII	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
	433887	AW204232	Hs.279522	ESTs	3.6
25	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
	435703	AW630133	Hs.83313	GK003 protein	3.6
30	445674	BE410347	Hs.13063	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.6
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	3.6
	439726	AW449893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
35	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55958		gb:yb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431263	AW129203	Hs.322915	ESTs	3.6
	431952	Z70695	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (Iazaro	3.5
	419440	AB020689	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
	419241	AA523939	Hs.165258	ESTs	3.5
50	410762	AF226053	Hs.66170	HSKM-B protein	3.5
	413384	NM_000401	Hs.75334	exostoses (multiple)	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449563	Hs.151393	glutamate-cysteine ligase, catalytic sub	3.5
55	420390	AA330047	Hs.191187	ESTs	3.5
	416662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0990 protein	3.5
	413950	AA249096	Hs.32793	ESTs	3.5
60	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-fin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.269128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410506	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
70	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF086431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
	432589	AL135725	Hs.131708	ESTs	3.5
75	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI624707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE439899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AI391470	Hs.158618	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

	456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
5	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	3.5
10	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AI969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BE613337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.4
	434966	AA657494		gb:n166f04.s1 NCL_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902: Homo sapiens progesterone induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheli	3.4
20	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056: Plasma membrane calcium	3.4
25	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AI655662	Hs.197698	ESTs	3.4
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	3.4
	436805	AA731533	Hs.270751	ESTs	3.4
	437367	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
30	407908	BE379758	Hs.110853	uncharacterized hemalopoietic stem/proge	3.4
	430144	AI732722	Hs.187694	ERGL protein; ERGIC-53-like protein	3.4
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
35	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	408267	AW380525	Hs.343664	tubulin-specific chaperone e	3.4
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AI148006	Hs.222120	ESTs	3.4
40	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
45	442910	AI365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheli	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
	445469	AW298370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.4
50	433037	NM_014158	Hs.279938	HSPC067 protein	3.4
	423044	AA320829	Hs.97266	protocadherin 18	3.4
	434128	W93170	Hs.284164	protein x 0004	3.4
	449645	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
55	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
	446874	AW968304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA406293	Hs.41167	ESTs	3.4
60	423178	AI033140	Hs.124983	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapi	3.3
65	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
70	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
	436664	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
	421476	AW953805	Hs.21887	ESTs	3.3
75	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263: HSPC213.	3.3
80	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443884	N20617	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

5	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450582	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143838	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_tetal_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H56196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (lr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/th	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AL080050	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (lr	3.3
	432363	AA534489		gb:mf76g11.s1 NCI_CGAP_Co3 Homo sapiens	3.3
	435102	AW899053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288684	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hibr1)	3.3
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.3
30	411373	BE326276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AI077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zcp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MGC2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426775	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279906	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200596	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20369	ESTs, Weakly similar to gonadotropin ind	3.2
60	442562	BE379584		dolichyl-diphosphooligosaccharide-protei	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chal	3.2
	421029	AW057782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44656	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-88 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001853	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.75574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein vezatin; hypotheti	3.2
80	452295	BE379936	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI635386	Hs.142846	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.105200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
	408784	AW971350	Hs.63386	ESTs	3.2
15	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.2
	405558			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
25	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	3.2
	440351	AF030933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08286	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220950	ESTs	3.1
	406627	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082597	Hs.244862	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	419965	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	3.1
	446146	AI287533	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	3.1
55	423947	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447726	AL137638	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gbzo65a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	H80696	Hs.233313	ESTs	3.1
	437756	AA767537	Hs.197096	ESTs	3.1
70	438979	AW976218	Hs.32565	ESTs	3.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
	438308	AI343469	Hs.127685	KIAA1627 protein	3.1
75	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440099	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29669	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412088	AI689496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
5	400664			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	AI879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152675	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPCO34 protein	3.0
	430280	AA361258	Hs.237858	Interleukin 7 receptor	3.0
15	445919	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294909	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.0
	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	AI805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431962	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA292642	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW819403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H09323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443967	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128387	ESTs	3.0
	441889	AI090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
	415954	AA171850	Hs.42251	ESTs	3.0
50	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	AI066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59522	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299688	Hs.24183	ESTs	3.0
	448264	AI478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hecl domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW698533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	AI791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.0
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:z97g10.r1 NCI_CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIKE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	438986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	AI932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

80

TABLE 60B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
5	411479	1247077_1 AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	411667	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	414372	143909_1 AA143654 AW753140 AA213770 AW970865 AA569075 AA492132
10	414680	147525_1 AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	415989	156454_1 AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416288	1585983_1 H51299 H44619 H46391 R86024 H51892 T72744
	416882	162718_1 AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AJ333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
15	416913	163001_1 AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	417379	167238_1 AA196390 AA507837 AA196468
	418304	173658_2 AA215702 AA368006 AA215703 BE066555 BE006876
	418647	177521_1 AA226198 AA226513 AA383773
20	418866	179788_1 T65754 AA229857 AA229658
	419536	185688_1 AA603305 AA244095 AA244183
	419544	185760_2 AI909154 AA526337 AA244193 AI909153
	423412	228001_1 AF109300 AI299378 AI202654
	423800	232161_1 AA331156 AA331157 AA331155
25	426226	262918_1 AA769045 AA372590 AW963633
	426413	266650_1 AA377823 AW954494 AI022688
	426503	268283_1 AA380153 AA380233 AW963529
	426775	271683_1 AA384564 AW966475 H02121 N41297 D63213 AA886888 AI922414 AW044240 AW196808 AI076736 AA599294 AI954433 AW117617 AI640323 H98134
30	426991	27415_1 AK001536 AA191092 AW510354 AI554256 AI353968 AA134266
	428342	290035_2 AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340
	429163	300543_1 AA884766 AW974271 AA592975 AA447312
35	429220	301384_1 AW207206 AW341473 AA448195 AI951341
	429258	301917_1 AA448765 C04967 C03045 AA658293
	430935	325772_1 AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI473611 AW841126 D60937
	430968	326269_1 AW972830 AA527647 AA489820 AA570362
	431429	33313_1 AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA056148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T35956 BE618035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 AL120308 AA187561 AA311680
40	432093	341283_1 H28383 AW972670 H28359 AA525808
	432125	341776_1 AW972667 AA526539 AI057032 AW167842
	432189	342819_1 AA527941 AI810508 AI620190 AA635266
	432340	345248_1 AA534222 AA632632 T81234
45	432363	345469_1 AA534489 AW970240 AW970323
	432600	350959_1 AI821085 AW973484 AA554802 AI821831 AA657438 AA640756 AA650339
	432810	354375_1 AA863400 AI991439 AW016017 AW014704 AI367512 H17550 AA744752 R46187 AW471324 AI126670 AA626033 AI276287 AI094253 AI286003 AI147163 AI911443 AW512612 AA972102 AA999975 AI684428 AI335035 D63102 AI524234 AI539156 AA565542 T55958 T57205 AF147346
50	434966	396504_1 AA657494 AI582663 AI581639
	435023	398093_1 AI692552 AI393343 AI800510 AI377711 F24263 AA661876
	437866	44433_2 AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733 AA812489 AW874142 AI47188
55	438147	45074_1 AW250553 L07876 Z36843 R30593 AI190097 AW965317
	439092	468554_1 AA830149 AW978407 M85983 AW503637
	439518	47334_1 W76326 AF086341 W72300
	439904	479942_1 AW892676 AA853877 D44747
60	440840	50357_2 AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI797207 AA921877
	441102	509604_1 AA973905 AI298888 AA917019 H63235 T90771
	442562	54500_2 BE379584 R34211 BE544768 AW973709 AI653056 AI653173 AI266043 AI656750 H74180 AI492630 AI376090 AW472184 D59940 AW170056 AI082443 AW021142 AI167921 AI348677 AI278577 AW130886 AA761517 AI698203 AA115535 AI264790 R34328 D59939 AW205074 AA554902 D62102 AI0007
65	443161	561305_1 AI038316 AI344631 AI261653
	445808	65133_1 AV655234 AW966332 AA340239
	447082	707248_1 T85314 AI360684 T85528 T91254
	448212	755099_1 AI475858 AW969013
70	449625	8113_1 NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486 N40087 H12925 AA60779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095 AA164518 AA730973 W00417 W65303
75	450582	83933_1 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	452260	9074_1 AA453208 NM_004251 U44103 AI571547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228 BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI659875 AW272338 AI423136 AI089270 AI160904 AA664354 BE1
	452598	92338_2 AI831594 AW970667 AW027959 AI129800 AI927949 AI650270 AI625105 AW514661 AI708393 AI138076 BE180510 AI926721 AI399955 AA749139 AI862160 AW874011 AI242763 AA262795 AA039864 H73499 AI093249 BE245661 AI816834 N25206 AA828301 AI084565 AI302815 AA026905 AA77255
80	452815	93255_1 AA418841 AI452657 AI768876 AA028973 BE179873 C00215 AA418930
	453802	981589_1 AL134757 AW079131
	455100	1253334_1 BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853_1 AW974811 AA651634 AA650072

5 TABLE 60C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400664	8118496	Plus	13558-13721,13942-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29335,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59968
403790	8084957	Minus	87826-87947,89835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102999-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

Pkey: Unique Eos probeset Identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*-HSPC213.	3.0	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79069	cyclin G2	8.4	8.4
421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose Induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
420120	AL049610	Hs.95243	transcription elongation factor A (Sil)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	9.4	7.3
425018	BE245277	Hs.154196	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026692	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20356	2.6	6.0

	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9	5.9
5	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.3	5.9
	431548	AI834273	Hs.9711	novel protein	15.7	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
10	422538	NM_006441	Hs.118131	5,10-methenyltetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5	5.5
	414516	AI307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
15	451684	AF216751	Hs.26813	CDA14	3.9	5.4
	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA626509	Hs.122329	ESTs	5.1	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	3.3	5.0
25	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
30	439024	R96696	Hs.35598	ESTs	5.4	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
35	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464		gb:tt88f04.x1 NCI_CGAP_Pr28 Homo sapiens	9.1	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			C15000476*.gij12737279[rel]XP_012163.1}	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
40	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
	408380	AF123050	Hs.44532	diubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
45	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
50	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
	426826	AL048842	Hs.194019	atractin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	418701	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2	4.2
55	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
60	443822	AI911527	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1	4.1
	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
65	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433687	AW204232	Hs.279522	ESTs	4.1	4.1
	436556	AI364997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443546	AI085198	Hs.164226	ESTs	4.1	4.1
70	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9	3.9
75	444755	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-amino adipate aminotra	3.9	3.9
80	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

5	422975	AA347720	Hs.122669	KIAA0264 protein	2.2	3.8
	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	2.7	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	4.1	3.8
	418821	AA436002	Hs.183161	ESTs	2.8	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.1	3.8
	453160	AJ263307	Hs.239884	H2B histone family, member L	9.2	3.8
10	424906	AJ566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked moi	3.7	3.7
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7	3.7
	448807	AJ571940	Hs.7549	ESTs	3.6	3.7
	439209	AF087993	Hs.91954	ESTs	2.1	3.6
	420077	AW512260	Hs.87767	ESTs	4.4	3.6
15	451009	AA013140	Hs.115707	ESTs	4.1	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6	3.6
	452561	AJ692181	Hs.49169	KIAA1634 protein	3.2	3.6
	447033	AJ357412	Hs.157601	ESTs	7.7	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6	3.6
20	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6	3.6
	414680	AA743331		hemoglobin, alpha 2	3.5	3.5
	417380	T06809	Hs.332086	ESTs	3.5	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5	3.5
25	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoieli	3.5	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KOX 4, clone HF.1	2.2	3.5
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5	3.5
	432101	AJ918950	Hs.123642	EphA3	16.5	3.5
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.3	3.5
30	435513	AW404075	Hs.42785	DC11 protein	2.2	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	2.1	3.5
	418293	AJ224483	Hs.16063	hypothetical protein FLJ21877	6.7	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	2.1	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	2.1	3.4
35	440749	W22335	Hs.7392	hypothetical protein MGC3199	2.5	3.3
	408374	AW025430	Hs.155591	forkhead box F1	4.3	3.3
	400277			Eos Control	2.4	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3	3.3
40	443912	R37257	Hs.184780	ESTs	3.3	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	9.9	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3	3.3
	450094	AJ174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.4	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.6	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.3	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	11.5	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	2.0	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2	3.2
50	402802			NM_001397:Homo sapiens endothelin conver	4.3	3.2
	419169	AJ336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	2.7	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.8	3.2
55	444489	AJ151010	Hs.157774	ESTs	3.2	3.2
	453124	AJ139058	Hs.125790	leucine-rich repeat-containing 2	3.2	3.2
	453078	AF053561	Hs.31584	melaxin 2	2.1	3.1
	439444	AJ277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	10.6	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	2.8	3.1
60	434804	AA649530	Hs.348148	gb:ns44R05.s1 NCL_CGAP_Alv1 Homo sapiens	2.1	3.1
	445840	AJ277811	Hs.146291	ESTs	3.1	3.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	2.2	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1	3.1
65	430519	AF129534	Hs.49210	F-box only protein 4	3.1	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	16.2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	9.0	3.1
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	20.9	3.1
70	420154	AJ093155	Hs.95420	JM27 protein	27.4	3.1
	453293	AA382267	Hs.10653	ESTs	3.7	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothe	2.4	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	2.9	3.0
75	433285	AW975944	Hs.237396	ESTs	7.7	3.0
	450671	AJ356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0	3.0
	445921	AW015211	Hs.146181	ESTs	4.3	3.0
	416882	AJ633044		tryptophanyl tRNA synthetase 2 (mitochon	3.5	3.0
80	414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	2.5	3.0
	450580	N40087		ESTs	3.0	3.0
	447726	AL137638	Hs.19368	matrilin 2	3.9	2.9
	447816	NM_007233	Hs.274329	TP53 target gene 1	7.2	2.9
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	5.1	2.9
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	2.6	2.9

5	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	2.9	2.9
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisoku	2.9	2.9
	445808	AV655234		ESTs, Moderately similar to PC4259 femi	2.9	2.9
	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
10	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AK033930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
	451796	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (I	2.9	2.9
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.0	2.9
15	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
	453628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
	412324	AW978439	Hs.69504	ESTs	2.0	2.8
20	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
	433865	N28862	Hs.44104	ESTs	2.8	2.8
	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
25	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
	427144	XS5097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654650	Hs.262906	ESTs	2.2	2.8
30	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
	448206	BE622585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
35	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AI000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
	412576	AA447718	Hs.107057	ESTs	2.7	2.7
40	413336	AI569936	Hs.296178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA534163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
45	409519	AK001015	Hs.55220	BCL2-associated athanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
50	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	446238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
55	417173	U51397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
	447509	AF107454	Hs.107537	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
60	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191060	ESTs	2.6	2.6
65	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	8.7	2.6
70	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.4	2.6
	425815	R94023	Hs.94560	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
	431474	AL133990	Hs.190642	ESTs	9.3	2.5
	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
75	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
	445424	AB028945	Hs.12696	cartactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005655: Homo sapiens transmembrane pr	21.1	2.5
80	416198	H27332	Hs.99598	hypothetical protein MGC5338	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

5	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRN	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA448765		gb:zx10e09.r1 Soares_t0tal_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone e	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0685 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AI493046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258576	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107056	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:QV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424602	AK002055	Hs.151046	hypothetical protein FLJ11193	2.1	2.3
	450693	AW450461	Hs.203965	ESTs	2.3	2.3
	452387	AI680772	Hs.306094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
40	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
	419438	AA406400	Hs.12482	glyceronephosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134757		gb:DKFZp547G1090_r1 547 (synonym: hfbt1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AI027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gil4507689[ret]NP_003298.1) tra	2.3	2.3
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW249181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452016	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPLIC	2.6	2.2
	431555	AI815470	Hs.260024	Cdc42 effector protein 3	4.5	2.2
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478*:SECRETOGNAN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	tol-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 feni	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935962	Hs.26289	ESTs	11.9	2.2
	422380	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66052	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
433444	AW975324	Hs.129816	ESTs	11.7	2.2
446354	AW449650	Hs.346335	ESTs	2.6	2.2
438869	AF075009		gb:Homo sapiens full length insert cDNA	5.9	2.2
425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
424036	AA770688		H2A histone family, member L	3.8	2.2
440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.8	2.2
404641			NM_021965:Homo sapiens phosphoglucomuta	2.2	2.2
407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
406068			C2002008:gi7303957[gb AAAF59000.1 (AE00	3.1	2.1
415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
448966	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
449897	AW819642	Hs.24135	transmembrane protein vezatin; hypothei	2.1	2.1
452959	AI933416	Hs.189674	ESTs	2.1	2.1
427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
418727	AA227609	Hs.94834	ESTs	2.1	2.1
440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.5	2.1
434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
438520	AA706319	Hs.98416	ESTs	2.7	2.1
414269	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
450861	AI523898	Hs.17617	ESTs	2.4	2.1
419193	D29643	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.2	2.1
416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
407182	AA312551	Hs.230157	ESTs	2.1	2.1
421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
432833	N51075	Hs.110028	ESTs	2.1	2.1
425170	AU077315	Hs.154970	transcription factor CP2	2.6	2.0
436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.6	2.0
424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
413627	BE182082	Hs.246973	ESTs	3.3	2.0
414133	AW022188	Hs.41167	ESTs	2.3	2.0
411096	U80034	Hs.68583	mitochondrial intermediate peptidase	14.7	2.0
450244	AA007534	Hs.125062	ESTs	3.1	2.0
422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
409219	AA393383	Hs.133331	ESTs	2.1	2.0
419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
434128	W93170	Hs.284164	protein x 0004	2.7	2.0
434503	T96231	Hs.17762	ESTs	2.0	2.0
443292	AK000213	Hs.9196	hypothetical protein	2.0	2.0
443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
448172	N75276	Hs.135904	ESTs	6.0	2.0
452039	AI922988	Hs.172510	ESTs	2.0	2.0
400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
449625	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	10.1	2.0
441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
451359	AA017321	Hs.269691	ESTs	2.1	2.0
434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
408806	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C	5.4	2.0
433388	AI432672	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	5.5	2.0
446783	AW138343	Hs.141867	ESTs	4.4	2.0
437323	AA371145	Hs.194397	leptin receptor	2.5	2.0
410076	T05387	Hs.7991	ESTs	2.9	2.0
421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	2.5	2.0

TABLE 61B

Pkey: Unique Eos probeset Identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150955 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59488 AI040666 W60959 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW663548 T90114 AI139947 AA809643 AA846232 AA581966 AA789002
15	424036	23460_1	AA770688 H15373 AW161070 BE304523 BE378517 AA989300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290558 C15404
	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA48765 C04967 C03045 AA658293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H56457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AA193203 N5581
	438869	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF086341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173296 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV655234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 M48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T613
	450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86550 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

40

Pkey	Ref	Strand	Nt_position
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401558	7139578	Plus	103510-104090
402802	3287156	Minus	53242-53432
403047	3540153	Minus	59793-59968
404641	9796810	Minus	32247-32362
405685	4508129	Minus	37956-38097
406068	9114084	Plus	382-543

45

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Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60

Pkey: Unique Eos probeset Identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigenelD: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal prostate tissue

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	Pkey	ExAccn	UnigenelD	Unigene Title	R1
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
	427274	NM_005211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
	420729	AW964897	Hs.290825	ESTs	15.8
75	412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
	416188	BE157260	Hs.79070	v-myc avian myelocytomatosis viral oncog	13.6
	417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activati	13.1
	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
80	401197			ENSP00000229263:HSPC213.	12.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
	449155	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3
	443271	BE588568	Hs.195704	ESTs	11.6
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419553	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	slit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.105768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
10	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
	456614	AV653110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
20	425174	D87450	Hs.154978	KIAA0261 protein	8.6
	445701	AF055581	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protei	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	8.4
25	434217	AW014795	Hs.23349	ESTs	8.3
	417363	AW129357	Hs.329700	ESTs	8.3
	425782	U66468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI984625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
35	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finge	7.3
	451900	AB023199	Hs.27207	KIAA0982 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-fin	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000643	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153584	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocalcin-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20196	adenylate cyclase 9	6.9
55	426759	AI590401	Hs.21213	ESTs	6.8
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam	6.7
60	451957	AJ796320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA622037	Hs.166468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415752	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	6.3
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	minichromosome maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0874 protein	6.2
	418195	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1
80	437147	AL049954	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447965	AW292577	Hs.94445	ESTs	5.9

5	449118	R67477	Hs.23103	Bet1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	5.9
	431548	A1834273	Hs.9711	novel protein	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
10	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
	435080	A1831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
15	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157645	Hs.48793	sialyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA905097	Hs.85050	phospholamban	5.7
20	445467	A1239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
	406672	M26041	Hs.198253	major histocompatibility complex, class	5.5
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.5
25	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90866	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
	414516	A1307802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
30	412490	AW803554	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undutin)	5.4
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
35	418758	AW959311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449907	AA004825	Hs.103281	ESTs	5.4
	419159	AW974945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
40	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	A1088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
	403851			C5002154:gi 7299015 gb AA54217.1 (AE0	5.3
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
45	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.153023	ESTs	5.2
50	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp27C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fis, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
55	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
	414212	AA136569	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
60	417318	AW953937	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
	434170	AA626509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
65	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	5.0
	433560	A1925195	Hs.130891	hypothetical protein MGC4400	5.0
70	410762	AF226053	Hs.66170	HSKM-B protein	5.0
	421823	N40850	Hs.28625	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
75	453370	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	4.9
	434094	AA305599	Hs.238206	hypothetical protein PRO2013	4.9
	452323	W44356	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
80	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
	445800	AA126419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96896	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301663	ESTs	4.7
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	AI692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	AI685464		gb:tt88f04.x1 NCL_CGAP_Pr28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor I	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C15000476.gi112737279[ref]XP_012163.1]	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	D80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	diubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425907	AA365752	Hs.155965	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	AI676062	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.5
	408705	AA312135	Hs.46967	HSPCO34 protein	4.5
30	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	426673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	4.5
	456974	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31595	ESTs	4.4
40	443250	AI041530	Hs.132107	ESTs	4.4
	411962	AA099050		gb:ztk85d12.r1 Soares_pregnant_uterus_NbH	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
45	430259	BE550182	Hs.127826	RalGEF-like protein 3, mouse homolog	4.4
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4
	436446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014493	Hs.126727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428826	AL048842	Hs.194019	atractin	4.3
	444212	AW503976	Hs.10649	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW067805	Hs.172665	methyltetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408088	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	4.2
	408554	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814948	Hs.95343	ESTs, Weakly similar to ALUC_HUMAN !!!!	4.2
70	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b57	4.2
	439518	W76326		gb:zdf60d04.r1 Soares_fetal_heart_NbHH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	AI421645	Hs.139851	caveolin 2	4.2
	414291	AI289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA677577	Hs.99732	Homo sapiens Chromosome 16 BAC clone CIT	4.2
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	AI911527	Hs.11805	ESTs	4.1

	436576	AI458213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430383	AI861854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	446468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.238039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.279522	ESTs	4.1
20	436556	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.26146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19904	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443646	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452186	AA120761	Hs.28307	VW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA689292	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H67220	Hs.169681	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0456 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09848	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40697	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	405934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444755	AA431791	Hs.113823	CipX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abi subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine/alpha-aminoacidipate aminotra	3.9
60	450899	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110537	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0665 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450506	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	415156	X84908	Hs.78060	phosphorylase kinase, beta	3.8
70	422975	AA347720	Hs.122669	KIAA0264 protein	3.8
	403100			C2001027:gi7296271 gb AAF51562.1 (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424806	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gb:mf78g11.s1 NC1_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.92195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861896	Hs.304506	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmob33 protein, 3'	3.7
	446554	AA151730	Hs.301789	nudix (nucleoside diphosphate linked mol	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.198425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087993	Hs.91954	ESTs	3.6
	434927	H46612	Hs.293815	Homo sapiens HSPC265 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-like	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439506	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452561	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA380328	Hs.865	RAP1A, member of RAS oncogene family	3.6
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350:gij65781261gb AA17706.1 AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658299	Hs.163959	ESTs	3.5
	449008	AW578003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		gb y12c04.r1 Soares infant brain 1N18 H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440643	M78878	Hs.7314	KIAA0614 protein	3.5
70	409068	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		gb y59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
75	401744			Target Exon	3.4
	432723	D29677	Hs.3085	KIAA0054 gene product; Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

	432741	A1732358	Hs.185118	ESTs, Moderately similar to A37413 calbi	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	A1207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
5	428466	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	A1224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AL046851	Hs.153053	CD37 antigen	3.4
10	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	425900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
15	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc:beta 1,3-galactosyltr	3.4
	444480	A1150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
	403389			C3001393*.gij3327090jdbjBAA31613.1j (AB	3.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
20	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidylprolyl isomerase F (cyclophilin	3.3
	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
25	417295	AW993524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
30	445270	A1762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW955696	Hs.90960	ESTs	3.3
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	418700	A1963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
35	435499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6631	hypothetical protein FLJ20373	3.3
	450094	A1174947	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
40	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	A1652236	Hs.49376	hypothetical protein FLJ20644	3.3
	453548	AL079983	Hs.116774	integrin, alpha 1	3.3
45	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
50	410366	A1267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
	421246	AW582962	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
55	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV660179	Hs.282431	ESTs	3.2
	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
60	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419168	A1336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
65	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
70	417386	AL037228	Hs.82043	D123 gene product	3.2
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
	442355	AA456539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
75	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	A1381659	Hs.267086	ESTs	3.2
80	424894	H83520	Hs.153678	reproduction 8	3.2
	416959	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QV0-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypothei	3.2

	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
5	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothei	3.1
10	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CDC14 (cell division cycle 14, S. cerevi	3.1
	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0280 protein	3.1
15	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
	427399	NM_014883	Hs.177664	KIAA0914 gene product	3.1
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
20	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
25	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
30	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
35	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypothei	3.1
	422481	AL050163	Hs.117339	DNAX-activation protein 10	3.1
	430487	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
40	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
45	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
50	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
	434398	AA121098	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
55	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fis, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
	411315	AW836547		gb:PM3-LT0032-030100-006-e08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothei	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
60	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxic)	3.0
	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypothei	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
65	421786	AI188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
70	445345	AW003850	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
75	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X63692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R05054		gb:ye89g07.r1 Soares fetal liver spleen	3.0
80	445921	AW015211	Hs.146181	ESTs	3.0
	406673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochond	3.0
414052	AW578849	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Key: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Key	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411952	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 AI537404 R45431 AJ333439 AI741845 AI674468 R44190 R52535 R52617 AI220925 AI979148 AI744688 AW242437 AA618148
414680	147525_1	AI983937 AA399623 AI676204 AI420077 N24944 D51042 AA282786 AA137264 AW236107 AW769
415528	1539409_1	AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288
416128	157163_1	AA708749 AA644620 AA652769 AA242975 AA151074 T19890
416882	162718_1	R17236 R52580 F11642
422673	219674_1	AA173632 AI174858 AA581361 AI700024 AA173988 BE165417 AI366964
426448	267323_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AJ333114 AI277384 AI088297 AI468477
430935	325772_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
430968	326269_1	N59027 AA314694 N53937 R08100
431304	331286_1	R06054 AA378789 AW956453
431676	336411_1	AW072916 AI184913 AA489195 AW466994 AW469044 N59350 AI819642 AI280239 AI220572 AA789302 AI73611 AW841126 D60937
432125	341776_1	AW972830 AA527647 AA489820 AA570362
432363	345469_1	BE157283 BE157287 AA502438
437159	43392_5	AI685464 AW971336 AA513587 AA525142
437866	44433_2	AW972667 AA526539 AI057032 AW167842
439047	468139_1	AA534489 AW970240 AW970323
439518	47334_1	AW090198 AW173544 AW439860 AW007307 AI762577 W86516 AA160485 AA974203 AI589521 AW451857 AW450602 AI702529 AA630766
450506	838_1	AI801808 AW611634 AI393606 AW235356 AW000736 AW468599 AI582546 AA962057 AA523012 AW51
450580	83929_1	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
452260	9074_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA04
453024	944876_28	AW979177 AA846994 AA829672
454473	1292917_1	W76326 AF086341 W72300
456719	222707_1	NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772
		AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296
		N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
		AA453208 NM_004251 U44103 AI671547 N57463 AW007521 AI479232 T82809 R67109 AW796099 AI833027 AI765395 AI763029 AI758228
		BE326331 AI934576 AI922378 AW276431 AI718466 N36566 AA904753 BE464245 AI338752 AI
		AW846787 AW903370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984802 AW984802 AW984800 AW984799 AW984825 AW984782 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632555 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863
		AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW2

TABLE 62C

Key: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Key	Ref	Strand	Nt_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199168,199316-199548
401197	9719705	Plus	176341-176452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-66031
401744	2576349	Plus	14595-14751
401807	7331536	Plus	152325-152912
402474	7547175	Minus	53526-53628,55755-55920,57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671,86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	69340-69615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39624-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160605
406038	8389537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75th percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75th percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of normal prostate tissue to prostate tumor tissue

Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M81650	Hs.1968	semenogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC:12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X83957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73980	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.99949	prolactin-induced protein	11.8
415337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	AI738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	AI791314		gb:ae46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
405001	U58196		interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455649	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	ankylosis, progressive (mouse) homolog	5.6
404606			Target Exon	5.6
432326	AI280308	Hs.274351	amiloride-sensitive cation channel 2, na	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C11000936.gi 3746443 gb AAC63969.1 (AF0	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 93	4.8
442082	R41823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440965	AI523646	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N1B H	4.6
441040	AW449782	Hs.178803	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
458895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004348*-Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
458840	AI580296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435866	AA704538	Hs.119740	ESTs	4.2
423871	AA331906		gb:EST35805 Embryo, 8 week 1 Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AI218950	Hs.125461	hypothetical protein FLJ11539	4.1
	425094	AI955956	Hs.21417	ESTs	4.1
5	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AI028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24185		hypothetical protein	4.0
	449233	BE048401	Hs.196511	ESTs	3.9
15	435457	AA682421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	AI821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-008-e05 LT0032 Homo	3.8
	409679	BE250521		ras homolog gene family, member A	3.8
20	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL036568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:np86b01.s1 NCL_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
	455887	BE154173		gb:PM1-HT0340-201299-004-f12 HT0340 Homo	3.8
25	443313	AI796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:ze85d01.r1 Soares_fetal_heart_NbHH19W	3.8
	400499			C10001858:gil6679124[ref]NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
30	427318	AF186081	Hs.175783	zinc transporter	3.7
	417620	R02530	Hs.191198	ESTs	3.7
	404660			C9000841*:gil12654691[gb]AAH01185.1 AAHO	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
	436524	AA922236	Hs.221037	ESTs	3.7
35	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
40	426736	AA431615	Hs.130722	ESTs	3.7
	434552	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	AI222422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
	442097	AW015799	Hs.128474	ESTs	3.6
45	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
	400749			NM_003105*:Homo sapiens sortilin-related	3.6
50	450295	AI766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:aa63f08.r1 NCL_CGAP_GCB1 Homo sapiens	3.5
	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
55	429043	AI824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	AI371978	Hs.128326	ESTs	3.4
60	445045	AI652576	Hs.147256	ESTs	3.4
	406177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:KJAA1578 protein (Fragm	3.4
	445797	AI253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	AI625304	Hs.190312	ESTs	3.4
	442027	AI652926	Hs.128395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gil2695979[emb]CAA70854.1] [Y0	3.4
	448516	AW898595		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
70	450588	AA010319	Hs.60389	ESTs	3.4
	447600	AI420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
	418672	L44284	Hs.12915	ESTs	3.3
75	446593	W79572	Hs.13277	hypothetical protein FLJ22054	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415895	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
	458539	AI733837	Hs.145661	ESTs	3.3
80	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413361	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10954	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AI423317	Hs.164680	ESTs	3.2
	418092	R45154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AI010063	Hs.343603	titin-cap (telathonin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.110293	ESTs	3.1
20	423837	AW937063	Hs.275150	gb:PM3-DT0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961613	Hs.127838	ESTs	3.1
	421813	BE048255		gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW293237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.166767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	AB040919	Hs.210958	KIAA1486 protein	3.1
	421894	AI418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658*HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD002 protein	3.0
	426349	AI308855	Hs.301497	arghnyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430661	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459647	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	3.0
	456103	Z39430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI636539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NhHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-160400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp761071 (tr	2.9
	453126	AA032155	Hs.61622	ESTs	2.9
	459421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	419254	AI469453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipooxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	2.9
	422482	AI439905	Hs.344476	gb:z57g08.x1 NCI_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:z199b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AI023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fis, clone A	2.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALU6_HUMAN A	2.8
	451632	BE005934	Hs.310625	EST	2.8

	426481	AW963941	gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656		Target Exon	2.8
	407269	AJ245210	gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	ESTs	2.8
	433565	AA599763	ESTs	2.8
	451004	AA044957	gb:z53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770		NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	ESTs	2.8
	454445	AW749432	gb:RC3-BT0385-301299-011-a09 BT0385 Homo	2.8
	419494	W01060	ESTs	2.8
	427639	AW444530	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	ESTs	2.7
15	406337		C14000021:gij7242973 dbj BAA92547.1 (AB	2.7
	401884		Target Exon	2.7
	406881	D16154	gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	ESTs	2.7
	450044	R66444	ESTs	2.7
20	403630		C3001708*:gij4758028 ref NP_004360.1 co	2.7
	445514	AI241280	ESTs	2.7
	446362	AW612481	ESTs	2.7
	432492	AW275110	ESTs	2.7
	430889	U22491	G protein-coupled receptor 7	2.7
25	434316	AW411330	annexin A6	2.7
	413155	BE067952	gb:CMO-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	numb (Drosophila) homolog-like	2.7
	446523	NM_003063	sarcolipin	2.7
	449923	BE258051	gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129	gb:DKFZp547F152_r1 547 (synonym: hibr1)	2.7
	405678		CX001454:gij8393794 ref NP_058681.1 myo	2.7
	432789	D26361	KIAA0042 gene product	2.7
	455791	BE090689	gb:RC1-BT0720-280300-011-108 BT0720 Homo	2.7
	449109	AW270992	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	zinc finger 1111	2.7
	415984	R19046	gb:yg21111.r1 Soares infant brain 1N1B H	2.7
	402844		C1000118*:gij9951913 ref NP_062832.1 pr	2.7
	456666	AA452512	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	ribosomal protein S14	2.7
40	404979		Target Exon	2.7
	412318	AW936911	hypothetical protein MGC11082	2.7
	424361	AK001551	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	ESTs	2.7
	441975	AW173248	EST	2.7
45	457021	AW968934	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457861	AW450205	BCL2-like 1	2.7
	439204	AF087987	EST	2.7
	415642	U19878	transmembrane protein with EGF-like and	2.7
50	446847	T51454	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
	443359	AI792583	ESTs	2.7
	447336	AW139383	ESTs	2.7
	449045	BE072483	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	DKFZP434B172 protein	2.7
	436030	R02287	ESTs	2.7
55	449589	AW752437	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	436092	AI345995	ESTs	2.6
	415054	AI733907	gb:z086h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	ESTs	2.6
60	410483	BE163567	gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083	wee1 (S. pombe) homolog	2.6
	426629	AI203933	ESTs	2.6
	415831	H15145	ESTs	2.6
	412281	AI810054	ESTs	2.6
65	434898	AW500458	KIAA0460 protein	2.6
	422229	AF134414	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061	gb:yd22108.s1 Soares fetal liver spleen	2.6
	458546	AI215667	ESTs	2.6
	438648	AA813125	ESTs	2.6
70	450399	AW511049	ESTs	2.6
	420833	R47948	ESTs	2.6
	453903	AW299606	ESTs	2.6
	443550	AI698330	ESTs	2.6
	427419	NM_000200	Histatin 3	2.6
75	423741	AA330362	gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	ESTs	2.6
	441358	AW173212	ESTs	2.6
	402706		Target Exon	2.6
	436054	AI076262	ESTs	2.6
80	402749		Target Exon	2.6
	442472	AW806859	gb:MRO-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872	gb:oc57d07.s1 NCI_CGAP_Lu5 Homo sapiens	2.6
	405554		Target Exon	2.6

	405003		Target Exon	2.6
	459584	AI910884	ESTs	2.6
	441597	AW135032	ESTs	2.6
5	411280	N50617	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	tumor necrosis factor receptor superfam	2.6
	445060	AA830811	ESTs	2.6
	436260	BE172762	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	hypothetical protein FLJ21120	2.6
10	401716		C16000902:gij403440[gb]AAA73168.1j (M817	2.6
	416628	W03955	gb:za62d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	ESTs, Weakly similar to I38022 hypothei	2.6
	440702	AA904178	ESTs	2.6
	456310	AA225522	gb:nc25c06.r1 NCI_CGAP_Pr1 Homo sapiens	2.6
15	451255	AA020857	ESTs	2.6
	455737	BE072246	gb:QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	AI220072	ESTs	2.6
	408432	AW195262	gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens	2.6
	445874	BE326671	ESTs	2.6
20	441063	AA913819	ESTs	2.6
	455505	AW970640	ESTs	2.6
	453491	AL040177	gb:DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749	gb:PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456990	NM_004504	HIV-1 Rev binding protein	2.6
25	444130	AI125263	ESTs	2.5
	422210	BE269319	steroid dehydrogenase-like	2.5
	424241	AW995948	Homo sapiens pyruvate dehydrogenase kina	2.5
	451606	AA018791	AlE-75 binding protein protein	2.5
	400427	AB044934	histamine H4 receptor	2.5
30	410443	BE062906	KIAA1546 protein	2.5
	455210	AW866599	gb:QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	CGI-203 protein	2.5
	441191	AI693930	ESTs	2.5
	413489	BE144228	gb:MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
35	448215	N34740	ESTs	2.5
	419354	M62839	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	ESTs	2.5
	450724	R55428	gb:yl79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	ESTs	2.5
	412671	AW977734	gb:EST389963 MAGE resequences, MAGO Homo	2.5
	456401	W28146	gb:43f11 Human retina cDNA randomly prim	2.5
45	404678		Target Exon	2.5
	408520	AA225063	ESTs	2.5
	411332	AW837212	gb:QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	alkylglycerone phosphate synthase	2.5
	429906	AL080137	ESTs	2.5
50	433712	AF090887	Homo sapiens clone HQ0085	2.5
	438353	BE539951	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probe set identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048462_1	AW176091 H24234
	408432	1058667_1	AW195262 R27868 AW811262
	409679	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 AJ221491 AA194239 D63046 AA193426 AA773243 AA193293
65	410483	1204995_1	BE163567 BE073689 BE073747 BE073780 BE073739 BE073748 BE163495 AW750178 BE163491 BE073763 BE073671
	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845893 AW845989
70	411829	1260309_1	AW865749 BE179419 BE179492
	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946
	413381	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
75	415054	151827_1	AJ733907 AA159708 AI732614
	415098	1522174_1	D59687 D59694 D59656 D59589
	415131	1523680_1	D61119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35694 H12035 R53312
	416628	1604848_1	W03955 H82332 H69247 H72486
80	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	419896	1888662_1	Z99362 Z99363
	420778	196389_1	AW970512 AA280251 AI652287 BE466438 AI650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 H87796
	423772	23188_1	AA306537 NM_007241 AF155102 BE388339 BE614027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519 AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW468227 AI680027 AW090513 AA662830 F30995 AI351985 AI424349 AW009599 C02215 AI6525
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421765 AA456076 AI290275 AA455579
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	435383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
	436190	41555_1	AK001059 AA633055
15	438535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
	447518	724787_1	T80061 AI382804
20	447600	728288_1	AI420990 AI399725 AI401757
	448516	766241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI525093
	449923	81926_1	BE258051 R45758 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
25	452351	91233_1	AA026647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866611 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455649	1348708_1	BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072256 BE072211 BE072242
	455791	1365954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380836_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844649_2	W28146 W28187

TABLE 63C

45	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham l. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham l. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
50	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400461	9929654	Plus	32727-32846,32929-33051
	400499	9796071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7799787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	89182-90053
	401896	8569194	Plus	115129-115294
	401917	9502466	Plus	25054-25229
	402422	9796344	Minus	32843-33008
65	402460	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797648	Plus	149982-150929
	402706	8894426	Minus	148640-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-15930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8469080	Minus	94723-94859
	403630	8569999	Minus	13909-14466,15251-15760,16898-17431,41742-42440
	403649	8705159	Minus	27141-27247
75	404260	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	9212936	Minus	22310-23269
	404660	9797068	Plus	168215-168916
	404678	9797204	Plus	115196-115448
80	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9929758	Plus	126475-126773

405152	9965561	Minus	137662-137969
405258	7329310	Plus	129930-130076
405422	7243869	Minus	101938-102079, 102261-102443, 102896-103202
405564	2114222	Minus	16766-17344
405678	4079670	Plus	151821-152027
405735	9931101	Minus	29854-29976
405770	2735037	Plus	61057-62075
406003	8247800	Plus	42079-42516
406085	9123888	Plus	18665-18843
406177	7279760	Minus	18930-19148
406337	9213455	Plus	90117-90337
406398	9256276	Minus	118691-118959
406600	8248616	Minus	36296-36610

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Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to normal adult body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
420154	AI093155	Hs.95420	JM27 protein	49.6
425747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	47.2
419526	AI821895	Hs.193481	ESTs	43.6
432441	AW292425	Hs.163484	ESTs	42.7
431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothe	30.2
407202	N58172	Hs.109370	ESTs	26.1
432101	AI918950	Hs.123642	EphA3	25.8
400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	25.5
425075	AA506324	Hs.1852	acid phosphatase, prostate	24.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	24.4
410929	H47233	Hs.30643	ESTs	21.1
400287	S39329	Hs.181350	kallikrein 2, prostatic	20.3
446057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	19.8
423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, D	18.6
415989	AI267700		ESTs	17.8
428336	AA503115	Hs.183752	microseminoprotein, beta-	17.3
450693	AW450461	Hs.203965	ESTs	16.7
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	16.7
407168	R45175	Hs.117183	ESTs	15.5
408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	15.5
454119	BE549773	Hs.40510	uncoupling protein 4	14.5
428819	AL135623	Hs.193914	KIAA0575 gene product	14.5
400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	14.4
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	14.3
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	14.2
433444	AW975324	Hs.129816	ESTs	13.8
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	13.5
428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	12.9
401424			NM_001172:Homo sapiens arginase, type II	12.7
432435	BE218886	Hs.282070	ESTs	12.5
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	12.3
446100	AW967109	Hs.13804	hypothetical protein dJ452023.2	12.0
425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.9
407275	AI364186		gb:qw34h07.x1 NCI_CGAP_U14 Homo sapiens	11.8
452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.7
432473	AI202703	Hs.152414	ESTs	11.3
410330	AW023630	Hs.159425	ESTs	11.2
431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	11.2
452792	AB037765	Hs.30652	KIAA1344 protein	11.2
418848	AI820961	Hs.193465	ESTs	10.9
400292	AA250737	Hs.72472	BMP-R1B	10.9
433647	AA603367	Hs.222294	ESTs	10.8
453160	AI263307	Hs.239884	H2B histone family, member L	10.8
409262	AK000631	Hs.52256	hypothetical protein FLJ20624	10.6
431474	AL133990	Hs.190642	CEGP1 protein	10.3
429220	AW207208		ESTs	10.3
428134	AA421773	Hs.161008	ESTs	10.2
408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA	10.1
456497	AW967956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	9.8
434792	AA649253	Hs.132458	ESTs	9.7
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	9.5
428398	AI249368	Hs.98558	ESTs	9.4

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.7130	copine IV	9.1
	453096	AW294631	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
	450642	R39773	Hs.7130	copine IV	8.7
15	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
	446336	AW815036	Hs.151251	ESTs	8.4
20	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA767382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z ³ -1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
	433923	AI823453	Hs.146625	ESTs	7.7
30	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441690	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	7.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
35	431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739*Homo sapiens E3 ubiquitin lig	7.3
	409557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.155689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	7.1
	449300	AI656959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799909	Hs.156989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415785	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA354940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCL_CGAP_Pr3 Homo sapiens	6.3
	435375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403667			Target Exon	6.1
	424846	AU077324	Hs.1832	neuropeptide Y	6.1
	439569	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	6.0
	415621	AI648602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N99828		gbza32c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
5	447156	AW274731	Hs.157920	ESTs	5.9
	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
10	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
15	434485	AI623511	Hs.118567	ESTs	5.8
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155694	Hs.191060	ESTs	5.6
25	404571			NM_015902*:Homo sapiens progesteron induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	439092	AA830149		gb:acc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AL049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		odt (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE584205	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
	432682	AI376400	Hs.159588	ESTs	5.5
35	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-05 CT0261 Homo	5.5
	426581	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
	443635	AI080230	Hs.134214	ESTs	5.5
40	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125062	ESTs	5.3
	400294	N95796	Hs.278595	Homo sapiens prostein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	448715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
60	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	5.3
	423101	MB3941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82065	interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI459306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCI_CGAP_Pt3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
75	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	445238	AA883971	Hs.187506	ESTs	5.1
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
80	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
5	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	5.0
	407198	H91679		gb:yy04a07.s1 Soares fetal liver spleen	5.0
	403696			C4001100:gi15852342[gb]AAD54015.1] (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCL_CGAP_Thy1 Homo sapiens	5.0
10	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
15	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	435937	AA830893	Hs.119769	ESTs	4.8
20	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	447058	AJ939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29882		ESTs	4.8
25	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8
	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	431657	AJ345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	4.7
30	452843	AJ796769	Hs.208320	ESTs	4.7
	458229	AJ929602	Hs.177	phosphatidylinositol glycan, class H	4.7
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
35	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AJ792628	Hs.133273	ESTs	4.6
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AJ831190	Hs.166876	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
40	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AJ031771	Hs.132586	ESTs	4.6
	454024	AA939527	Hs.293907	hypothetical protein FLJ23403	4.6
45	447805	AW627932	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
50	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AJ655499	Hs.161712	ESTs	4.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AJ760833	Hs.293971	ESTs	4.5
55	437252	AJ433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	420133	AA426117	Hs.155543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 67	4.5
	439752	T78968	Hs.14411	ESTs	4.5
60	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
	445372	N36417	Hs.144928	ESTs	4.5
	452055	AJ377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
65	418019	R68911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412643	AW971239	Hs.136433	ESTs	4.4
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420608	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
75	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
	435655	AW105663	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376:PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
80	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432960	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	4.3

	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW958065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
5	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	4.3
	420111	AA255652		gb:zs21h11.r1 NCL_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
10	405348			C7001664:gil12698061[jdbj]BAB21849.1 (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
15	420905	AA521307	Hs.186651	ESTs	4.2
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
20	450597	AI701635	Hs.207077	ESTs	4.2
	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	AB040907	Hs.278436	KIAA1474 protein	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
25	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
30	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
35	435714	AA728964	Hs.293399	ESTs	4.1
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
40	445206	AI350199	Hs.269990	ESTs	4.1
	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	449907	AA004825	Hs.103281	ESTs	4.1
	430487	D87742	Hs.241552	KIAA0268 protein	4.1
45	448152	AI741053	Hs.170770	ESTs	4.1
	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL039402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58kD)	4.1
	400746			Target Exon	4.1
50	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	446416	AV658299	Hs.163959	ESTs	4.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
55	442338	AI761976	Hs.156080	ESTs	4.0
	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415861	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
60	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	432229	AW290976	Hs.143587	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.0
65	421312	AA824627	Hs.291670	ESTs	4.0
	448131	AI675054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partia	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
70	434844	AF157116	Hs.22350	hypothetical protein LOC56757	4.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346335	ESTs	4.0
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	4.0
75	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441735	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
80	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	416288	HS1299	gb:yp07c06.s1 Soares breast 3NbHBst Homo	3.9
	420301	AA767526	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	ESTs	3.9
5	435878	R08330	ESTs	3.9
	446862	AV660697	ESTs	3.9
	447530	AW192063	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Homo sapiens, clone IMAGE:4298026, mRNA,	3.9
	401403		Target Exon	3.9
10	448779	BE042877	ESTs	3.9
	420533	AI809510	ESTs	3.9
	411084	T18987	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	KIAA0888 protein	3.9
	423453	AW450737	CGI-09 protein	3.9
15	434833	AF156548	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AW848047	gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	ESTs	3.9
	421129	BE439899	ESTs	3.9
20	424332	AA338919	ESTs	3.9
	441766	R53790	hypothetical protein FLJ14393	3.9
	447033	AI357412	ESTs	3.9
	439306	BE220199	WD40 protein Cioa1	3.8
	410352	AW969725	KIAA0373 gene product	3.8
25	407961	AW672939	origin recognition complex, subunit 2 (y	3.8
	410252	AW821182	microfibrillar-associated protein 1	3.8
	439560	BE565647	hypothetical protein FLJ12820	3.8
	440450	AI333129	ESTs	3.8
	458811	AI268407	DC-specific transmembrane protein	3.8
30	419589	AW973708	Homo sapiens cDNA FLJ13446 fis, clone PL	3.8
	431576	M76665	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE617907	ESTs	3.8
	438379	N23018	C-terminal binding protein 2	3.8
	416009	Z43062	gb:HSC12E041 normalized infant brain cDN	3.8
35	416534	H69043	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	423044	AA320829	protocadherin 18	3.8
	424701	NM_005923	mitogen-activated protein kinase kinase	3.8
	433507	AI817336	ESTs	3.8
	437718	AI927288	ESTs	3.8
40	419831	AW448930	ESTs	3.8
	424830	AW270580	ESTs, Weakly similar to putative p150 [H	3.8
	426981	AL044675	KIAA0530 protein	3.8
	431447	AA505138	ESTs	3.8
	435932	W03928	ESTs	3.8
45	442447	AA999723	ESTs	3.8
	403242		Target Exon	3.8
	433908	AW298141	ESTs	3.8
	452323	W44356	ESTs, Weakly similar to T33468 hypothe	3.7
	412095	AI624707	Homo sapiens cDNA: FLJ21592 fis, clone C	3.7
50	418759	AA227879	ESTs	3.7
	422299	AK000181	hypothetical protein FLJ20174	3.7
	452462	BE173515	gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	423096	AA732684	progesterone induced protein	3.7
	454037	AW998716	gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420564	ESTs	3.7
	447785	AL041765	ESTs	3.7
	451746	M86178	ESTs	3.7
	453293	AA382267	ESTs	3.7
	436671	AW137159	ESTs	3.7
60	407437	AF220264	gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963897	KIAA1435 protein	3.7
	420092	AA814043	ESTs	3.7
	446947	AF146747	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384726	hypothetical protein FLJ23316	3.7
65	419875	AA853410	proenkephalin	3.7
	431231	AA653552	ESTs	3.7
	418348	AI537167	hypothetical protein FLJ23560	3.7
	419261	X07876	wingless-type MMTV integration site fami	3.7
	422899	D16471	Human mRNA, Xq terminal portion	3.7
70	429163	AA884766	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	ESTs	3.7
	440947	AA910403	ESTs	3.7
	404561		trichorhinophalangeal syndrome I gene (T	3.6
	430096	U91935	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	ESTs	3.6
	426991	AK001536	Homo sapiens cDNA FLJ10674 fis, clone NT	3.6
	431316	AA502663	ESTs	3.6
	414178	AW957372	ESTs, Weakly similar to I38022 hypothe	3.6
	450530	AA010429	ESTs	3.6
80	411067	AI681006	ESTs	3.6
	436326	BE085236	aldo-keto reductase family 1, member B1	3.6
	410268	AA315181	six transmembrane epithelial antigen of	3.6
	423590	AW952412	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
10	433563	AI732637	Hs.277901	ESTs	3.6
	425465	L18954	Hs.1904	protein kinase C, ι ola	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517*:gi 4758712 ref NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
15	435177	AI018174	Hs.42936	ESTs	3.5
	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
20	427304	AA761526	Hs.163853	ESTs	3.5
	434763	AA648618		gb:ns07a11.1 NCI_CGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
25	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.190555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	419964	AA811657	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19928	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
65	429165	AW009886	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
70	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
	427615	BE410107	Hs.179817	CGI-82 protein	3.3
75	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
80	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
5	447182	BE241858	Hs.17585	KIAA0801 gene product	3.3
	423545	AI215632	Hs.147487	ESTs	3.3
	429227	AI961456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975590	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
15	411435	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	436962	AW377314	Hs.5364	DKFZP564I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	3.3
20	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW665130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61893	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	3.2
	423595	R82826	Hs.220702	ESTs	3.2
	407021	U52077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450587	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.2
	425557	T89839	Hs.119471	ESTs	3.2
	459546	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338:gij7459502[pir]S74665 outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40		436995	AI160015	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049610	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X81895	Hs.194765	Hsapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437866	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.66731	homeo box B13	3.2
	438899	AF085833	Hs.135624	ESTs	3.2
	415862	R51034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI458682		gb:tk13e01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405548			Target Exon	3.1
	439584	AA838114	Hs.221612	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	D54745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
75	423855	AA331761	Hs.254859	ESTs	3.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
80	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
	433610	AA806822	Hs.112547	ESTs	3.1
	435295	N73895		gb:za62d05.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
10	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogeni	3.1
	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fis, clone H	3.1
15	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	425480	AB023198	Hs.158135	KIAA0981 protein	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
20	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	3.1
	433852	AI378329	Hs.126629	ESTs	3.0
	446558	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	Hs.159993	glycosyltransferase	3.0
	424690	BE538356	Hs.151777	eukaryotic translation initiation factor	3.0
25	405264			NM_030813*:Homo sapiens suppressor of po	3.0
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothe	3.0
	434497	AI821803	Hs.136580	ESTs	3.0
	420355	AW968263	Hs.123126	ESTs	3.0
30	403481			Target Exon	3.0
	412988	BE046680		gb:tn42h03.x1 NCL_CGAP_RDF2 Homo sapiens	3.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
35	426174	AA547959	Hs.115838	ESTs	3.0
	430459	BE178539	Hs.278634	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448686	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
40	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132950	ESTs	3.0
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450863	AI864668	Hs.48832	ESTs	3.0
45	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.0
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
50	420407	AA814732	Hs.145010	lipopolysaccharide-specific response S-II	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CMO-CT0103-120899-037-g07 CT0103 Homo	3.0
55	437323	AA371145	Hs.194397	taplin receptor	3.0
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.0
	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
60	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fis, clone PL	3.0
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	428634	AA811845	Hs.106290	Kelch motif containing protein	3.0
65	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.162898	ESTs	3.0
	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retrovira	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

80	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW846433 AW846159 AW846377 AW846528

411479	1247077_1	AW848047 AW848202 AW848531 AW848142 AW848702 AW848121 AW848532 AW848140 AW848571 AW848009 AW848067 AW848059
412988	1342150_1	AW848905 AW848214
413081	1348563_1	BE046680 BE046738 BE044958
413525	1374635_1	BE064415 BE064430 BE064448
415989	156454_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
416009	1566379_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
416288	1585983_1	Z43062 R13213 H14422
416882	162718_1	H51299 H44619 H46391 R86024 H51892 T72744
418259	173388_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
418866	179788_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
418948	180808_1	AA215404 AI990909 BE464132 AW271459 N74332 AI262061
419536	185688_1	T65754 AA229857 AA229658
420111	190755_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
420352	192979_1	AA603305 AA244095 AA244183
423412	228001_1	AA255652 AA280911 AW967920 AA262684
424200	236595_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
426413	266650_1	AF109300 AI299378 AI202654
426503	268283_1	AA337221 AA336756 AW966196
426991	27415_1	AA377823 AW954494 AI022688
428002	285602_1	AA380153 AA380233 AW963529
428342	290035_2	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
429163	300543_1	AA418703 AA418711 BE071915 BE071920 BE071912
429220	301384_1	AI739168 AA426249 AI199635 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
430535	319643_1	AI092404 AI085630 AA731340
432600	350959_1	AA884766 AW974271 AA592975 AA447312
432765	353907_1	AW207206 AW341473 AA448195 AI951341
433523	368873_1	AW968485 AW968670 AA480922 BE350425
434763	392847_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
436295	41733_1	AJ003429 AJ003367 AA564825
436326	41795_2	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
437866	44433_2	AA648618 AW974389 H51771
439092	468554_1	N73895 AJ001872
439306	47088_1	BE085236 BE085317 X04236 AA577534 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281
440840	50357_2	AW593405 AI825755 AI350499 AI655710 AI972281 AI654949 BE073961 BE073962 BE041399 AW750214 AA228488 BE074016 AI908706
440947	505904_1	AW270601 AW873282
442481	543588_1	AA156781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
445432	63943_1	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866688 AI572124 AA043777 AA040926 D20160 AI536733
448044	747196_1	AA812489 AW874142 AI47188
449343	80517_2	AA830149 AW978407 M85983 AW503637
449570	81018_1	BE220199 W01813 AF086118 N70760 BE221405
449625	8113_1	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW051920 AI288591 AW236114 AI302852 AI038548 AA534496 AI979207
450317	831956_1	AA921877
450580	83929_1	AA910403 AI815593 W58361 AW162520 AI816550
450582	83933_1	N99828 BE079873 AI110738 AF074645
450687	84327_1	AV653771 BE089370
452462	918580_1	AI458682 H24240 R14537 R18428 AW867082
453682	977454_1	AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053
454037	996287_1	AW889353 AA521308 AA001203 W92828 AI207778 AA746655 R78710 W24617 AA024605 C01747 AW173095 W61229 W92685 AA742467
454096	1007449_1	H00789 R76925 AW1828
454171	1049240_1	AA001793 AA001871
454457	1207274_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760
454860	1237732_1	AI8674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
455276	1272541_1	AI692689 R14223 R18395
455646	1348557_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
455710	1352368_1	AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
457374	328758_1	AA164518 AA730973 W00417 W65303
458912	823104_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
		AA495800 AA495737 AA010736 AA654716 AA640726
		BE173515 BE173560 AI902860
		T79703 T96307 AL079725
		AW998716 AW022148 N68020
		AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
		AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
		AW753456 AW753036 AW854868 AW854862
		AW835767 AW835537 BE160187
		AW849046 AW847956 AW849039 AW847957 AW848279 AW848598 AW849034 AW849033
		BE176479 BE176678 BE176357 BE176550 AW888079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
		BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
		BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
		AA493662 AW897396 BE154814
		AJ911066 AJ933734 AI680888 AJ003599

TABLE 64C

Pkey: Unique number corresponding to an Eos probe set
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
------	-----	--------	-------------

5	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710966	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9965004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532158	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85th percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

35	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to prostate tumor tissue		
	Pkey	ExAccn	Unigene ID	Unigene Title
	428134	AA421773	Hs.161008	ESTs
	446336	AW815036	Hs.151251	ESTs
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K
	400533			ENSP00000209376*-PRED65 protein (Fragmen
	418310	AA814100	Hs.86693	ESTs
	404592			NM_022739:Homo sapiens E3 ubiquitin lig
45	454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo
	400080			Eos Control
	459546	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo
	420352	BE256835		gb:601117374F1 NIH_MGC_16 Homo sapiens c
	438231	AW594539	Hs.155689	ESTs
50	418387	R18085		gb:yg16b12.r1 Soares Infant brain 1N1B H
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe
	404867			Target Exon
55	430635	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo
	423789	AK002084	Hs.132651	hypothetical protein FLJ11222
	412988	BE046680		gb:tm42h03.x1 NCI_CGAP_RDF2 Homo sapiens
	400440	X83957	Hs.83870	nebulin
60	454171	AW854832		gb:QV2-CT0261-201099-011-f05 CT0261 Homo
	400086			Eos Control
	440911	AA909536	Hs.143562	ESTs
	425312	AA354940	Hs.145958	ESTs
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence
65	419015	T79262	Hs.14463	ESTs
	453789	AA628517	Hs.118502	ESTs
	424940	AA985308	Hs.283902	ESTs
	403667			Target Exon
70	429014	AI800518	Hs.118158	ESTs
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte
	419999	AI760942	Hs.191754	ESTs
	405348			C7001664:gi12698061[jdbj]BAB21849.1] (AB
	404003			Target Exon
75	453200	AA033832	Hs.212433	ESTs
	428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi
	432319	AW510770	Hs.128386	ESTs
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi
	443361	AI792628	Hs.133273	ESTs
	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo
80	439079	AF085937	Hs.38348	ESTs
	422081	AW136820	Hs.196011	ESTs
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked
	423529	T87318	Hs.120411	ESTs

	436578	AI091435	Hs.134859	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	5.4
	433087	AI720586	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothel	5.3
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
15	435375	AI733810	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
20	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421188	AA284658	Hs.261493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*:Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fts, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442295	AE827248	Hs.224398	Homo sapiens cDNA FLJ11469 fts, clone HE	4.6
	434589	AF147383		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*:Monocytic leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*:gij4758712[ref]NP_004659.1] al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.153287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn56d05.s1 Stralagene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424586	AA345504		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	4.3
70	441620	R59595	Hs.26675	ESTs	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	405500	U08098	Hs.54576	sulfotransferase, estrogen-prefering	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
80	430124	AW204894	Hs.253450	ESTs	4.2
	410790	AW803357		gb:JL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	H54253	Hs.205241	ESTs, Weakly similar to S65657 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AF741053	Hs.170770	ESTs	4.1
	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
5	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-105-g05 DT0020 Homo	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
10	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, molo	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
15	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453387	AI990741	Hs.252809	ESTs	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	454806	AW872430	Hs.273743	ESTs	3.9
20	429056	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9658, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 gatac	3.9
	407834	AW084991	Hs.26100	ESTs	3.9
25	400398	AF137396	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C140004822:gil9790241[refl]NP_062628.1] S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthine dehydrogenase	3.9
	436350	AA713661	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321'Homo	3.8
	452320	AA042873	Hs.160412	ESTs	3.8
	402145			Target Exon	3.8
35	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized Infant brain cDN	3.8
	434381	AA631834		gb:mp77h05.s1 NCL_CGAP_Pr2 Homo sapiens	3.8
40	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29882		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
45	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
50	449264	AI637649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
55	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311259	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
	448135	AI470874	Hs.343799	ESTs	3.7
60	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-e04 CT0328 Homo	3.7
	409189	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	3.7
65	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
	419261	X07876	Hs.89791	wingless-type MMTV Integration site fami	3.7
70	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
75	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AA446167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
	455057	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI671141	Hs.211122	ESTs	3.6
	451193	N29850	Hs.44098	ESTs	3.6
5	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517*:g 4758712 ref NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813*:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:ns07a11.1 r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769*:BG153O3.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AIW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	410551	R36730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765337	Hs.145095	ESTs	3.4
	442388	AW663442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_total_fetus_Nb2HF8_	3.3
50	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW292635	Hs.346145	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	449256	AA059050	Hs.59847	ESTs	3.3
	432550	AW297206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.65641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW968263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothe	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501*:g 129092 sp P23270 OLF7_RAT O	3.2
	411552	AW851255		gb:IL3-CT0220-160200-066-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.26085	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426629	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457136	AA428240	Hs.126083	ESTs	3.2
	443585	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AI754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
15	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445758	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	438142	T90309	Hs.269651	ESTs	3.1
	416423	H54375	Hs.268921	ESTs	3.1
25	448765	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
30	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	435628	W88732	Hs.36107	ESTs	3.0
	444326	AI939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H60457		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140: Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71886 Sla20-lik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458187	D56919	Hs.265848	myomegalin	3.0
	429430	AI381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0

55 TABLE 65B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 AW810325 AW810443 AW8
65	409189	110687_1	AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 NB4829 AA084752 AA076512 AA085119 AA085208 AA085045
	410559	1208283_1	AW754192 W00554 AW857797 AW754203 AW754197 AW754193
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
70	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1	AW845433 AW846159 AW846377 AW846528
	411518	1248692_1	AW850246 AW850251 AW850302
75	411552	1249255_1	AW851255 AW851432 AW850955
	412701	1322288_1	AW984757 AW984797 AW984734 AW984745
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
80	416422	1593811_1	H60457 H68709 H73528 H54335 R87154
	418059	171879_1	AA211586 F35799 AA211641 F29720 AW937387 AW937408
	418387	174731_1	R18085 AA219028 R17712 Z44345
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043

5	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300591 AW963893 AA300493
	424200	236595_1	AA337221 AA336756 AW966196
	424686	242486_1	AA345504 AA345251 AW963243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003367 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE089370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173560 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE068023 AW809375
	454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW861677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW953477 Z41970 F12435 T73989 T09387
	455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074935
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225060 AA225101
	457374	328758_1	AA493662 AW897396 BE154814

45

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probeset
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

55	Pkey	Ref	Strand	Nt_position
	400533	6981826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
65	403305	8099945	Plus	114632-114805
	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	105655-106050
	403433	9719511	Minus	72225-72437
	403481	9965004	Plus	93496-93633
70	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
75	404592	9943965	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	404967	7523744	Minus	89944-90729
	404995	6006247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
80	405321	3419846	Minus	44554-45210
	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85th percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AI202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AI354186		gb:qw34h07.x1 NCI_CGAP_UI4 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508353	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453387	AI930741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoleti	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.306201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023630	Hs.159425	ESTs	7.2
449300	AI656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AI472078	Hs.303662	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-R05 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N98828		gb:za32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145598	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PREDE65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436396	AI683487	Hs.152213	wingless-type MMTV Integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AI623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sepi	5.7
424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443361	AI792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF085937	Hs.38348	ESTs	5.5
430535	AW968485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AI091435	Hs.134859	ESTs	5.5
424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	5.4
421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AI733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278081	ESTs	5.4
416602	NM_006159	Hs.79389	nel (chicken)-like 2	5.4
433087	AI720686	Hs.152520	ESTs	5.3
439092	AA830149		gb:oc44f08.s1 NCI_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypothe	5.3

	423101	M83941	Hs.123642	EphA3	5.3
	437587	A1591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	A1359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA865818	Hs.174936	ESTs, Weakly similar to S71885 Ste20-lik	5.1
15	445238	AA883971	Hs.187506	ESTs	5.1
	450582	A1339732		G-rich RNA sequence binding factor 1	5.1
	420533	A1809510	Hs.118971	ESTs	5.1
	438447	A1082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889385	Hs.125468	ESTs	5.0
20	452891	N75582	Hs.212875	ESTs, Weakly similar to OYH9_HUMAN CILIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	A1820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	4.9
25	450497	H64159	Hs.15328	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
30	450317	A1692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
	443635	A1080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	A1796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
35	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
40	405348			C7001684:gil12698061 dij BAB21849.1 (AB	4.6
	419511	AA429750	Hs.75113	general transcription factor IIA	4.6
	447058	A1939456	Hs.160870	ESTs	4.6
	428218	AA424266	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211867	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	A1671141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	A1377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	A1093155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:zsz21h11.r1 NCI_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	A1692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
65	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	A1911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	A1701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	A1350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	A1741053	Hs.170770	ESTs	4.1
80	438875	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
5	435136	R27299	Hs.10172	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
15	412988	BE046680		gb:hn42h03.x1 NCL CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020695	Hs.91662	KIAA0888 protein	3.9
	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
20	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW569118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
30	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433908	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0067-250300-002-f11 BN0067 Homo	3.7
	432101	AI918950	Hs.123642	EphA3	3.7
40	418759	AA227879	Hs.187621	ESTs	3.7
	452462	BE173515		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	448568	AA149121	Hs.71947	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	436345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660697	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:zw05b07.s1 Soares_NhlHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
55	422899	D16471	Hs.121571	Human mRNA, 3' terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophalangeal syndrome I gene (T	3.6
	417565	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021987	Hs.59970	ESTs	3.6
	450630	AA010429	Hs.191939	ESTs	3.6
65	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
70	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C12000517*:g 4758712 ref NP_004659.1 a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ns07a11.r1 NCL CGAP_Ew1 Homo sapiens	3.5
80	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

5	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
10	436714	AA728964	Hs.293399	ESTs	3.4
	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfam	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBPI-like protein	3.4
20	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prol	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP3 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126288	Hs.192232	ESTs	3.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170685	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	418719	AW975580	Hs.161707	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f05 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53126	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein Claf1	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	3.2
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA768296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1	
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/ln	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	433444	AW975324	Hs.129816	ESTs	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypothe	3.1
	415861	Z43123	Hs.144513	ESTs	3.1
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	3.1
10	432527	AW975028	Hs.102754	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	417958	AA767382	Hs.193417	ESTs	3.1
15	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	405548			Target Exon	3.1
	423595	R82826	Hs.220702	ESTs	3.1
	412533	AA679863	Hs.69506	ESTs	3.1
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	3.1
25	405264			NM_030813*:Homo sapiens suppressor of po	3.1
	410869	AW608361		gb:MR1-ST0111-111099-003-R04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
30	435021	AA922192	Hs.54709	ESTs	3.0
	408832	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087		ESTs	3.0
	432319	AW510770	Hs.128386	ESTs	3.0
	453713	R20640	Hs.79133	cadherin 8, type 2	3.0
35	445784	AI253155	Hs.146065	ESTs	3.0
	416642	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
40	404995			ENSP00000251890*:Monocytic leukemia zinc	3.0
	444794	AI419991	Hs.145225	ESTs	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	420133	AA426117	Hs.155543	ESTs	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338	ESTs	3.0
50	449745	AI668593		gb:yl38a05.x5 Soares breast 3NbHBst Homo	3.0
	428412	AA428240	Hs.126083	ESTs	3.0
	428200	AI039624	Hs.98388	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
55	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 66B

60	Pkey: Unique Eos probeset identifier number CAT number: Gene cluster number Accession: Genbank accession numbers		
65	Pkey _i	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
	410869	1225123_1	AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
70	411436	1245660_1	AW846433 AW846159 AW846377 AW846528
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
	412988	1342150_1	BE046680 BE046738 BE044958
	413081	1348563_1	BE064415 BE064430 BE064448
75	413525	1374635_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
	416009	1566379_1	Z43062 R13213 H14422
	418948	180808_1	AI217097 AW886090 W38035 W38792 AA232835 AW936043
	420111	190755_1	AA255652 AA280911 AW967920 AA262684
80	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	424200	236595_1	AA337221 AA336756 AW966196
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	426002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912

428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AJ377728 AW293682 AI928140 AA731438
		AI092404 AI085630 AA731340
430535	319643_1	AW968485 AW968670 AA480922 BE350425
432765	353907_1	AJ003429 AJ003367 AA564825
433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW854390 AW864320
434763	392847_1	AA648618 AW974389 H51771
436295	41733_1	N73895 AJ001872
439092	468554_1	AA830149 AW978407 M85983 AW503637
439306	47088_1	BE220199 W01813 AF086118 N70760 BE221405
440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
442481	543588_1	N99828 BE079873 AI110738 AF074645
445432	63943_1	AV653771 BE089370
448044	747196_1	AI458682 H24240 R14537 R18426 AW667082
449570	81018_1	AA001793 AA001871
449745	814534_1	AI688593 AI820774 R86205 H39971 H22177 H26241
450317	831955_1	AI692689 R14223 R18395
450580	83929_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
		AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
		AA164518 AA730973 W00417 W65303
450582	83933_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
452462	918580_1	BE173515 BE173560 AI902860
453682	977454_1	T79703 T96307 AL079725
454037	996287_1	AW998716 AW022148 N68020
454096	1007449_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
454171	1049240_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454457	1207274_1	AW753456 AW753036 AW854868 AW854862
454665	1228599_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
454860	1237732_1	AW835767 AW835537 BE160187
454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
455067	1252050_1	AW854538 AW854418 AW854412
455276	1272541_1	BE176479 BE176678 BE176357 BE176550 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176382
455646	1348557_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
457374	328758_1	AA493662 AW897396 BE154814
458912	823104_1	AI911066 AI933734 AI680888 AJ003599

TABLE 66C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11297-12511
403481	9965004	Plus	93496-93633
403510	7652047	Plus	61866-62027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404561	9795980	Minus	69039-70100
404592	9943965	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404967	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28556-28684
405321	3419846	Minus	44654-45210
405348	2914717	Minus	43310-43462
405510	7630909	Minus	101028-101174
405548	1532158	Plus	11552-11686

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigeneID	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292425	Hs.163484	ESTs	56.0
	446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
10	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
15	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400287	S39329	Hs.181350	kallikrein 2, prostatic	28.8
20	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	25.5
25	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
30	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
35	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
40	431548	AI834273	Hs.9711	novel protein	16.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	16.5
	413597	AW302885	Hs.117183	ESTs	16.1
45	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	426501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
	418951	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278695	Homo sapiens prostate mRNA, complete cds	13.2
55	418848	AI820961	Hs.193465	ESTs	13.1
	428398	AI249368	Hs.98558	ESTs	13.0
	429220	AW207206		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
60	419078	M93119	Hs.89584	insulinoma-associated 1	12.3
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
65	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	412446	AI768015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
70	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AI088489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AU57019	Hs.116467	small nuclear protein PRAC	10.2
75	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449825	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
80	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935962	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

	447033	AI357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	LIM domain only 4	9.3
5	411687	AW182924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
10	432101	AI918950	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
15	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	8.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	8.5
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.5
	416182	NM_004354	Hs.79059	cyclin G2	8.5
20	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0866 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
30	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
	428728	NM_016625	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410889	X91652	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.5
	433285	AW975944	Hs.237396	ESTs	7.5
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	432586	AA568548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279490	Hs.86368	catmegin	6.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	6.8
	436962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18964	Hs.1904	protein kinase C, iota	6.6
60	450377	AB033091		KIAA1265 protein	6.6
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U28926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (6.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	6.2
	452744	AI267552	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
	448045	AJ297436	Hs.20166	prostate stem cell antigen	6.0
80	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189838	ESTs	6.0
	424036	AA770688		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
5	441866	BE464341	Hs.21201	nectin 3; DKFZP56680846 protein	5.8
	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	5.7
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	415621	AI648602	Hs.55468	ESTs	5.7
15	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens prolein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	5.4
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	5.4
20	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
30	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.1
35	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptotagmin 2	5.0
	403046			NM_005656:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-tryptophan/alpha-aminoadipate aminotra	5.0
	450164	AI239923	Hs.63931	ESTs	5.0
	417318	AW953937	Hs.240845	ESTs	4.9
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.126629	ESTs	4.9
	452879	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LIV-1 protein, estrogen regulated	4.8
	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
50	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.268126	spondin 2, extracellular matrix protein	4.8
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DEME-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	4.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
65	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	4.5
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JCS238 galactosy	4.5
75	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423583	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	FSDH region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456382	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

5	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
10	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheli	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.2
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23128	ESTs	4.2
15	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436556	AI364997	Hs.7572	ESTs	4.2
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
20	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
25	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
	432363	AA534489		gbn776g11.s1 NCL CGAP_Co3 Homo sapiens	4.1
	447574	AF162666	Hs.18895	tousled-like kinase 1	4.0
30	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gb:zp99b10.s1 Stralagene muscle 937209 H	4.0
35	418818	AA228699	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
40	415276	U88666	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
45	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
	432435	BE218886	Hs.282070	ESTs	3.9
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
50	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
55	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40334	ESTs	3.9
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
60	432675	AI791855		ESTs	3.8
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	3.8
	427479	BE410092	Hs.178471	KIAA0798 gene product	3.8
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249096	Hs.32793	ESTs	3.8
65	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
70	447620	AW290951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
75	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437957	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ21033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
80	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	3.7
	453469	AB014533	Hs.33010	KIAA0633 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calsarcin-1	3.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

5	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
	422424	AI186431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.6
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-85 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
10	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein DEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
15	429686	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	3.5
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
20	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	3.5
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
30	443884	N20617	Hs.194397	leptin receptor	3.4
	403752			NM_002753*:Homo sapiens mitogen-activate	3.4
	427723	AI355260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gbye53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	AJ026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.3
45	435655	AW105663	Hs.6947	HSPC069 protein	3.3
	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420568	F09247	Hs.247735	protocadherin alpha 10	3.3
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409960	BE261944		hexokinase 1	3.3
	433891	AA613792		gb:nc97h03.s1 NCL_CGAP_Pr2 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
60	419972	AL041465	Hs.182982	golgin-67	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.3
65	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26591	ESTs	3.2
70	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPUC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
	401519			C15000476".gil12737279[ref XP_012163.1]	3.2
75	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.2
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
80	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439593	BE073597	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	AI249502	Hs.29669	ESTs	3.2
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272608	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
	417193	AI922189	Hs.268390	hypothetical protein FLJ22795	3.1
15	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	435489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
	445943	AW898533	Hs.181574	ESTs	3.1
20	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
	423453	AW450737	Hs.128791	CGI-09 protein	3.1
25	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expressed	3.1
	436278	BE396290	Hs.5097	synaptogyrin 2	3.1
	432908	AI861896		ESTs	3.1
	432962	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.1
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	409757	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278962	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806583	Hs.125291	ESTs	3.1
	448807	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435551	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
45	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.211192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	3.0
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.195048	ESTs	3.0
	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412652	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10669	ESTs, Weakly similar to T00050 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78106	phosphodiesterase 8B	2.9
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420051	AW024937	Hs.29410	ESTs	2.9
80	431663	NM_016569	Hs.267182	TBX3-iso protein	2.9
	417622	AW298163	Hs.82318	WAS protein family, member 3	2.9
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195922	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

5	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
	445880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 fem	2.9
	437396	BE140396	Hs.21621	hypothetical protein DKFZp7620076	2.9
	413125	BE244589	Hs.75207	glyoxalase I	2.9
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	2.9
10	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
15	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bromodomain-containing 1	2.8
20	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	2.8
	441345	AW068579	Hs.7780	Homo sapiens mRNA: cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
	418166	AI754416		Cdc42 effector protein 3	2.8
25	448734	BE614070	Hs.326416	Homo sapiens mRNA: cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306881	MSTP043 protein	2.8
	426170	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
30	425320	U29344	Hs.83190	fatty acid synthase	2.8
	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
40	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
45	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
55	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	2.7
60	438157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	2.7
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
70	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
75	409550	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
80	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.7
	406627	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

5	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	nlban protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
	401197			ENSP00000229263*.HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
10	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA: cDNA DKFZp566L203 (fr	2.6
	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
	408157	AA047685	Hs.62946	ESTs	2.6
15	420805	L10333	Hs.99947	reticulin 1	2.6
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AI015709	Hs.172089	Homo sapiens mRNA: cDNA DKFZp586I2022 (f	2.6
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	2.6
20	425174	D87450	Hs.154978	KIAA0261 protein	2.6
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
25	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 krueppel-	2.6
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406670	W79632	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
30	449518	BE395253	Hs.30861	ESTs	2.6
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type 1 transmembrane receptor (seizure-r	2.6
35	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
	434672	AW294020	Hs.117721	ESTs	2.6
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.6
	452576	AB023177	Hs.29900	KIAA0960 protein	2.6
40	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor 1	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
45	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheli	2.6
50	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	2.5
	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidemolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheli	2.5
55	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	2.5
	436165	AI373544	Hs.331328	intermediate filament protein syncollin	2.5
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
60	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA825425	Hs.192375	ESTs	2.5
	421091	W22821		ribosomal protein L26	2.5
65	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.5
	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheli	2.5
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
70	431615	AW295859	Hs.235860	ESTs	2.5
	433037	NM_014158	Hs.279938	HSPC067 protein	2.5
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
75	450628	AW382884	Hs.204715	ESTs	2.5
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	2.5
	431122	AI267593	Hs.250535	Homo sapiens mRNA: cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
80	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.5
	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414869	AA157291	Hs.21479	ubiquitin 1	2.5
	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothel	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibito	2.5
	414556	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
10	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.5
	443837	AI984625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
15	435021	AA922192	Hs.73962	ESTs	2.5
	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
	449458	AI805078	Hs.208261	ESTs	2.5
20	428013	AF151020	Hs.181444	hypothetical protein	2.5
	424369	R87622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.5
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.5
	427515	T79526	Hs.179516	integral type I protein	2.5
	418700	AI963808	Hs.85970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

35	Pkey	CAT Number	Accession
40	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF090208 BF090980 BF095153 BG285837 AI720344 BF541715 AA355086 AA172236 AW341473 AA448195 AW207206 AI951341 AA969259
	429220	15103_7	BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962632 BF952020 BF963134 BI036538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721
	412446	63467_1	AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 BC009612 NM_003526 BI597616 AV761592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R08336 AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AA93770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AI829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379052 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49886 BF850422 BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548 AF075009 R63109 R63068
50	453160	6028_5	AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW253978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768485 AW512118 AA479302 AW770384 AW072470 AI041596 AI049699 AW592885 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925899 AL050294 BC010371 BF982270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164 AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593 AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI928140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF448026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW629495 AW505314 W74704 AI356361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166 NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI434589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI548505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AL531028 BG437151 BE868021 AA179427 AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192 AB032997 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295901 BF057835 BE465977 AI621269 BE465983 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333 AW970240 AA534489 AW970323
60	432586	6633_1	
	438869	52134_1	
	450377	12109_1	
65	436063	5483_1	
70	428342	6712_1	
75	424036	6226_1	
80	450203	19009_1	
	451752	10408_5	
	432363	1234917_1	

422890	61426_1	AK057805 AW162343 AI190479 AI093318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 AI632565 BE502530 B1792383 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AI453869 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 B1819428 AA683393 AA583376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
5	417379 1610005_1 407819 7392_2	AA196390 AA507837 AA195468 AK056626 AI800896 BF939022 BE644718 AI954754 BE218177 BE348567 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
10	419733 7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA805643 AW188870 BE706684 BE706539 BE153177 BF084925 AL133779 AW961788 AA559693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 B1045099 T84625 AW129678 BG770826
15	432675 1237917_1 447620 687223_1 409151 4123_1	AW973834 AI791932 AI791855 AI732640 AA558833 AA559897 AI821610 AI973051 AI400921 AI796154 AW241817 AW290951 NM_004892 AF047442 BE275338 BF724863 B1917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 AI902726 AA354813 B1092644 BG778400 B1260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
20	409960 39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI055394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF947619 BE883026 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI188988 AA931831 AA134972 BF217480 BF111012 AA908246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AL544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW980808 BM360872 AA319160 AA130778 AL514257
25	433891 647290_1 414922 1563_2	AW182329 AA613792 T05304 AW858385 BG107484 AA632009 AI432670 AI656660 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 B1091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI695677 AL562079 AI700926 AI470561 BF063058 AW196387 AU132984 B1064046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003 AW339821 AA805951 AI287969 AW564827
30	414222 18695_1	BC021085 AL527872 AL526296 AL557087 B1255090 AU143499 AI460356 BG823170 BE736988 AU141388 AL580262 B1764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 B1770885 B1911394 BE901426 B1918039 BG760842 BE883026 B1254761 BF763690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AI564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 B1222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI420449 AW275385
35		AA336950 BE501521 BF740566 AA311404 AA384639 B1772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE901342 BG746358 BF374053 AL564430 AU143835 AI635077 BF195492 AI280559 BF741685 AA385257 BE247655 W84974 BE163702 AI025167 B127118 H78641 AI581093 AI158954 AU158917 AI282516 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 B1284986 AA857926 BF372568 AA570172 AI753825 AA171566 AU159257 BM194320 W93390 AW132101 AA550898 B1259678 AA522554 N55172 AW013929 AI282674 AI871237 C75260 AA934846 AA555036 AA526579 AA526466 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AU166667 AU159238 AI282517 AA406317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI005500 AW328268 AI244886 AA948424 AA700604 AA832317 AA011555 H97671 AA988711 AW150529 N70983 H44325 AV657614 AA902238 AA644018 AA034050 T71053 N71444 AA831158 T40892 AA706106
40		AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 B1043873 AA019433 B1862088 BM468657 AU128438 BE384458 AI353967 B1857117 BF686525 B1465223 BM460132 AU129877 B1222283 BG171592 B1043544 BG496295 BG750710 B1256542 BG108520 AU150719 AW510354 AL554256 AI353968 AA191092 BF132635
45	426991 29771_1	AF119847 AA437261 AA436987 AI132965 AF150424 AI861896 AA570057 AV738855
50	434194 62680_1 432908 452541_1 412652 18858_2	AI801777 BE577762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF72912 AI891780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981
55	437179 12239_1	AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 B69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656538 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020058 B1491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422
60	418166 18858_1	AK055915 BE867252 AI523348 AA765350 BF446858 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 AI754416 AA213816 BF592044 B1811729 AW514842 AI633486 AI096810 AW183016 AI635738 N27524 BE645916 AI247842 AW991230 AI754277 H16814 AI766892 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680060 AW953899 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA249732
65	431416 120918_1 447881 44623_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974 AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 B1019798 B1019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 B1035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102
70	407192 2200202_1 434747 117643_1 410297 2990_1	AA602964 AA609200 AW976537 AI033582 AA837085 AA745261 AA648395 BC013939 B1494590 B1491211 AI928393 AA843540 BG938644 AU185628 B1495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA928759 AW118737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460355 AW662760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 B1911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 B1602483 BE889592 AW954311 BM052986 B1962893 AI989299 Z42328 BF029504 T35658 BG402602 AU185770 AI023271 AA147719 AI434079 AI569000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 AI356299 R70463 AI383586 AA827189 B1494872 AW021094 B1494871 AA905500 AA460923 B1492041 AW028965 AI624611 BG271780 AI497723 H88862 D59858 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370663 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N75273 AA148710 B1597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954386
75		NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530054 AL525377 BG474596 BG473144 BE251553 BG706099 AL538039 BG703131 BE255806 BF805256 F12128 AL566773 B1826686 BF761480 AI204971 BG818818 B1199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164
80	424339 50559_1	AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257148 AL561833

445636	8561_5	BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672
419175	35068_1	AB018322 BC012480 BI524873 AW665554 AI934469 AI479916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916688 AI678811 AI693109 AI308135 AA669046 AA961054 AI018062 H80618 BE221942 R52609 AI915164 AA365626 Z44671 BI052776 BF882486 BG286184 AI589558 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H80652 AA360728 F10618 AA953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
441128	20932_1	BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322 AI041403 Z49148
406789	0_0	AK057700 BC015899 BE867108 AI526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AI567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896
421091	24941_2	Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF669862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084

TABLE 67C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham l. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham l. et al., Nature (1999) 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
Nt_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401519	6549315	Plus	157315-157950
401785	7249190	Minus	165776-165996, 166189-166314, 166408-16655
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 995 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 995 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigenelD:	Unigene number
Unigene Title:	Unigene gene title
R1:	Ratio of tumor to normal body tissue

Pkey	ExAccn	UnigenelD	Unigene Title	R1
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.5
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	AI420227	Hs.149358	Trp-p8 transient receptor potential cal	65.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	AI821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424059	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	40.9
453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
5	400292	AA250737	Hs.72472	BMP-R1B	31.4
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL135623	Hs.193914	KIAA0575 gene product	31.2
	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	30.3
10	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
	415539	A1733881	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
15	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microsaminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
20	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI267700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
25	437052	AA861697	Hs.120591	ESTs	22.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-[prop	20.8
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
30	427958	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
	431548	AI834273	Hs.9711	novel protein	19.8
	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
35	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
40	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
	428398	AI249368	Hs.98558	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
45	449625	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AU076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448519	AW175685	Hs.278695	Homo sapiens protein mRNA, complete cds	14.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
	418848	AI820961	Hs.193465	ESTs	14.3
	429918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
55	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	13.9
	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	13.3
	432101	AI918950	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
60	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	12.5
65	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
70	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA429834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
75	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
80	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothei	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
5	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
10	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247676	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
15	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	9.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.190044	ESTs	9.6
20	443180	R15875	Hs.258576	claudin 12	9.5
	406964	M21305		GENES predicted novel secreted protein	9.5
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
25	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	cathepsin	9.3
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
30	437124	AA554458		KIAA0666 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431892	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.9
35	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AJ655499	Hs.161712	ESTs	8.8
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
40	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	8.7
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	8.7
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	8.7
	425465	L18964	Hs.1904	protein kinase C, iota	8.5
45	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP5641052 protein	8.4
	450164	AJ239923	Hs.63931	ESTs	8.4
	452744	AJ267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AJ420611	Hs.153934	ESTs	8.3
50	444922	AJ921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418584	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
55	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-1	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432588	AA568548		ESTs	8.0
60	426108	AA622037	Hs.166468	programmed cell death 5	8.0
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	7.9
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kallikrein 4 (protease, enamel matrix, p	7.7
65	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
	451952	AL120173	Hs.301663	ESTs	7.7
	452387	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
70	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.6
	440749	W22335	Hs.7392	hypothetical protein MGC3199	7.6
	418866	BE464341	Hs.21201	necln 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
75	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AJ648602	Hs.55468	ESTs	7.4
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AJ623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	436063	AK000028		ribosomal protein S24	7.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414564	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
10	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
15	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
20	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	409648	AW451449	Hs.57749	ESTs	6.4
	481148	NM_016578	Hs.20509	HBV pX associated protein-8	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
25	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
30	410762	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
35	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
40	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
	449845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U79293	Hs.159264	Human clone 23948 mRNA sequence	6.0
45	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Droso	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
50	446416	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 [Clona savignyi	5.9
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.9
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	5.7
60	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (hls	5.7
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	5.7
	433852	AI378329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020689	Hs.90419	KIAA0882 protein	5.6
65	435706	W31254	Hs.7045	GLD04 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
70	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	429638	AI916662	Hs.211577	kinecin 1 (kinesin receptor)	5.5
	403046			NM_005656*:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49951	Hs.9029	DKFZP434G032 protein	5.4
75	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	5.4
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
80	409151	AA306105		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453082	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88666	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
5	417318	AW953937	Hs.240845	ESTs	5.3
	429467	NM_004477	Hs.203772	FSHD region gene 1	5.3
	416276	U41060	Hs.79136	UV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004505	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
	450832	AW970602	Hs.105421	ESTs	5.1
15	448807	AI571940	Hs.7549	ESTs	5.1
	420568	F09247	Hs.247735	protocadherin alpha 10	5.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
20	452576	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
	407103	AA424881	Hs.256301	hypothetical protein MGC13170	5.0
25	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.9
30	446880	AI811807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R55784	Hs.140942	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784	Hs.2256	ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.33718	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.27495	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.179909	prostate cancer associated protein 7	4.9
	458362	AW973003	Hs.23128	hypothetical protein FLJ22995	4.8
40	442501	AA315267	Hs.142846	ESTs	4.8
	439735	AI635386	Hs.129836	hypothetical protein	4.8
	451752	AB032997	Hs.131740	KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
45	432363	AA534489	Hs.296039	gbn176g11.s1 NCI_CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.123073	ESTs	4.8
	408101	AW968504	Hs.35861	CDC2-related protein kinase 7	4.8
	453857	AL080235	Hs.27373	DKFZP586E1621 protein	4.7
	451982	F13036	Hs.18895	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	4.7
50	447574	AF162666	Hs.347408	tousled-like kinase 1	4.7
	429299	AI620463	Hs.98541	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390	Hs.34892	gbzpz99b10.s1 Stragene muscle 937209 H	4.7
	411031	W37943	Hs.2839	KIAA1323 protein	4.7
55	431725	X65724	Hs.7753	Norie disease (pseudoglioma)	4.7
	441224	AU076964	Hs.40109	calumenin	4.7
	407813	AL120247	Hs.10669	KIAA0872 protein	4.7
	440074	AA863045	Hs.32976	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI538226	Hs.137396	guanine nucleotide binding protein 4	4.7
60	415082	AA160000	Hs.55999	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723	Hs.79953	glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.154978	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.102406	ESTs	4.7
	425174	D87450	Hs.59757	KIAA0261 protein	4.7
65	420380	AA640891	Hs.8859	ESTs	4.7
	410193	AJ132592	Hs.236557	zinc finger protein 281	4.7
	440300	N39760	Hs.61796	Homo sapiens, Similar to RIKEN cDNA 5830	4.6
	436761	AI817776	Hs.7572	ESTs	4.6
	410275	U85558	Hs.198899	transcription factor AP-2 gamma (activat	4.6
70	404922	AI364997	Hs.18953	NM_003071:Homo sapiens SWUSNF related,	4.6
	436556	AU076674	Hs.190223	ESTs	4.6
	429302	AW379130	Hs.41143	eukaryotic translation initiation factor	4.6
	447595	BE242758	Hs.101307	phosphodiesterase 9A	4.6
75	433006	AJ278313	Hs.111460	ESTs, Moderately similar to T29285 hypot	4.5
	407894	AA228899	Hs.272808	phosphoinositide-specific phospholipase	4.5
	418818	W56321	Hs.94210	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	AA094538	Hs.28482	calcium/calmodulin-dependent protein kin	4.5
	443123	AJ000098	Hs.188691	putative transcription regulation nuclea	4.5
	419991	AA013051	Hs.184598	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA862496	Hs.50477	topoisomerase (DNA) II binding protein	4.5
	453390	AI675944	Hs.184598	ESTs	4.5
	417051	AA468183	Hs.184598	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	N23874	Hs.50477	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873			RAB27A, member RAS oncogene family	4.5

	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
5	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
10	417958	AA767382	Hs.193417	ESTs	4.4
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp762O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
15	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	lg superfamily receptor LNIR	4.3
	429259	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
20	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
25	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
	450402	BE218027	Hs.89969	ESTs	4.3
	428055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
30	432675	AI791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
	445707	AI248720	Hs.114390	ESTs	4.2
	410297	AA148710		lumican	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
35	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
40	446237	AW270515	Hs.149596	Homo sapiens, similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
	423337	NM_004655	Hs.127337	axin 2 (conductin, axl)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AI355260	Hs.279789	histone deacetylase 3	4.2
45	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
50	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypothei	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calcarcin-1	4.1
	407192	AA609200		gb:ca12e02.s1 Soares_testis_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0798 gene product	4.1
55	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4096694, mRNA,	4.1
	449459	BE546846	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
60	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
	448663	BE614599		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433647	AA603367	Hs.222294	ESTs	4.0
65	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
70	418827	BE327311	Hs.47166	HT021	4.0
	446791	AI632278	Hs.195922	ESTs	4.0
	443884	N20617	Hs.194397	leptin receptor	4.0
	416857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476*gi12737279 ref XP_012163.1	4.0
75	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.9
	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW105663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
80	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.9
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubiquitin 1	3.9
	429163	AA884766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
5	435021	AA922192	Hs.73962	ESTs	3.9
	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	AI249502	Hs.29669	ESTs	3.8
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.8
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
15	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.8
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	AI272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	AI186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429886	AI871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nuclear protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	AI861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041455	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kalikrein 11	3.7
	432205	AI806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*HSPC213.	3.7
	420061	AW024937	Hs.29410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284192	ESTs	3.7
50	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
	420805	L10333	Hs.99947	reticulum 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dvt-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*:Homo sapiens Williams-Beuren	3.7
55	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451945	BE504055	Hs.211420	ESTs	3.7
60	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0806 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPLIC	3.6
	408096	BE250162	Hs.83765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272269	Hs.121429	zinc-binding protein Rboc728	3.6
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	3.6
75	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
	427715	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	3.6
	403752			NM_002753*:Homo sapiens mitogen-activate	3.6
80	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	AI049624	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.6
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.5
5	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gbno97h03.s1 NCI_CGAP_P12 Homo sapiens	3.5
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (I	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
10	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW898533	Hs.181574	ESTs	3.5
15	412628	AI972402	Hs.306051	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
20	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
	436087	BE300296	Hs.5054	CGI-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty acid-Coenzyme A ligase, long-chain	3.5
25	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
30	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW016669	Hs.29190	ESTs	3.5
	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
35	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30965	neuronal Shc adaptor homolog	3.4
40	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
45	438279	AA805166	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CoccolCrisp	3.4
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
50	431674	AA098901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
	431578	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.4
55	452295	BE379936	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
	439593	BE073597	Hs.124863	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
60	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412652	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
65	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	3.3
	425010	T16837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
70	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_016569	Hs.267182	TBX3-iso protein	3.3
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	3.3
	420818	AW959635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	3.3
75	408681	AW953853	Hs.292833	ESTs, Weakly similar to I38022 hypothei	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418166	AI754416		Cdc42 effector protein 3	3.3
80	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase I	3.2

5	435551	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.2
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	3.2
	423396	AI382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275*:Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA460775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	3.2
	422173	BE385828	Hs.250619	phorbol-in-like protein MDS019	3.2
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371:Homo sapiens hydroxysteroid (1	3.2
15	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW665130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	3.2
20	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
	437179	AA393508		serologically defined colon cancer anti	3.2
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.2
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	3.2
25	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01556	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638:Homo sapiens hypothetical prot	3.2
30	452941	AL110347	Hs.31074	N-guloglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75909	KIAA0182 protein	3.1
	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
35	423551	AA327598	Hs.89633	ESTs	3.1
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413550	W03011	Hs.306881	MSTP043 protein	3.1
	431933	AI187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99364	putative transmembrane protein	3.1
40	448044	AI458882		gb:tk13e01.x:1 NCI_CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-cop	3.1
	424339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ectonucleoside triphosphate diphosphohyd	3.1
45	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE161085	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.106534	hypothetical protein FLJ22625	3.1
	417622	AW298163	Hs.82318	WAS protein family, member 3	3.1
50	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433036	AA574091	Hs.105964	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	406380	AF123050	Hs.44532	diubiquitin	3.1
55	407910	AA650274	Hs.41295	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169841	Hs.270134	hypothetical protein FLJ20280	3.1
	437295	AA350994	Hs.20281	KIAA1700	3.1
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
60	448913	AA194422	Hs.22554	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
65	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
70	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	3.0
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406827	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
75	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	3.0
	411089	AA456454		cell division cycle 2-like 1 (PITSLRE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548906	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
80	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	3.0
	450937	R49131	Hs.26267	ATP-dependant interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC067 protein	3.0

	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
5	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear trans	3.0
	434392	AW983709	Hs.250824	Homo sapiens cDNA: FLJ23435 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
10	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445596	R89543	Hs.12942	vesicle trafficking protein	3.0
	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439690	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	3.0
	408298	A1745325	Hs.271923	Homo sapiens cDNA: FLJ22785 fis, clone K	3.0
15	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409927	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
	447881	BE620886		GCN1 (general control of amino-acid synt	2.9
20	439584	AA838114	Hs.221612	ESTs	2.9
	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
25	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	2.9
30	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
35	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
	430462	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98806	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
40	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens	2.9
	432140	AK000404	Hs.272688	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
	452256	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371048	Hs.93758	H4 histone family, member H	2.9
	409650	T08490	Hs.288969	HSCARG protein	2.9
50	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	438621	AJ200281	Hs.123910	ESTs, Highly similar to B34087 hypotheti	2.9
	437050	AA766420		ESTs	2.9
55	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
	416941	BE000150	Hs.48778	nilban protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
60	436823	AW749865		ESTs, Weakly similar to I38022 hypotheti	2.8
	441266	H15968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
	426761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413746	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
65	400860			Target Exon	2.8
	436165	AI373544	Hs.331328	Intermediate filament protein syncollin	2.8
	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNA/R	2.8
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
70	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	435703	AW630133	Hs.83313	GK003 protein	2.8
	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
75	418196	AI745649	Hs.26549	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
80	435586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.8
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	2.8

5	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.256549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571835	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4816	2.8
	417517	AF001176	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266619	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
	440080	AW051597		ESTs	2.8
15	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10600	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
	453038	AW282415	Hs.20509	HBV pX associated protein-8	2.8
25	419175	AW270037		KIAA0779 protein	2.8
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75360	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975063	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.298258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AL050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp586L141 (fr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	M30599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gbm178f05.x5 NCI_CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rii-related antigen, integr	2.7
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	2.7
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.7
55	400263			Eos Control	2.7
	435750	AB029012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107056	CED-6 protein	2.7
	421077	AK000981	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972657	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW206942	Hs.253594	intron of trichorhinopharyngeal syndro	2.7
	420223	N27807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411960	R77776	Hs.18103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613416	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.296141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA806164	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.7
	451558	NM_001089	Hs.26630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418649	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFp434N2412 (f	2.7
	438682	AA354489	Hs.222103	EBP50-PDZ interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
15	451356	AA748418	Hs.164577	ESTs	2.7
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_006218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL035633		Human DNA sequence from clone RPS-1046G1	2.7
	444034	AL161957	Hs.10177	pleckstrin homology domain interacting p	2.7
20	404913			NM_024408*:Homo sapiens Notch (Drosophil	2.7
	407378	AA299264	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AI815395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	U6 snRNA-associated Sm-like protein LSM8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AI458179	Hs.41528	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE15037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.6551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	426797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410935	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
35	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.6
	430341	NM_005348	Hs.239631	golgi transport complex 1 (90 kDa subuni	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0556 protein,	2.6
	408212	AA297567	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW009892	Hs.31924	ESTs	2.6
	420164	AW339037	Hs.24908	ESTs	2.6
	443444	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	429925	NM_000786		cytochrome P450, 51 (lanosterol 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004922	Hs.81964	SEC24 (S. cerevisiae) related gene famil	2.6
50	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110246	Hs.47367	KIAA1785 protein	2.6
	434011	AW953437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated atlanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	446258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410645	Hs.164649	hypothetical protein DKFp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaa1p, yeas	2.6
	416751	T48130	Hs.5897	Homo sapiens mRNA; cDNA DKFp586P1622 (f	2.6
75	458946	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183684	eukaryotic translation initiation factor	2.6
	449458	AI805078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425863	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L35	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
15	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	456050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	2.5
	408796	AA688292	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62620	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synth	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15573	Hs.50027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypotheri	2.5
35	449500	AW956345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016831	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	419430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypotheri	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypotheri	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40696	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R06859	Hs.193172	ESTs, Weakly similar to I38022 hypotheri	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogenas	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Ste-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W05656	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437762	T78028	Hs.154679	synaptotagmin I	2.5
	425722	AI659076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153937	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [H.s	2.5
	446054	AB014537	Hs.13604	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101067	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433683	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AI469633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153	
			BG285837 AI720344 BF541715 AA355088 AA172236	
	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	

5	449625	249224_1	B1918168 AW779760 N48674 A1375997 AA235370 BG699146 A1913631 A1498402 A1016320 AA323193 R49021 D59344 BG886750 N45526 BG886917 T61382 R49391 R45432 A1203107 R35004 F07491 R25094 R35360
10	412446	63467_1	BC021735 A1669212 A120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 B1035538 BF908052 BF908057 BF090026 BF943158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 A1633838 AA617929 BF947001 B1035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815
15	433404	7392_1	BC022980 BF224081 B149908 AW672842 BE670687 A1702161 AW341832 BE222503 N71836 A1026061 AW953116 AW083132 A1979261 AV725377 A1423288 A1640707 AW675518 A1032611 A1818044 A1295508 A1911386 A1270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32982 R54110 BF115783 F09044 BF808433
20	453160	6028_5	BC009612 NM_003526 B1597616 AV761592 AV760377 AL501008 B1604131 BE645918 BG187760 BG181525 BG210634 BG192999 A1263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 A1143991 AA084581 AA033610 AV742510 AV735788 R08336
25	420218	191547_1	AW958037 R42557 A137047 AA948360 A1638005 AA459950 A1624915 A1638047 A1467856 A1521826 AA860305 A1932315 AW003092 AW271756 AW779380 AA609879 A1634791 A1493770 A1565211 Z41145 A1627952 AA303734 BE349457 AW196765 AA256527 BE089727
30	437124	59408_1	AL050013 BG939500 AW969191 AA769925 A1377973 A1625545 AA811365 AA521114 N24705 A1379579 AA424899 A1684671 AA829715 A1453010 N35401 AA677452 AA504340 A1209149 AA883574 A1379062 A1084455 A1280147 AA644327 BF432508 N27392 AA7364 N34880 A1147024 T86860 A1219716 AA960926 H25544 B1857123 AW960489 AA599099 A7655246 AA328537 BG434703 AA890373 AA424765 A1292318 AA829886 N95742 A1218758 H25588 N36282 AA024987 N36687 B1919187 N49471 AA889970 AW166152 AA468546 A1262504 A1452782 AA554458 AA807080
35	438869	52134_1	AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 A1016509 AW663972 BM127686 C15552 N83435 N51744 T98800 N56980 B108636 N49381 R49886 D61278 B1756612 AA508234 R49885 BF850422
40	428342	6712_1	AF075009 R63109 R63068 AK056315 A1015524 AA724079 B1713619 A1377728 AW293682 A1928140 A1092404 A1085630 AA731340 BM469629 AW966804 AA425658 AA769094 BF446026 AW118719 A1332765 AW500888 AW576556 A1859571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 AW070509 A1521500 A1042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA905524 AA635311 AA649040 A1392620 Z40708 A1985564 AW265313 AA913892 A1983486 AW263502 A1806164 AW291137 B1061872 B1059498 AA134476 AW084888 AA036967
45	450203	19009_1	AW370823 T55263 B1002756 AA489664 BF827281 W74741 BF963166 AK055952 BG182168 BG220105 BG191569 B1618894 BG187388 BG220104 BG183714 BE645998 A1819354 AW974068 A1393635 A1580846 A1024796 AW020098 B1491127 A1393644 N74993 AW472959 BM478854 B1597437 H12165 B458612 BE543192
50	432586	6633_1	BC022881 A1150944 BG750783 AW754175 AW557737 A1911659 A1050036 AA554053 A1826259 AA586548
55	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 A1561910 AA280655 BE710392 AV705100 AW293978 AW444556 AA281459 A1679751 A1873695 B1070089 B1553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 A1857643 A1768486 AW512118 AA479302 AW770384 AW072470 A1041596 A1049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 A1050294 BC010371 BF982270 A1042656 BF095732 AW812618 BF095731 BG212397 BF678765 B1038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 A1693720 AA743364 A1915793 N48185 A1573107 AA043474 A1351615 A1969490 A1910763 R50866 A1699181 N73808 H08164
60	436063	5483_1	AK000028 AA494483 A1298674 AA720773 AV761529 A1884670 A1936202 AW294235 D61652 BF881184 AV711384 N27154 A1926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
65	424036	6226_1	NM_033445 BC001193 A1885781 BF794032 AA476620 AA810906 AA810905 A1291244 A1885097 A1359708 A1335629 H97396 A1344589 AA300377 AA457566 AW771833 BE465621 A1364068 A1364452 A1648505 A1918342 A1928670 AA886580 AL531029 AA886344 A1185419 BG329096
70	407819	7392_2	BM045465 AL531028 BG437151 BE868021 AA179427 AK055626 A1800895 BF939022 BE644718 A1954754 BE218177 BE348567 A1952406 AW293122 A1968798 A1457321 BE327228 BG913531
75	409151	4123_1	AW939055 T03280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185 NM_004892 AF047442 BE275338 BF724863 B1917206 BE276993 AL602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA456385 AA234796 A1902726 AA354813 A1902644 BG778400 B1260001
80	451752	10408_5	BG007325 A1267455 AA426574 A160782 A1472186 AA255500 AA434006 BG435520 A1356111 H00525 AV749060 BG944497 BG292031 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R65766 AW958448 BE090972 BF693195 AV738979 R65855 R80136 AA484677
85	422890	61426_1	AK057805 AW162343 A1190479 A1093318 BE048820 A1198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964436 AW004030 A1632565 BE502530 B1792383 BF056928 AA449241 A1651825 AA805324 A1264853 A19196918 AA948267 A1953735 A1263703 BF056387 AW594171 A1867447 AA319159 A1903440 AW956110 A1366013 A1867923 BG911906 D81142 C15616 A1538697 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 B1819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
90	451752	10408_5	AB032997 A1141678 AW978722 BE467119 A1761408 BF727385 AW237035 A1934521 BF436248 A1479668 Z40632 AA832081 AW295901 BF057835 BE465977 A1621269 BE465983 BF755639 N74056 A1817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE883333
95	432363	1234917_1	AW970240 AA534489 AW970323 AA196390 AA507837 AA196468
100	417379	1610005_1	BG107484 AA632009 A132670 A1856660 A1650884 A1521919 A1264653 AW150793 AW611894 A1917098 B1091245 A1651454 BF434889 A1580286 A1880735 BE301995 A1392959 AW613965 BM023828 AW515374 A1460102 BM023318 BE328188 A1952820 A1581363 AA557165 A1695677
105	414922	1563_2	AL562079 A1700926 A1470561 BF063058 AW196387 A132984 B1064046 A1970157 R02122 H55924 A1521721 AA808206 AA725223 A1766003 AW339821 AA805951 A1287969 AW664827
110	419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 A1951970 AW663548 A1139947 AA514302 AA845232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706564 BE706539 BE153177 BF084925 AL133779 AW961788 AA658693 AA347970 AA295134 AA526037 AA449282 B150454 H61476 T91396 N20018 T90114 H75644 BE710736 BF687723 H28581 AA249370 BF726698 BE841554 B1045099 T84625 AW129678 BG770826
115	432675	1237917_1	AW973834 A1791832 A1791855 A1732640 AA558833 AA559897 A1821610
120	410297	2990_1	BC013939 B1494690 A1491211 A1928393 AA843540 BG938644 A1185628 B1495842 AW173255 BM052709 A1743999 A1690144 A1922209 A1740907 AW340368 AA928759 A118737 BF513970 AA707807 BF435295 A1339463 A1373842 A1433809 BE222392 AA602308 AA428261 A1460355
125			AW662760 A1888087 A1342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 A1150479 A1016166 AA779515 AA661791 BM474307 B1911169 BG575154 AW953303 T33604 D59141 AA385785 AA148648 BM461951 BG681168 B1602483 BE889592 AW954311 BM052986 B1962893 A1989299 Z42328 BF029504 T35668 BG402602 A1185770 A1023271 AA147719 A1434079 A1569000 A1276488 AA992453 AA342821 AA648303 A1493364 A1051008 AA926841 AA350894 AW071451 N22249 A1784138 AA083847 N22258 AW440825 AA661570 AA376687 AA659125 A1356299
130			R70463 A1383586 AA827189 B1494872 AW021094 B1494871 AA905500 AA460923 B1492041 AW028965 A1624611 BG271780 A1497723 H88862 D59858 N89979 AA658425 N81154 D62341 A1274437 N66697 H96993 A1370663 A1728850 H05232 R59374 H12223 A1935759 A1362553 D60006 N29572 A1916833 N75273 AA148710 B1597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 A1910374 A1865262 R55325 A1468927 R34681 H96211 Z39807 BF954386
135	447620	687223_1	A1973051 A400921 A1796154 AW241817 AW290951
140	407192	2200202_1	AA602964 AA609200
145	434194	62680_1	AF119847 AA437261 AA436987 A112965
150	448663	16112_4	BE966763 AA659765 A1961656 A1520918 AA761743 AA281477 N66431 BE463652 AA281329 AW272944 AA058687 BM145087 AA045516 AW341820 AA112515 AA258766 A1886639 AA714133 AA768245 AA035533 A1630459 T20165 AW971268 BE966269 AA522722
155	429163	1238297_1	AW974271 AA592975 AA447312 AA84766

	426991	29771_1	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AI353967 BI857117 BF686525 BI465223 BM460132 AU129877 BI222283 BG171592 BI043544 BG496295 BG750710 BI256542 BG108520 AU150719 AW510354 AI554256 AL353968 AA191092 BF132635
5	432908 433891 409960	452541_1 647290_1 39576_1	AF150424 AI861896 AA570057 AV738855 AW182329 AA613792 T05304 AW858385 BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW654149 AA283782 BF509538 AW296868 AI268977 AI168133 BM352065 AI262769 BF941976 AI058920 AA481861 BF763697 AL565888 BM352383 AA427768 AA385346 AI186988 AA931831 AA134972 BF217480 BF111012 AA080246 AA319849 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AI544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257 BC021085 AL527872 AL526296 AL557087 BI255090 AU143499 AL560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU141330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW328267 AL135173 AA102674 BF726986 AL564735 BE155962 BE155979 BF741679 H67776 H59234 H89665 AW117774 AW274435 L29008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW069877 AW015214 AI948718 BE219706 AI953605 BE217755 AI991382 AI245005 BF431179 AI521843 BE048908 AI240449 AW275385 AA336950 BE501521 BF740566 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012986 BE242693 BE801342 BG746358 BF374053 AL564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AL581093 AU158964 AU158917 AI282516 AU146399 AI713947 AI280528 AA101228 AI338522 AA832316 AI284986 AA857926 BF372568 AA570172 AI753825 AA171568 AU159257 BM194320 W93390 AW132101 AA550898 BI259678 AA522554 N55172 AA013929 AI826274 AI871237 C75260 AA934846 AA555036 AA525579 AA526486 N80270 AI538347 AW615805 AU158875 AU158883 AU159396 AI016667 AU159238 AI282517 AA06317 AI285043 N53050 AA969446 N57718 H93323 W93374 AI873751 H56011 AI936174 AA937830 AW438877 AI800550 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AL523284 AL568203 AL534419 BF981182 BE257148 AL561833 BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 AI688568 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393380 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI097532 AW451563 AA459408 AA459633 AA418444 W23807 BC940150 AI493445 AW054729 AI221929 AI868744 AA215405 AA766713 AA621546 BF928317 BE464132 AI990909 AW271459 AI262061 AA215404 N74332 BG940151 BG952261 AA972115 W96315 AA689588 R69057 BF766886 BE769254 W05240 BI009308 BI009893 BF922023 BF922909 BF922913 BF922096 BF957733 BE701791 AA456454 AA579876 BF933710 AA091294 BI007291 AW905577 AW975593 AA713730 AW836781 AA663371 AA651106 BF594606 AI082382 AI955808 AI678995 AI679386 BF435555 AA586369 AA551351 AA595822 AA565188 BF080855 AA584921 N86077 AA601031 AA633188 AA514764 AA454562 AA551297 AA936109 BI009389 AW897806 BE815442 BF739374 BI009310 BF925422 BF933709 BF922034 BF925465 BI009680 AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654206 F27974 AL079283 BF792538 AA744861 AI871888 AI478580 AI720775 AI888937 AI808966 BE463436 BF725510 AW675767 BF589111 BE855951 AI197232 AW272173 AI480335 BF589044 AA443540 AI420128 AI066029 AI650755 AW274589 AW183510 AI440198 AI271801 AW080345 AW189508 AW008293 AA884731 AA579802 AI968645 AI620822 AI222117 AA677146 AI346296 BI792788 AA446515 AI183488 AA892113 AW271851 AW241299 W90134 AA482921 AI049496 AA492010 AA846639 AA983603 AA969293 AI890036 BI254992 AA463513 AA476659 AW673442 AL557763 AA688312 H28886 AA778711 AA081838 AI989340 AL557762 N99654 Z28545 N28874 AA442388 AW887818 AW663156 BG252539 BG501262 BG714174 BG499052 AA058524 BE881198 C75278 R59648 AI829311 AA037656 AW026747 N64518 AW103253 BF529731 AW241677 AW194855 AA917531 R95578 H94036 AA856665 T10342 AW439112 AI090044 AA661591 N71704 AI474928 AU152235 D53426 N21634 R59590 R51072 R96601 H06171 AA084440 H84172 AW118714 C04928 W90092 AA039267 AA136445 R52391 T66024 BG778916 AA428153 N41394 AA283639 R96600 H94122 BF743684 AA147009 T65867 Z19487 BF697478 AW971213 AA493925 AA493567 AA876839 AA934462 T69981 T69924 AA078476 AK074291 AW293424 BE676135 AI832125 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF924261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726604 AA077560 BE272975 BF949119 AW814195 BE879126 AI897926 BF594155 BE205787 BF063513 N35828 AI948557 AI433839 AI379679 BG056182 AI589094 N23123 AA588805 AW316581 AI080272 AI421980 AI493318 BF194830 N87590 AA495993 N32996 AA699844 H96845 H96592 N28741 BI035539 BF747723 BF171066 W01350 H05495 AI243785 Z39622 AA887432 AI350659 R46102 AA761668 AA573621 R09670 R92814 BI918715 BF594193 AI073494 AI363077 AI656655 AA121979 BF983131 AA491795 BG152545 AI350401 BF939121 AI479401 BI493099 BF057693 AI970550 BF111919 BF448282 BI493100 AW043768 AW006202 AI564010 BF433292 AI58202 AI954746 BE220962 AI375411 AI361048 AA115853 AI364474 AI669815 AA133407 AI928647 AW016610 AA133334 AA504948 AI291629 AI161208 AA837042 AI867138 AA987255 AI830219 AU150404 AI680674 AW969901 AW976442 AA743319 AA766420 BG180003 AW975741 AW749865 AA731828 AA731829 AW974812 AI821822 AI821820 AI821075 AI821073 AA651643 AA651662 BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AI926504 AA041551 AW043754 AI086702 AW008105 AA974849 AW614693 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW358482 AW388420 BF374777 W01360 N94710 H87967 AW051597 AI733052 AI167287 AI732999 AI566918 AI476787 AI791542 AA887204 AW025394 AA863338 AI240285 AI791393 AB018322 BC012480 BI524873 AW665554 AI934469 AI79916 BF096179 BF096162 BF096132 AA744972 AI951988 AI858339 BE076331 AA886998 AI570585 AI916888 AI678811 AI693109 AI308135 AA669046 AA961064 AI018062 H08018 BE221942 R52609 AI915164 AA355626 Z44571 BI052776 BF882486 BG286184 AI589588 AA931663 AA534979 AI275392 AI273455 R52553 AA829920 H08052 AA360728 F10618
70	433009 412719	2142268_1 1634_2	
75	437050 436823 457733 453912	1240141_1 MH1660_153 119160_1 32562_3	
80	440080 419175	517737_1 35068_1	

			AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI857450 AI341191 AI434143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW952314
5	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527436 BG913023 AI884867 BE858461 AI885227 AI935218 BE645596 AI922406 AA778161 BF345973 AW195853 AI687121 AI336147 AI091364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812396 AI358396 AA932022 BE222881 AW016109 BM352667 BF528099 BG818616 AI935916 AA912295 BG910887 AI568301 AI567278 BI522445 BI754384 BG819375 BF835950 AA323718 AA860955 AI089847 AL520776 AL526045 AL538507 AL567798 AL536876 AL574332 BF834531 BF340116 BF835954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AI581327 AL565842 H43568 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896 BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG874574 BE903322 AI041403 Z49148
10	441128	20932_1	AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL583737 BG029709 W52882 AI439658 BE551237 AA283724 BF109530 AI457096 AI085992 BE467735 AA693467 AI697593 AI887863 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AI18634 T31586 AA436630 AI366472 AA706191 AI422304 AI204899 AI041169 AA211402 AW827081 AA788593 T32736 AI767935 AA747914 T03534 AW959843 AI119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113 AA658826 AI821925 AI791191 AA635129 AA564492 Z11692 X51466 NM_001951 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI091978 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084 BG256892 HI0532 N48614 R52610 AW977698 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123683 AW006831 BE831162 AW452753 AV742717 W86152 BF115102 AI633815 BF921562 AA094230 BE092587 W86151 AA526153 AI672166 BF914496 R12579 BF852352 AA699780 T57386 BF903022 R09933 AA678298 BF339388 AI345516 BG391657 BE708957 BG026034 BE261703 H56718 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 AA090672 N27807 AA256634 BE276324 AF263306 BF851698 T66089 F11783 F11794 H29379 R19493 HI8042 AI133995 AW134660 AI299437 AA057405 AA917450 AI002692 T09262 R43839 H29290 T65008 N78357 AI221207 AI689856 AA913591 AI220302 NM_000786 U23942 BI01050 BG771947 BG773455 BI561558 BI460206 BG714348 BM126447 AU129411 AU129401 AI119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 W79867 W74235 AV709052 AI217668 AA399409 BE182318 BM128040 AI939998 AW615411 AW070426 AI124550 AW778736 AA477781 AW263013 AI459619 AA860513 BF809548 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 BI916393 BM470755 BI333211 AA095636 BI265415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56883 BE813131 C03646 BG287974 AA386261 H4780 R48858 T91611 H42019 BI869421 BG502073 BG425943 W37290 W31363 BE004451 BF208311 BI048717 N78122 AA226597 AI525334 AI953821 AA657925 AA935436 AW975068
15	405789 410099	0_0 16732_1	BC000222 AL136871 NM_002321 BC009497 BM481705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI277161 BG820180 AA454463 AA255685 N31549 AA326504 BC019924 BG257230 BI092368 BI869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF686779 AI755222 AA452272 AW241170 AU156565 F28259 T16319 AA362506 N64153 BM016416 BM458963 BG739972 AV729565 BE268285 BE867433 BM011110 BG285856 AI922439 BE270975 AL119339 BF956085 AI565178 AL554305 AL573240 AL572917 AI129627 AL548640 BE392285 AI092843 AI371057 BE302410 AI608753 AW674261 AI750057 AI052649 H47822 AL516249 AI589903 BG258439 AI123562 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA775369 AA858195 W73625 AA216784 AW513778 AW243958 AI061112 AI783806 AL569622 AD070466 BF229936 N58159 H80288 N32598 H80293 H80279 AI581253 AW571884 AI361698 AW073321 AA876464 H95640 T34421 AA331419 N99897 H80274 BI262120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA382527 BG056668 AW118162 AW073071 BE293868 BF792321 BF792258 BG107176 T56604 BM193566 H03238 AA618045 AA906004 BI085686 AA564566 AI221630 D52045 C14510 AA029390 W60153 H98743 AI682641 H28485 AA723093 AI081730 AA641309 AA687083 BI224818 AW204722 AI309186 AI215122 AI200785 BE467373 BM352502 AI304400 AI193071 AI742483 AW003408 AI600911 AI558740 AW655173 AI215120 AI147599 AI803429 AI076110 AI754349 AW205103 AI262491 AI088243 AI281007 AI051273 AI004801 AW466918 AW103289 AI474637 AI264446 AI699509 BE704420 AA889278 AA918256 AA830856 AA89425 AA911929 AA262598 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94863 N69544 AA181762 D02132 T55734 T60692 R76858 AA022948 AW770291 R50934 AA205918 R97811 H40328 R86252 AA936029 AI813809 AA933607 AA129695 AA548261 AA714393 AA775006 AA653439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51696 D55942 D62740 AI000118 AL516304 AL534259 N54940 AL579194 AI669399 AI342925 BE939201 AA633000 BI222963 AI619676 AW190306 BF035010 AW087897 AI864969 T57243 R48211 AA113880 R26594 C14467 C14444 BI195459 BE896346 BE270780 AL568073 BG389833 BE891549 BI223147 AW381001 AA448464 AW799744 AA412194 AA948107 AA927157 AA983841 BF752571 BE731304 AI380443 AI240179 AA977516 AA84643 AW079380 AW294316 AI913755 AI864320 AI685770 H25135 AI972654 AI538592 AI174783 R12271 R83569 AI274757 AI559500 AW022192 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D60181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60556
20	432745 400263	112643_1 18977_1	Z11692 X51466 NM_001951 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 BM016525 AI560409 AL562866 AI091978 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG674499 BG774174 BI015084
25			
30	411605	10026_3	
35	445636	8561_5	
40	420223 423476 441054 429925	191648_1 32437_1 2641490_1 33135_1	
45	434976 440191	121716_1 MH790_2	
50			
55			
60			
65	440409 444610 446091 431843	588375_1 2145292_1 515091_1 445334_1	
70	400262	18977_1	
75			
80			

TABLE 68C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796668	Plus	45096-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719705	Plus	176341-176452
401866	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165776-165996, 166189-166314, 166408-16656
406214	7342036	Plus	86320-86523
403532	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104, 152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigenelD	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37976	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AJ077196	Hs.82985	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63984	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.59
425139	AW630488	Hs.25338	protease, serine, 23	1.63
402463			NM_014624:Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AJ878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93847	NM_016931:Homo sapiens NADPH oxidase 4 (2.06
447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
446500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW986651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	1.87
413795	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AI750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432673	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones Z3549 a	1.42
453085	AW954243		KIAA0251 protein	1.47
438887	R68857	Hs.265499	ESTs	1.49
436729	BE621807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970*:CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolipi	1.55
414476	AA301887	Hs.76224	EGF-containing fibulin-like extracellula	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AJ004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419983	W55956	Hs.94030	Homo sapiens mRNA: cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AJ076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448674	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:H.sapiens PTX3 gene promotor region.	1.33

5	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.62
	401234			mitogen-activated protein kinase 8 inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	AJ249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	1.49
	422099	AA156022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	445119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.269651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein (Homo sapien	1.76
	418825	AA228881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb:gb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AJ821409	Hs.304471	EST	1.45
40	426113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.52
	453983	H94997	Hs.16450	ESTs	1.94
45	406506			Target Exon	1.97
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW580939	Hs.97199	complement component C1q receptor	2.36
	426696	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	E1B-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22958	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptotagmin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412564	X83703		cardiac ankyrin repeat protein	1.51
	414785	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiotensin-2	1.91
	406627	T64904	Hs.163760	ESTs	1.76
	405025			Bone morphogenetic protein 6	1.69
65	422648	D86983	Hs.118893	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfam	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.65
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL035668	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.79067	MAD (mothers against decapentaplegic, Dr	1.71
	450689	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
80	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	1.83
	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412765	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	456977	AK000252	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

	425234	AW152225	Hs.165909	ESTs, Weakly similar to I380222 hypotheti	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1359	decay accelerating factor for complement	1.74
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	416940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	endothelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453467	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219591	Hs.73625	RAB6 Interacting, kinesin-like (rabkines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleotide phosphorylase	1.99
	405121			mitogen-activated protein kinase 8 inter	2.99
	425811	AL039104	Hs.159557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
30	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.109706	hematological and neurological expressed	1.65
	408669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA486620	Hs.41135	endomucin-2	2.34
	407891	AA486620	Hs.41135	endomucin-2	2.34
40	436032	AA150797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs;similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
45	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
	432128	AA127221	Hs.296502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439265	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	2.08
50	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	2.37
	442573	H93366	Hs.7567	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE280074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422603	BE242687	Hs.118651	hematopoietically expressed homeobox	2.15
	406954	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
	408989	AW381656	Hs.49500	KIAA0746 protein	1.43
60	429663	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW388533	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400666			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom	2.25
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.76
70	451979	F06972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	3.11
	414577	AI066548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI597655	Hs.49265	ESTs	3.08
	424244	AI186431	Hs.296638	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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453085	10017_1	BC017336 BG176430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745642 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI025328 AI298436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05751 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AM70033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI916523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI866240 BE773500 AI244845 AI565439 AI918453 AI472527 AA446740 AA035576 AA191414 AW674145 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AL568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C05111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL550096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AI556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG428896 BE392486 AW961686 BG721056 BE906365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA853496 AA360401 AW956168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882 AA156511 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018667 AU139209 BE924924 BE924899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA969184 BE924898 BF229066 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943776 AA488072 AA486364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 CD4160 CD4483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787			
442506	29197_1	TABLE 69C Pkey: Unique number corresponding to an Eos probeset Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. Strand: Indicates DNA strand from which exons were predicted. NL_position: Indicates nucleotide positions of predicted exons.			
436772	1239464_1	Pkey	Ref	Strand	NL_position
434596	14701_1	402463	9796886	Minus	8818-8952
412564	18571_1	400494	9714719	Plus	169845-170272
		401234	9929642	Plus	120173-120337
		406506	7711374	Minus	6843-8077
		405025	7107727	Plus	105267-105343,106184-106294,106387-10653
		405121	8102330	Minus	35816-36004,36587-36684
		400666	8118496	Plus	17982-18115,20297-20456
442006	1239046_1	TABLE 70A: Pkey: Unique Eos probeset Identifier number ExAccn: Exemplar Accession number, Genbank accession number UnigenelD: Unigene number Unigene Title: Unigene gene title R1: Ratio of the mean of the vessel AI's to the mean of the HUVEC AI's			
428928	BE409838	UnigenelD	Unigene Title	R1	
439180	AI393742	Hs.199067	cadherin 1, type 1, E-cadherin (epithelial)	0.99	
412636	NM_004415	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06	
426158	NM_001982	Hs.199067	desmoplakin (DPI, DPL)	1.25	
414320	U13616	Hs.75893	v-erb-b2 avian erythroblastic leukemia v	1.36	
417878	U90916	Hs.82845	ankyrin 3, node of Ranvier (ankyrin G)	1.50	
414572	AU077174	Hs.288181	Homo sapiens cDNA: FLJ21930 fls, clone H	1.55	
415314	N88802	Hs.5422	cathepsin H	1.64	
431103	M57399	Hs.44	glycoprotein M6B	1.70	
406973	M34996	Hs.198253	pleiotrophin (heparin binding growth fac	1.75	
456974	M12529	Hs.169401	major histocompatibility complex, class	1.88	
430560	Z28942	Hs.243960	apolipoprotein E	1.90	
406828	AA419202	Hs.84298	N-myc downstream-regulated gene 2	1.91	
422048	NM_012445	Hs.288126	CD74 antigen (invariant polypeptide of m	1.97	
			spondin 2, extracellular matrix protein	1.99	

	406826	AW516005	Hs.84298	CD74 antigen (invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AI223328	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
5	406824	AW515961	Hs.84298	CD74 antigen (invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437536	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.26
	446945	AI193115	Hs.16511	tumor protein D52-like 1	2.27
10	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690916	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	2.38
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.39
	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
15	415994	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB029018	Hs.177635	KIAA1095 protein	2.47
	414217	AI309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB class II histocompatibi	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431359	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.58
	437952	D63209	Hs.5944	solute carrier family 11 (proton-coupled	2.58
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	p8 protein (candidate of metastasis 1)	2.62
30	425751	T19239	Hs.1940	crystallin, alpha B	2.63
	414194	BE175494	Hs.75811	N-acylsphingosine amidohydrolase (acid c	2.63
	443907	AU076484	Hs.9953	TYRO protein tyrosine kinase binding pro	2.66
	453464	A884911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410677	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
35	452685	AI634651	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453767	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
40	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W25005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plakophilin 4	2.94
45	429123	AB011099	Hs.196647	KIAA0527 protein	2.97
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fis, clone L	3.01
	425822	AW360847	Hs.16578	ESTs	3.01
	420195	N44348	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.04
50	446584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
	423915	AF039018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	calsequestrin 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
55	414840	R27319	Hs.23823	hair/enhancer-of-split related with YRP	3.14
	424651	AI493206		ESTs	3.17
	443932	AW888222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
60	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	perforin (OSF-2os)	3.24
	447384	AI377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
65	420136	AW801090	Hs.195851	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.26
	410132	NM_003480	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	Indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipsin)	3.29
70	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI091195	Hs.65029	growth arrest-specific 1	3.35
	451529	AI917901	Hs.208541	ESTs	3.35
	430310	U60115	Hs.239069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	frizzled-related protein	3.37
75	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
	421913	AI934365	Hs.109439	osteoglycin (osteoinductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fis, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
80	407938	AA905097	Hs.85050	phospholamban	3.48
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L36531	Hs.91296	integrin, alpha 8	3.52
	404277			NM_019111*:Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (ponsin)	3.64
	447111	AI017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV657778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
15	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE:4183312, mRNA,	4.01
20	449925	AI342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
	453500	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245188	tissue inhibitor of metalloproteinase 3	4.09
	421823	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.26
	450912	AW839251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	4.37
	419938	AU076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78065	complement component 7	4.37
30	414176	BE140638	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22687	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	AU1518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108823	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI568801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276858	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	lumican	5.20
45	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.65
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	5.87
	416585	X54162	Hs.79386	telomodulin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426406	AI742501	Hs.169756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.75445	SPARC-like 1 (mast9, hevii)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey	CAT Number	Accession
55	412636	1438_1
60		M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 HZ7408 BE931630 BE167165 AW370827
		AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592
		BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316
		BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737
65		AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R68704 AA852212 AW366566 BI090358 BF087707 BE819046
		BE819005 AA377127 BE073467 BE819059 BE819048 BI036305 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674
		BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510
		AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476856 BF086994 BF592276
		BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421
70		BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG958545
		AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705966 BE705968 AW848723
		AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211
		AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599
		BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583
75		AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516
		AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI417612
		AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AA346078 W95070 AA149191 AA026864 AI830049 AW780435
		AI078449 AI819984 AI685828 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207
80		AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12052 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181
		H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654
		AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320
		AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW106614 AI887258 AI538577 BE926474
		BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763
		BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406

5

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25

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35

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45

50

55

60

65

70

75

80

454042

30254_1

440820

3091_1

424651

46029_5

TABLE 70C

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

Pkey

Ref

Strand

NL_position

404277

1834458

Minus

91665-91946

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 75th percentile of ewing sarcoma to 85th percentile of body map

Pkey

ExAccn

UnigeneID

Unigene Title

R1

104659

AW969769

Hs.105201

ESTs

70.3

101447

M21305

gb:Human alpha satellite and satellite 3

64.7

105782

H09748

Hs.57987

B-cell CLL/lymphoma 11B (zinc finger pro

50.5

115881

NM_005756

Hs.184942

G protein-coupled receptor 64

48.8

121792

AW969726

Hs.98381

ESTs, Weakly similar to serine protease

46.7

101104

AW862258

Hs.169266

neuropeptide Y receptor Y1

46.6

110278

AF061573

Hs.19492

protocadherin 8

46.1

126645

AA316181

Hs.61635

six transmembrane epithelial antigen of

41.4

116752

AL008583

Hs.91622

neuronal pentraxin receptor

40.9

119717

AA918317

Hs.57987

B-cell CLL/lymphoma 11B (zinc finger pro

39.6

104691

U29690

Hs.37744

Homo sapiens beta-1 adrenergic receptor

36.9

110728

AA737106

Hs.32250

ESTs, Moderately similar to I78885 serin

35.5

121362

AF050147

Hs.97932

chondromodulin I precursor

34.7

131291

NM_004350

Hs.170019

nunt-related transcription factor 3

33.0

101063

D54745

Hs.80247

cholecystokinin

31.7

121619

AA528339

Hs.178062

ESTs, Weakly similar to phosphatidylseri

28.7

122651

AW976398

Hs.293836

ESTs

28.0

100299

D49493

Hs.2171

growth differentiation factor 10

26.5

129977

NM_000399

Hs.1395

early growth response 2 (Krox-20 (Drosop

26.2

123619

AA602964

gb:nc97c02.s1 NCI_CGAP_P12 Homo sapiens

26.1

124006

A1147155

Hs.279727

ESTs; homologue of PEM-3 (Clona savigny)

23.1

116301

AW969706

Hs.293332

ESTs

22.6

121231

AA814948

Hs.95343

ESTs, Weakly similar to ALUC_HUMAN !!!!

22.3

106533

AL134708

Hs.145998

ESTs

22.3

109166

AA219691

Hs.73625

RAB6 interacting, kinesin-like (ratkines

21.3

131313

R96290

Hs.75874

ribosomal protein L44

20.8

116790

AW161357

microtubule-associated protein tau

18.7

105316

A1671245

Hs.24835

hypothetical protein FLJ14594

18.2

102123

NM_001809

Hs.1594

centromere protein A (17kD)

17.8

126218

AL049801

Hs.13649

Novel human gene mapping to chromosome 13

17.8

119791

AA554907

Hs.58291

ESTs

16.7

113003

AW292315

Hs.7215

ESTs

16.3

102836

U94320

Hs.158330

neuropeptide Y receptor Y5

16.3

126799

AW753865

Hs.74376

olfactomedin related ER localized protei

16.3

105298

BE387790

Hs.26369

hypothetical protein FLJ20287

15.5

107160

AA314490

Hs.27669

KAA1563 protein

14.8

115313

AA808001

Hs.184411

albumin

14.6

123308

C14187

Hs.103538

ESTs

14.2

	126077	M78772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	106821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40665	Hs.31564	ESTs	13.8
	106498	AI221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	128639	AW582962	Hs.102897	CGI-47 protein	13.2
10	125698	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119456	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
15	132968	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
	104968	AI249502	Hs.29669	ESTs	11.1
20	123532	AA608733		gb:ae56f06.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125556	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
	123049	BE047680	Hs.211869	clckapf (Xenopus laevis) homolog 2	10.6
25	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
	110730	N67655	Hs.26411	ESTs	10.3
30	119186	AI979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133181	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA457211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22995	9.6
	106146	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.5
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AI204800	Hs.96978	hypothetical protein MGC10764	9.2
	130625	AF176012	Hs.260720	J domain containing protein 1	9.2
	129755	R42216	Hs.7759	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247529	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	AI940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA862257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AI085153	Hs.143764	ESTs, Weakly similar to unknown [H.sapie	8.8
55	113903	AI368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AJ077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159156	protocadherin 11	8.5
	130298	AJ347487	Hs.132781	class I cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106575	AW970602	Hs.105421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119499	AI918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244930	Hs.166895	ESTs	8.0
70	107098	AI823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	7.9
75	133063	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.5364	DKFZP564I052 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	7.8
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP586D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AI608657	Hs.95097	ESTs	7.7
	129075	BE250162	Hs.83765	dihydrofolate reductase	7.6

	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypotheti	7.6
	132438	AW363687	Hs.82916	chaperonin containing TCP1, subunit 6A (7.6
	118036	AI471862	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	7.6
5	131170	NM_014253		odz (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE568452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
10	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1580	7.3
	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW693940	Hs.59698	ESTs	7.1
	105127	AA045548	Hs.301957	nudix (nucleoside diphosphate linked moi	7.1
15	128478	AA708205	Hs.100343	ESTs	7.1
	110456	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50695	homeo box C4	7.1
	120934	AA226198		gb:nc26a07.s1 NCL_CGAP_Pr1 Homo sapiens	7.1
	128132	AA225632		gb:nc08a07.r1 NCL_CGAP_Pr1 Homo sapiens	7.0
20	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 ferri	7.0
	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	N45018	Hs.6769	hypothetical protein DKFZp761J17121	6.9
	118013	AI674126	Hs.94031	ESTs	6.9
25	120147	AI917116		hemoglobin, beta	6.8
	118267	N34905	Hs.44653	Homo sapiens cDNA: FLJ22669 fis, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195651		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
30	127742	AW293496	Hs.180138	ESTs	6.7
	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIIC, polyp	6.6
	121553	AA412488	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
35	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
	115197	R18656		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
40	126967	AA205976		gb:zq48a10.r1 Stratagene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AI669372	Hs.17207	Homo sapiens cDNA FLJ11922 fis, clone HE	6.3
	127958	AA830201	Hs.124347	ESTs	6.3
45	134719	AA852885	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121885	AA934883	Hs.98467	ESTs, Highly similar to AF257737 1 cilia	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
50	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp586M0723 (f	6.2
	135186	U73328	Hs.172648	distal-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
55	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fis, clone PL	6.1
	114357	R41677	Hs.6107	Homo sapiens cDNA FLJ14839 fis, clone OV	6.1
	128501	AL133572	Hs.199009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
60	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-530115	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121830	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypotheti	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
65	109841	H01052		gb:yl32h01.s1 Soares placenta Nb2HP Homo	5.9
	115622	AI088691	Hs.208414	Homo sapiens mRNA; cDNA DKFZp554D0472 (f	5.8
	122969	AW821252	Hs.104336	hypothetical protein	5.8
	109872	R65841	Hs.28653	ESTs	5.8
	114208	AL049466	Hs.7859	ESTs	5.8
70	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
	129300	W94197	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01556	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
75	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI468004	Hs.278956	hypothetical protein FLJ12929	5.7
80	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW753865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

5	117357	N24829		gb:yr98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
	131185	BE280074	Hs.23960	cyclin B1	5.4
15	111227	T06701	Hs.12268	ESTs	5.4
	105516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
20	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares multiple sclerosis	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	5.3
	119040	R02394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothe	5.2
	120830	AI568170	Hs.96886	ESTs	5.2
30	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	103316	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49163	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	AI089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW975998	Hs.58595	ESTs, Weakly similar to I38022 hypothe	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102627	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	116814	H50834	Hs.77899	gb:yp86a10.s1 Soares fetal liver spleen	5.0
50	130622	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA971146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.96473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 serine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356764	Hs.17109	integral membrane protein 2A	4.8
	126769	AA083456		gbr:zn09g08.r1 Stratagene hNT neuron (937	4.8
	126086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21634	4.8
	105848	AW954064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129706	AA443241		ribosomal protein L44	4.7
	129598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AL096739	Hs.107260	hypothetical protein DKFZp586H0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	126521	AI475110	Hs.203933	ESTs	4.7
	110343	AW135703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

5	113974	AW969756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.149377	hypothetical protein DKFZp761L0424	4.6
	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
10	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.5
	104912	AA813192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
15	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
20	106489	AA452054	Hs.119338	ESTs	4.5
	122792	AW188551	Hs.99519	hypothetical protein FLJ14007	4.5
	112651	AA595802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
25	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334842	tubulin alpha 1	4.4
	127496	AI031650		ESTs	4.4
30	127315	AF116622		gb:Homo sapiens clone FLB4217 mRNA seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
35	120922	AA481003	Hs.97128	ESTs	4.3
	115167	AA749209	Hs.43728	hypothetical protein	4.3
	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PRO0659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
40	103616	NM_002647	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	135098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
45	133571	BE515037	Hs.177556	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
50	129650	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
	106073	AL157441	Hs.17834	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
55	134126	NM_003747	Hs.131814	tankyrase, TRF1-interacting ankyrin-rela	4.2
	115041	AA252457	Hs.86543	ESTs, Moderately similar to T00256 hypot	4.2
	106012	AI240685		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
60	130832	AW838006	Hs.20082	zinc finger protein 3 (A8-51)	4.2
	125960	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-tRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
65	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101266	L36645	Hs.73984	EphA4	4.2
	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S	4.1
70	116133	AW449597	Hs.313652	EST, Weakly similar to I38022 hypothetic	4.1
	129001	AA443323	Hs.107812	BPOZ protein	4.1
	119271	AI051118	Hs.65328	Fanconi anemia, complementation group F	4.1
	114767	AI859865	Hs.154443	minichromosome maintenance deficient (S.	4.1
	126107	H75477	Hs.93361	ESTs	4.1
75	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
80	129948	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW088276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15069	ESTs	4.1
	118872	AI039201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic acid)	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retrovirus	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
	100031			AFEX control - DapX-M	4.0
	106897	AF039023	Hs.167496	RAN binding protein 6	4.0
10	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo)	4.0
	126965	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR)	4.0
	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	118751	N74210	Hs.50454	ESTs	4.0
15	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
	118676	N45312	Hs.46506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
20	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_	4.0
25	126522	W31912	Hs.21168	gb:zc76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
30	105808	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
35	118967	AI686870	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
40	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomas	3.9
	131971	BE567100	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.106985	ESTs	3.9
45	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
50	106476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876B10	3.8
	122682	AA984531	Hs.159293	ESTs	3.8
	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
55	129785	H19008	Hs.184780	ESTs	3.8
	126127	N95428		gb:zb80d09.s1 Soares_senescent_fibroblas	3.8
	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H60720	Hs.81892	KIAA0101 gene product	3.8
60	105140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA256874	Hs.77494	deoxyguanosine kinase	3.8
65	127262	AA828125		gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UH-BI3-ata-a-12-0-UI.s1 NCL_CGAP_Su	3.7
	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.7
	113119	T47910		gb:zb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
70	116203	AW137166	Hs.87306	ESTs	3.7
	123377	AW969183	Hs.271297	ESTs	3.7
	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123654	PCF11p homolog	3.7
75	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
	126708	AW962593	Hs.135260	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
80	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFP434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109260A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W96141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	AI300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	114118	F01598	Hs.175930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to I38022 hypotheti	3.6
	125174	W51835	Hs.231082	EST	3.5
	104799	AA029703		gbze95h08.s1 Soares_fetal_heart_NbHH19W	3.6
	128952	AL043463	Hs.6755	RaP2 Interacting protein 8	3.6
	135191	X16866	Hs.333497	cytochrome P450, subfamily IID (debrissoq	3.6
20	124367	AI683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	AI655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113988	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88252	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	AI738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	115691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23625	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zm92h12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	AI494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE161065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:rh16c10.r1 Soares Infant brain 1N1B H	3.5
	117265	AA451966		RAB9-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	AI002238	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	AI803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW029507	Hs.161102	ESTs	3.5
	100944	L07518		mucn 6, gastric	3.5
50	105226	R58958	Hs.26608	hypothetical protein MGC15880	3.5
	126032	T74884		gb:yc58d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like-protein	3.5
	116443	AW962196	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.5
	131244	AI638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	Insulin receptor substrate 2	3.5
	111223	AA852773	Hs.334838	KIAA1866 protein	3.5
60	104857	AI920902	Hs.19058	ESTs, Moderately similar to S65657 alpha	3.5
	105395	AI580880	Hs.268149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504583	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	106367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94563		gb:H.sapiens dbi/actp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fis, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp586L1121 (f	3.5
70	114096	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product, ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
75	109734	AI927212	Hs.3734	ESTs	3.4
	132786	BE083422	Hs.56851	hypothetical protein MGC2668	3.4
	106685	AU076617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
80	131381	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
	108687	BE544475	Hs.54347	ESTs	3.4
	113115	AI141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA486256	Hs.193510	EST	3.4
	131019	W28614		chorionic somatomammotropin hormone 1 (p	3.4

	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
5	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE:23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	ankylosis, progressive (mouse) homolog	3.4
10	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122365	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037766	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
15	106591	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE245294	Hs.180789	S164 protein	3.4
	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA649257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
20	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp56400122 (f	3.3
	108859	AL121500		ESTs	3.3
	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125693	H23989	Hs.169743	Homo sapiens clone 25121 neuronal olfact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
25	132994	AA112748	Hs.279905	clone HQ0310 PRO0310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	ghym37a05.r1 Soares infant brain 1NIB H	3.3
30	133363	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r	3.3
	107908	AF087999		ESTs	3.3
	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H63947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA295052	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com	3.3
35	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21801	3.3
	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gbk3517.seq.F Human fetal heart, Lambda	3.3
40	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133160	N54968	Hs.66309	hypothetical protein MGC11061	3.3
45	134076	AF086215	Hs.78980	gb:Homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76067	ribosomal protein L10a	3.3
50	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648886	Hs.151999	ESTs	3.3
	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
55	121292	AA401807		gb:zv55f11.s1 Soares_t0tal_fetus_Nb2HF8_	3.3
	123284	AA488988	Hs.293796	ESTs	3.3
	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	105014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
60	114988	AA251089		gb:zs04f05.s1 NCL_CGAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AJ521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
65	111520	AI985369	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA768242	Hs.80618	hypothetical protein	3.3
	129619	AA209534	Hs.284243	telraspan NET-6 protein	3.3
70	126770	AI292320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93796	DKFZP586D2223 protein	3.3
	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
75	129284	AA318224	Hs.296141	ESTs	3.3
	119127	AA708035	Hs.12248	ESTs	3.3
	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65657 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	118397	BE139479	Hs.161492	ESTs	3.3
80	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113626	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58508	Homo sapiens cDNA FLJ14205 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
5	123808	AA620552		gb:ae58g11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein I3	3.2
	110561	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29682	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	125722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
15	109517	AI631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039670	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
20	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	130338	AA926960		CDC28 protein kinase 1	3.2
	130553	AF062649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I78885 serine/th	3.2
	132305	AI806090	Hs.44344	hypothetical protein FLJ20534	3.2
30	131136	AB033099	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AI422951	Hs.146162	ESTs	3.2
	126153	H85692	Hs.40730	ESTs	3.2
35	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypothi	3.2
	104946	AW242407	Hs.73848	carcinoembryonic antigen-related cell ad	3.2
	122110	AI123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW286134	Hs.86999	ESTs, Weakly similar to S65657 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.62180	anillin (Drosophila Scrapie homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108812	hypothetical protein FLJ22004	3.2
45	134964	AI803516	Hs.272891	hippocampin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease H1, large subunit	3.1
	119750	AI538880	Hs.94812	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373062		nuclear receptor subfamily 1, group I, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	116429	AF191018	Hs.279923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	128721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW969025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AI652236	Hs.49376	hypothetical protein FLJ20644	3.1
	133461	NM_000762	Hs.334345	cytochrome P450, subfamily IIA (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 allele of SKP1, S. cere	3.1
60	134937	AI251449	Hs.171939	ESTs	3.1
	125756	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12650	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	126556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AI908006	Hs.295362	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AI914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:zn57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R56678	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
75	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nucleolar protein NOP5/NOP58	3.1
80	105024	AA126311	Hs.9879	ESTs	3.1
	123485	AI308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	UIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hn88a05.x1 NCI_CGAP_Kd11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AA443473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ20212	3.1
	129707	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like-protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84284	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
15	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
	106057	BE614474	Hs.289074	F-box only protein 22	3.0
20	106378	AA824298	Hs.21331	hypothetical protein FLJ10036	3.0
	128660	AA011597	Hs.177398	ESTs	3.0
	115467	AI365784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128604	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
25	126698	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypotheti	3.0
	133966	BE280478	Hs.182695	hypothetical protein MGC3243	3.0
	119155	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131586	AA460352	Hs.26956	KIAA1171 protein	3.0
	100237	D30715	Hs.26956	Human PAP (pancreatitis-associated prote	3.0
30	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
	129928	AI338993	Hs.134535	ESTs	3.0
35	118922	AW206193		hypothetical protein DKFZp761B2423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
	125165	W45350		gb:zc81h08.s1 Pancreatic Islet Homo sapi	3.0
	122219	AA436002	Hs.183161	ESTs	3.0
40	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) Interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp564O043	3.0
	126997	AI377150	Hs.150914	ESTs	3.0
	128902	AA036637	Hs.107052	ESTs	3.0
45	117186	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.0
	126096	F08208	Hs.283844	similar to rat tricarboxylate carrier-II	3.0
	106711	BE390125	Hs.143187	hypothetical protein	3.0
	114046	BE018658	Hs.141003	Homo sapiens cDNA: FLJ21691 fis, clone C	3.0
50	135029	H59818		hydroxysteroid (17-beta) dehydrogenase 7	3.0
	112003	AW978731	Hs.301824	hypothetical protein PRO1331	3.0
	106735	R77698	Hs.337778	ESTs	3.0
	126628	N49776	Hs.170994	hypothetical protein MGC10946	3.0
	133350	AI499220	Hs.71573	hypothetical protein FLJ10074	3.0
55	110312	BE256986	Hs.11896	hypothetical protein FLJ12089	3.0
	125659	T57693	Hs.87929	Homo sapiens cDNA FLJ13707 fis, clone PL	3.0
	129601	AB032964	Hs.115726	KIAA1138 protein	3.0
	123423	AA598484		gb:aa38f04.s1 Gessler Wilms tumor Homo s	3.0
	128695	NM_003478	Hs.101299	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
	101445	M21259		gb:Human Alu repeats in the region 5' to	3.0
	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
	116475	AA733050	Hs.334612	small nuclear ribonucleoprotein polypept	3.0
65	106573	AA223447	Hs.12835	A kinase (PRKA) anchor protein 7	3.0
	103106	W27172	Hs.1857	phosphodiesterase 6G, cGMP-specific, rod	3.0
	130755	BE293520	Hs.18910	prostate cancer overexpressed gene 1	3.0
	112246	R51321	Hs.25780	Homo sapiens cDNA FLJ12252 fis, clone MA	3.0
	126887	H20832		gb:ym48d03.s1 Soares Infant brain 1N1B H	3.0
70	117960	AA310417	Hs.47044	ESTs	3.0
	133626	AW836130	Hs.75277	hypothetical protein FLJ13910	3.0
	113179	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	3.0
	109968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
75	125770	AA143045	Hs.81665	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

Pkey: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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5	123619	371681_1	AI686652 AW389079 AA602099 AW134567 AW517843 AI682674 AI474874 AA374167
	131495	142008_1	AA602964 AA609200
			AA812434 AI831542 AA766261 AI769894 N63376 AA214392 AA135833 AW605017 AA135965 AW450072 H04812 AA446459
			AW439151 AA426273 AI061423 AA598549 Z40087 AI753216 AA743075 AA854268 AA458920 AA843893 AI566516 AI864957
			AI566634 AW971760 AA211795 AA430089
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	125165	1852047_1	W45350 W45406
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			AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221
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			AA476873 BE297387 AA292753 AA177048 NM_001826 X54941 BE314366 AA908783 AI719075 BE270172 BE269819 AA889955
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			AA740817 AI312104 AI911822 AA416871 AI185409 AA128784 AA701623 AI075239 AI139549 AA633648 AI339966 AI336880
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	125464	168460_1	N71807 AA203399
	126127	1205826_1	N95428 W24040 AW751366 H81987
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			AI953638 R31669 AW769278 R82398 AA131925 R21776 R79031 AI129553 N70340 AI276116 AA709381 N63734 AI342605
			AA327133 AI805980 AA005377 AW611716 T86946 AA369083 R67250 H00240 R32578 W85279 R80248 R23734 H00977 R21732
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			H12600 R82345 AA653499 AW953717 R63207 R33888 H54071 H66993 T48748 AI702300 R30775 H68996 AI014957 AA369082
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			H00188 R21233 H03055 R53822 AA367558 R75872 W04151 AI220869 AI090290 AA368730 R24434 H81153 H70950 AA367783
			H81514 H53536 C16968 C17797 C17677 C17064 AA082581 C17044 D63217 C18791 D78839 D63290 D78838 N91085 H54070
55			R80360 H78318 H40199 R33887 R02529 H94918 R00900 T87029 AA131924 R99891 AA004267 D78764 D78757 H61600 C18615
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	103898	187213_3	AA248884
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			AW898616 AA709126 AW898628 AW898544 AA947932 AW898625 AW898622 AI276125 AI185720 AW510698 AA987230 T52522
65			BE467708 AW243400 AW043642 AI288245 AI186932 D52654 D55017 D52715 D52477 D53933 D54679 AI298739 AI146984
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			AW196492

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30	131019 223488_3	AW303285 AW117396 AA888929 BE174517 Z70704 AL042292 H54958 AA310063 AW499643 AW501380 AW501202 AW501293 AW501596 AW630166 AL041326 AA780690 L40517 U21556 AI093182 AW062487 AA883387 AA931302 BE252601 BE258381 AA827330 AL043930 AA356337 AW962830 AW393814 Z70703 AW389484 T62231 AW780048 AL043931 BE149744 AW963292 BE439659 BE091737 BE091657 AA484004 AI673095 AA599106 AW601545 AI538739 AI538730 AI521786 AW366369 AW021010 AA362576 AI289927 AA382592
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55		D30715 AA251089 AA598484
60	124250 314220_1 101447 entrez_M21305 117357 genbank_N24829 103392 entrez_X94563 135029 H58818_at 105225 genbank_AA211777 121292 genbank_AA401807 105909 82840_1	
65		
70	100237 entrez_D30715 114988 genbank_AA251089 123423 genbank_AA598484	
75		

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigena Title for all of the sequences in Table 73.

80	Pkey:	Unique Eos probeset Identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigena number
	Unigena Title:	Unigena gene title

Seq ID No:	Seq ID number correlation for those sequences in Table 73			
Pkey	ExAccn	UnigenelD	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82932	cydin D1 (PRAD1: parathyroid adenomas
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi
	101104	AW862258	Hs.169266	neuropeptide Y receptor Y1
	447761	AF061573	Hs.19492	protocadherin 8
	428183	AW969726	Hs.98381	ESTs, Weakly similar to serine protease
10	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin
	121619	AA528339	Hs.178062	ESTs, Weakly similar to phosphatidylseri
	104659	AW969769	Hs.105201	ESTs
	105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro
	129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop
15	100299	D49493	Hs.2171	growth differentiation factor 10
	116301	AW969706	Hs.293332	ESTs
	106533	AL134708	Hs.145998	ESTs
	131313	R96290	Hs.75874	ribosomal protein L44
	105316	AI671245	Hs.24835	hypothetical protein FLJ14594
20	113003	AW292315	Hs.7215	ESTs
	102836	U94320	Hs.158330	neuropeptide Y receptor Y5
	102745	AW753865	Hs.74376	olfactomedin related ER localized protel
	123308	C14187	Hs.157208	ESTs
	120147	AJ917116		hemoglobin, beta
25	123049	BE047680	Hs.211869	diclkopf (Xenopus laevis) homolog 2
	119082	AF252297	Hs.91546	cytochrome P450 retinoid metabolizing pr
	105301	AW352357	Hs.7457	MAGE1 protein
	128478	AA708205	Hs.100343	ESTs
	106111	AW875398	Hs.6451	PRO0659 protein
30	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor
	120830	AJ568170	Hs.96886	ESTs
	127664	AA806164	Hs.116502	ESTs
	102725	AB026187	Hs.159156	protocadherin 11
	132520	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas
35	130637	AA356764	Hs.17109	integral membrane protein 2A
	117602	N35020	Hs.44585	C3HC4-like zinc finger protein
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr
	129703	BE388665	Hs.179999	Homo sapiens, clone IMAGE:3457003, mRNA
	125770	AA143045	Hs.81665	w-kit Hardy-Zuckerman 4 feline sarcoma v
40	414761	AU077228	Hs.77256	enhancer of zeste (Drosophila) homolog 2
	420462	AF050147	Hs.97932	chondromodulin I precursor
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of
	104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor
	416836	D54745	Hs.80247	cholecystokinin

Table 72B

Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT Number	Accession
131307	3138_1	NM_000025 X72811 X70811 M29932 X70812 S53291 AW015148 AW581776 AJ276134
131313	93372_1	R95290 H02411 C18327 AA367588 AA367557 H89632 C17954 AA568860 AJ752983 AA699451 H04260 AI128118 AW193364 N94503
		AA029995 T40536 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226
		AI200363 R79731 AA702947 A400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R65618 H73711 R58545 D79189 AW265710
		R77664 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156623 AA368336 H53662
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		AW969706 AA456258 AA491881 BE501639 D62113 AW869710 AI591236 AJ379869 AW968997 AA040053 AI807206 AW663917 AA454645
		AA489238 BE241958 AA743491
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		BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077
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		AI918938 BE168117 BE087369 AW995539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H66084
		AI146884 BE075154 AW992247 AI186525 AI752230 AW263140 W03329 N26056 AA948080 AA113073 H99284 AA227101 AA631077
		AA148042 AI740837 BE082728 AA149570 W44495 BE089351 AA375044 N26775 H27771 AA064705 BE091204 R89337 N32676 N27141
		BE164704 H98049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T09020 W23852 AA062709 BE167894 AA076515 R97329
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		AW298822 AW080962 AI073747 W24123 AA577596 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W48631 AA908347
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		AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA522062 AI055890 AI660881 AI366117 AA403090 AI272818
		AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079968 AI752231 AA076431 AA113245
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		AA207064 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526
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		AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086652 BE408324 AW292848 AI768962 BE540703 BE409478 AA931692

5	132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW838107 AW838106 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE000988 AA131806 BE180577 AW838269 AL039831 AJ754380 C06051 AA131737 AW838239 AI767465 AI480134 AA610312 AW838190 AA379252 AW838282 AA484027 AI423413 AI685064 BE328307 AI241857 AW838281 AW838284 AI671267 AI814928 AA828367 AI476306 AI270180 AA622362 AI076497 AI635919 AI444994 AI194028 AI659159 AI928131 AA448953 AI350143 AW079289 AW467807 AA480442 AA522935 BE180570 AW380087 AW380109 AI081015 AI690818 AI589485 AI698510 AA642019 AA714366 AI580430 AA985527 AI740475 C21398 AA257993 AI302393 AI689018 AW770194 AW753750 AI079164 BE550338 AA559851 T16108 AI864822 AI932827 AA045095 AA045062 AI954225 AA768569 AA709308 AW958363 N35020 AB026187 NM_014522 U79247 F13304 AA224524 F10902 R39431 AW753855 F07644 F11280 F06355 F08136 U79299 F07459 F08750 F12419 F12842 F06468 F08585 F13403 F05921 F05512 F11683 F05416 F12841 F12810 F05418 F12850 R24551 F06276 H11803 H10237 H11542 H22894 R59563 H19351 H18722 F11237 F08507 H23123 R61595 F07796 F06201 F12289 F07107 T78113 F08734 F13344 F05760 F11784 F08780 F05835 R20588 F07739 F11497 R17410 H17414 R20440 T66090 R25292 T66236 T78766 T79908 R25286 R60071 C14761 AW905192 AA331914 AW965291 H09000 F05212 F08313 F05825 H06399 H15135 H11378 R65424 R61541 AA235405 AI205041 R59564 H23124 H18638 R37359 AI571275 R41780 T66174 T66159 R54102 W07657 H10794 R52337 R42890 H14354 R40952 T17391 H12068 R56797 R51000 R60011 R37617 R39434 H28266 T16403 H09129 R49114 H15161 H11729 R39160 H10468 H24454 H11432 R54433 H08768 H24042 H09511 H17281 H15292 R37849 AI91965 R52815 R42650 T17390 T16438 T17388 T16285 R48963 R50782 R42427 R46729 R59558 R40696 R43575 R44420 T17403 R37754 R46637 R51039 R40513 T23785 F10433 T16350 H10191 R43688 T23543 H08591 R44351 R37575 R49508 F04379 F04056 F05067 F02010 F09158 F10036 F08900 F02559 F09914 F09434 F05034 H17415 F02644 H10650 F10451 H14589 F10444 T16440 R44517 R46643 F03993 F10443 F02170 F09343 F10414 F04794 F11122 F04997 F03894 AW005932 F02757 F10941 F01777 R45260 F03386 R45261 T65009 F10990 F08942 F01673 H23253 F04533 F02082 F01669 F03689 H09568 R40763 H06400 R50958 H08570 AI082296 AI198226 T23763 AA814486 AW015823 AI886272 H06514 AA515969 F10049 AI984267 AI886279 AA558516 F02071 AI783443 AI804884 F01468 AA730438 AF035301 R38389 R41440 R59468 R14437 T89036 R43560 H10821 R62850 R56722 R14559 T09299 H10467 R25829 F13546 R56796 R51151 D82657 T32952 T66257 H06569 F12430 T74326 H08489 R34430 R13083 H23364 R21134 T77098 AW957157 H24150 H11403 R52336 F12830 T77173 T74281 T77663 T74736 H10649 H12067 R20092 T74735 R54530 R17552 R59557 R54529 H17280 T75171 H14694 T74975 H15291 R18574 R54157 R13446 H15221 R35120 R35031 R21277 R19632 R35820 R50899 R13923 R36771 R26485 R33061 R20100 H24426 H09184 H15958 R19253 H15195 H09510 R36032 R19691 H14402 H14885 T17068 AF252297 N27888 F13415 R34552 R14377 AA323962 AW611514 AW614097 AW195487 AI026040 AI097663 AI0012834 AW969885 AA988198 R49069 AW873673 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AI948482 AI960966 AA548335 W72197 N32815 AA768073 AW338181 AW001742 AI819896 AI015666 N58011 AA677584 AI183750 AW105514 W37875 AW301679 AA775257
10	117602	10565_4	
	102725	11582_1	
	102745	13186_1	
15			
20			
25			
30	119082	34131_1	
	102836	25380_1	
	125770	16581_2	
35	120147	386607_2	
	113003	420161_1	
	104659	82594_1	
	104691	41308_1	
40	105301	27795_5	
45	105316	181763_1	
	127664	394361_1	
	106111	4671_1	
50	128478	370722_2	
	105782	246361_1	
	120830	244476_1	
	128797	20410_1	
55	108533	305354_1	
	121619	284072_1	
	123049	30801_1	
	129703	64196_1	
60			
65			
70			
75	100299	2801_1	
	129977	2039_1	
	123308	322009_1	
	101104	26442_2	
80	130637	7040_1	

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410102 117657_1
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420462 19379_1

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AA730357 AI128690 AA630149 AW241515 AI147003 AI183499 N90923 AI968582 AA354145 AI147297 BE550502 AI085777 AI709087
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D54745 AU077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571
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AW969726 AA424028 AI266636 AI271571 AA423998 AI266634 AA702780 AA452037 AI424866 AA742931 AA483361
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H26576 H95984 AA745021 AA639180 H26575
AF061573 NM_002590 AA780138 AW135620 AI197884 AA483348 R05468 AW969724 H29216

Table 73: Sequences

Seq ID NO: B1 DNA sequence

Nucleic Acid Accession #: NM_053056.1

Coding sequence: 210..1097

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	TCCCAGAGCTG	CCCAGGAAGA	GCCCCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCTCTCA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAATGT	GTGCAAGAGG	360
	AGGTCTCGCC	GTCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCGAGGAAC	420
15	AGAAGTGC	GGAGGAGGTC	TTCCCGCTGG	CCATGAACCTA	CCTGGACCGC	TTCTGTGCGC	480
	TGGAGCCCGT	GAAAAAGAGC	CGCCTGCAGC	TGCTGGGGGC	CACCTGTCATG	TTCTGTGCGCT	540
	CTAAGATGAA	GGAGACCATC	CCCCTGACGG	CCGAGAAAGCT	GTGCATCTAC	ACCGACAACCT	600
	CCATCCGCGC	CGAGGAGCTG	CTGCAAAATG	AGCTGCTCCT	GGTGAACAA	CTCAAGTGGA	660
	ACCTGGCCCG	AATGACCCCG	CACGATTTC	TGGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
20	CGGAGGAGAA	CAACAGATC	ATCCGCAAA	ACGCGCAGAC	CTTCGTGTCC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCATTTC	AATCCGCCCT	CCATGGTGGC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCAAG	CTGAACCTC	AGGAGCCCCA	ACAACTTCCT	GTCTACTAC	CGCTCACAC	900
	GCTTCTCTC	CAGAGTGATC	AAGTGTGACC	CAGACTGCCT	CCGGGCGTGC	CAGGAGCAGA	960
25	TGGAAGAGCT	AATGCAAA	AGCCTGCGCC	AGGCCAGCA	GAACATGGAC	CCCAAGCCG	1020
	CCGAGGAGGA	GGAAGAGGAG	GAGGAGGAGG	TGACCTGGC	TTGCACACCC	ACCGAGCTGC	1080
	GGGAGCTGGA	CATCTGAGG	CGCCAGGCG	GCGGGCGCCA	CCGCCACCCG	CAGCGAGGGC	1140
	GGAGCCCGCC	CAGGTGCTC	CCCTGACAGT	CCCTCTCTC	CGGAGCATTT	TGATACGACA	1200
	AGGGAAAGCT	TCATTCTCT	TGTTGTGTT	TGTTTTTCT	TTTGTCTCT	CCCCCTTCCA	1260
30	TCTCTGAGCT	AAGCAAAAG	AAAAGATTAC	CCAAAACCTG	TCTTTAAAG	AGAGAGAGAG	1320
	AAAAAAGAAA	TAGTATTG	ATAACCTG	GCGGTGGGG	AGGAGGGTTG	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATAATCAAC	TCGTTTTTAT	ATTAAGTAC	TTGTTTCTCT	1440
	GTGTGAAGAA	TAGGCATTAA	CACAAAGGAG	GCGTCTCGGG	AGAGGATTAG	GTCCATCCT	1500
	TTACGTGTTT	AAAAAAGC	ATAAAACAT	TTTAAACA	TAGAAAAAT	CAGCAAAACA	1560
	TTTTTAAAGT	AGAGAGGGT	TTTAGGTAGA	AAAACATATT	CTTGTGCTT	TCTGTATAAA	1620
35	GCACAGCTGT	AGTGGGGTTC	TAGGCATCTC	TGTACTTTGC	TTGCTCATAT	GCATGTAGTC	1680
	ACCTTTATAG	TCATTGTATG	TTATTATATT	CCGTAGGTAG	ATGTGTAACC	TCTTACACCT	1740
	ATTCATGCT	GAGTCACCT	CTTGGTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCCCT	1800
	TGCGCTGTG	ACCACCAACC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
40	TCGGGACCCA	GCGAGCGTAG	CAGGGTGGG	AAAGGCCACC	TGTCCCACTC	CTACGATACG	1920
	CTACTATAAA	GAGAAGACGA	AATAGTGACA	TAATATATTC	TATTTTATA	CTCTTCTAT	1980
	TTTGTAGTG	ACCTGTTTAT	GAGATGCTG	TTTTCTACCC	AACGGCCCTG	CAGCCAGCTC	2040
	ACGTCCAGGT	TCAACCCACA	GCTACTTGGT	TTGTGTTCTT	CTTCATATTC	TAAAAACCAT	2100
	CCATTTCCAA	GCACTTTCAG	TCCAATAGGT	GTAGGAAATA	GCGCTGTTT	TGTTGTGTGT	2160
45	GCAGGGAGGG	CAGTGTTCCTA	ATGGAATGGT	TTGGGAATAT	CCATGTACTT	GTTTGCAGAC	2220
	AGGACTTTGA	GGCAAGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGCCAG	TCAAGAAAGAA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCTCT	2340
	TTCTTTTCT	TTAAGAAAGT	TGAAGTTTAG	GAATCCTTTG	GTGCCAACTG	GTGTTTGAAA	2400
	GTAGGGAGCT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGGTTAT	CTTAGATGTT	2460
50	TCACACCCGA	AGGTTTTTCTA	ACACTAAAT	ATATAATTTA	TAGTTAAGCG	TAAAAAGTAT	2520
	ATTTATTGCA	GAGGATGTTT	ATAAGGCCAG	TATGATTTAT	AAATGCAATC	TCCCTTGAT	2580
	TTAAACACAC	AGATACACAC	ACACACACAC	ACACACACAC	AAACCTTCTG	CCCTTGTATG	2640
	TACAGATTGA	ATACAGTTTA	TTTTTAAAGA	TAGATCCTTT	TATAGGTGAG	AAAAAACA	2700
	CTGGAAGAAA	AAAAACCA	CAAGACAT	GATTGAGCCT	GTTTGGCGTT	TCCAGAGTCT	2760
55	ATCTGATTGG	ACAGGCATGG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTGCGTTCC	2820
	GATGAATCT	TATCCCTGTC	CCCTTCTCTT	AAAAACCTTA	GTGACAAAT	AGACAATTTG	2880
	CACATCTTGG	CTATGTAATT	CTTGTAAATT	TTATTTAGGA	AGTGTGGAAG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGGAGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGCTC	3000
	CCGAGGGGAA	GGGCGGTG	CCACACCGGG	GACAGGCGCG	AGCTCCATT	TCTTATTGCG	3060
60	CTGCTACCGT	TGACTTCCAG	GCACGGTTTG	GAAATATTCA	CATGCTTCT	GTGTATCTCT	3120
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	ATGTACTAGT	TTTAGTTTTT	TCTTAGAACA	TGTATTACCA	GATGCCTTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCTCTATT	CAAAAAGGTT	3300
	GCTGTTTTC	AATACCTCAT	GCTTCACTTA	GCCATGGTGG	ACCCAGCGGG	CAGGTTCTCG	3360
65	CTGCTTTGGC	GGGACAGAC	GCGGGGCGGA	TCCACACAG	GCTGGCGGGG	GCGGGGCGCG	3420
	AGGCGCGGTG	CGTGAGAAC	GCGCGGTGT	CCCCAGAGAC	CAGGCTGTGT	CCCTCTTCTC	3480
	TTCCCTGCGC	CTGTGATGCT	GGGCACTTCA	TCTGATCGGG	GGCGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATTCTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	CGGCGTTGTA	CCTGTAGGAC	TCTCATTCGG	3660
70	GATGATTGGA	ATAGCTTCTG	GAATTTGTTT	AAGTTTTGGG	TATGTTTAAT	CTGTTATGTA	3720
	CTAGTGTCT	GTGTTTAT	GTGTTGTAA	TTACACCATA	ATGCTAATTT	AAAGAGACTC	3780
	CAATCTCAA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCGG	GTCACTAGC	AAGCTGCCGA	3840
	ACCAAAAGAA	TTTGACCCCC	GCTGCGGGCC	CACGTGGTTG	GGGCGCTGCC	CTGGCAGGGT	3900
	CATCTGTG	TGCGAGGCCA	TCTCGGCGAC	AGGCCACACC	CGCCCCACCC	CTCCAGAAC	3960
75	CGGCTCACGC	TGACTCAAC	CATCTGGCT	GCGGCGTCTG	TCTGAACAC	GCGGGGCGCT	4020
	TGAGGGACGC	TTTGTCTGTC	GTGATGGGGC	AAGGGCACAA	GTCTGTGATG	TTGTGTGTAT	4080
	CGAGAGGCCA	AAGGCTGGTG	GCAAGTGAC	GGGGCACAGC	GGAGTCTGTC	CTGTGACCGG	4140
	CAAGTCTGAG	GGTCTGGGCG	GCGGCGGCT	GGGTCTGTGC	ATTTCTGTTT	GCACCGCGGC	4200
80	GCTTCCAGC	ACCAACATGT	AACCGGCATG	TTTCCAGCAG	AAGACAAAA	GACAAACATG	4260
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Seq ID NO: B2 Protein sequence

Protein Accession #: NP_444284.1

1 11 21 31 41 51

5 MEHQLLCCEV ETIRRAYPDA NLLNDRVLRA MLKAETCAP SVSYFKCVQK EVLPSMRKIV 60
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Seq ID NO: B3 DNA sequence
 Nucleic Acid Accession #: XM_044166
 Coding sequence: 1..1576

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1 11 21 31 41 51
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Seq ID NO: B4 Protein sequence
 Protein Accession #: XP_044166.2

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 LVVGPKGATI KRIQQQNTNY IITPSRDRDP VFEITGAPGN VERAREEIEI HIAVRTGKIL 300
 EYNNENDFLA GSPDAALDSR YSDAWRVHQP GCKPLSTFRQ NSLGCIGECG VDSGFAPRL 360
 GEQGGDFGYG GYLFPYGVGV KQDVYGVVAE TSPPLWAGQE NATPTSVLFS SASSSSSSSA 420

KARAGPFGAH RSPATSAGPE LAGLPRRPPG EPLQGFSLKG GGLRSPGGG RDCMVCPESE 480
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5 Seq ID NO: B5 DNA sequence
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209..1363

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25 TACCACCTCTC CTCTTGGTGC TGCAGTATTT TGGTCCACTT TGTTTTATAT TTATTGCTA 900
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55 TGTTTGATTT TAAAGGGCG GACATTTTAT TAAATCAAT ATTGTTTTTG CTTTCTCTGA 2700
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Seq ID NO: B6 Protein sequence
Protein Accession #: NP_000900.1

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65 CVSITVSIFS LVLIIVERHQ LIINPRGWRP NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180
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70 Seq ID NO: B7 DNA sequence
Nucleic Acid Accession #: NM_002590.2
Coding sequence: 204..3416

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5 AGGAGCAGTT CCGCTGGTG CACGTGGAGG TAGAGGTGAG GGACGTCAAC GACCACGCGC 600
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Seq ID NO: B8 Protein sequence
 Protein Accession #: NP_002581.2

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 VGRAGGAVST YVSVDPATGA IYALRSFDYB TLRQLDVRIQ ASDGGSPQLS SSALVQVRVL 600
 DQNDHAFVLV HPAPANGSLE VAVPGRTAKD TVVARVQARD ADEGANGELA FELQQEPRE 660
 APAIGRRTGE ILLTGDLSQL PPGRVFRALL VISDGGRPFL TTTATVSVFV TAGGGRGFAA 720
 PASAGSPERS RPPGSRGLVS GSVLQWDTPL TVIIVLAGSC TLLAAIIAI ATTQNRKKE 780
 80 VRKGGALREE RPGAAGGGAS APGSPPEEAR GAGPRPNMFD VLTFFGTGKA PFGSPAADAP 840
 PPAAVAAEVP GSEGGSTGSE SACHFEGQQR LRGAHAPEYG ASPFGKEPA PPVAVWKGS 900
 FNTISGREAE KFSGKDSGKG DSDFNDSDD ISGDALCKDL INHMQSLWA CTAECKILGH 960
 SDRCSPPSCS GPNAPHSFPH PAQMSTFCKS TSLPRDLRR DNYVQAQLPK TVGLQSVYEK 1020
 VLHRDYDRTV TLLSPFRFRG LPDLQSIGVP LYQSPPGRYL SPKKGANENV

Seq ID NO: B9 DNA sequence
Nucleic Acid Accession #: AL121939.12
Coding sequence: 185..1426

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5      1      11      21      31      41      51
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AGCGGAGTST CAGTGGCCGAG CTCGGGTGCG TGTGGCCCGG CCTTGGCCGG GCGGCCCTCCG 60
GCTCAGGCTG GCTGAGAGGC TCCAGCTGCG AGCGTCCCGG CCGGCTCCTC CGGGAGCTCT 120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAAGCCTG GCAGGACAAA ATTAGAAGAT 180
10     CAAAATGGAA AATATGCTGC TTTGGTTGAT ATTTTTCACC CCTGGGTGGA CCCTCATTGA 240
TGGATCTGAA ATGGAATGGG ATTTTATGTG GCACCTGAGA AAGGTACCCC GGATTGTGAG 300
TGAAAGGACT TTCCATCTCA CCAGCCCCGC ATTTGAGGCA GATGCTAAGA TGATGGTAAA 360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCACT CCCAGCCTTT CTGAATTGGA 420
GGATTATCTT TCCTATGAGA CTGTCTTTGA GAATGGCACC CGAACCTTAA CCAGGGTGAA 480
15     AGTTCAAGAT TTGGTCTCTG AGCCGACTCA AATATCACC ACAAGGGGAG TATCTGTTAG 540
GAGAAAGAGA CAGGTGTATG GCACCGACAG CAGGTTGAGC ATCTTGAGCA AAAGGTTCTT 600
AACCAATTTC CCTTTCAGCA CAGCTGTGAA GCTTTCACG GGCTGTAGTG GCATTCTCAT 660
TTCCCTCAG CATGTTCTAA CTGCTGCCCA CTGTGTTTCA TATGAAAGG ACTATGTCAA 720
20     AGGAGTAAA AAGCTAAGGG TAGGGTTGTT GAAGATGAGG AATAAAGTG GAGGCAAGAA 780
ACGTGAGGAT TCTAAGAGGA GCAGGAGAGA AGCTAGTGGT GGTGACCAA GAGAGGGTAC 840
CAGAGAGAGA CAGGTGTATG GAGCGAAGGG TGGGAGAAGA AGAAAAAAT CTGGCCGGGG 900
TCAGAGGATT GCCGAAGGGA GGCTTCCTCT TCAGTGGACC CGGCTCAAGA ATACCCACAT 960
TCCGAAGGGC TGGGACGAGG GAGGCAATGG GGAAGCTACC TTGGACTATG ACTATGCTCT 1020
25     TCTGAGCTG AAGCGTACTC ACAAAAAGAA ATACATGGAA CTTGGAATCA GCCCAACGAT 1080
CAAGAAATG CCTGGTGAA TGATCCACTT CTCAGGATT GATAACGATA GGGCTGATCA 1140
GTTGCTCTAT CGGTTTTCGA GTGTGTCYGA CGAATCCAAT GATCTCCTTT ACCAATAYTG 1200
CGATGCTGAG TCGGCTCCCA CCGGTTCCGG GGTCTATCTG GGTCTGAAG ATCCAGACAA 1260
AAAGAATTGG AAGCGCAAAA TCATTGCGGT CTACTCAGGG CACCAAGTGG TGGATGTCCA 1320
30     CGGGTTCAG AAGGACTACA ACGTTGCTGT TCGCATCACT CCGCTAAAAT ACGCCAGAT 1380
TTGCCCTGCG ATTCAGGGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAAC 1440
AGGCGGTGAT ATCATCTAAA TCACAGAGAA AACCACTCT CTCTACCGTA GTGAGATCAC 1500
TTCATAGGTT ATGCTGAGAC TTGAACCTCT TCAATAGCAT TTCACATTT TTCAAATCA 1560
GGAGATTTC GTCCATTAAA AAAATGTATA GGTGCAGATA TTGAACCTAG GTGGGCACCT 1620
35     CAATGCCAAG TATATACTCT TCTTTACATG GTGATGAGTT TCATTGTAG AAAAATTTTG 1680
TTGCCCTCTT AAAAATTAGA CACACTTAAA ACCTTCAAAC AGGTATTATA AATAACATGT 1740
GACTCCTTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTGG 1800
TTGTGTATTA AATGTGAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAAGTTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGCTCAT 1920
40     GCCCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGSGA CATTTAGTTT AGTTTTTTTG 1980
AAGAATTACA AATCAGAAGA AAAAGCAAGC ATTATAAACA AAACCTAATA CTGTTTTACT 2040
GCTTTAAGAA ATAACAATTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCT 2100
ATGAAATAAA CCTAGTTTAG AAATAGGGA GCTGAGACAT TTAAAGATCT CAAGTTTTTA 2160
TTAACTAAT ACTCAAAATA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCACAAAT 2220
45     TATGAATGAT CATGTGTTGA AAGCCACATT ATTTATGCT ATACATTCTA TGTATGAGGT 2280
GCTACATTTT TAGGACAAAG AATTCTGTAA TCTTTTCAA GAAAGAGTCT TTTCTCCTT 2340
GACAAAGAGA GCTTTTGTGA TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTGA 2400
TATGTCTCTT CCTAAAAATG AATAAAATTT ATGAATATGA CTTAAAAAAA AAARWCGACG 2460
CGGCCGGGAA TTTAGTAGTA GTAGTGGACC CGGGAATTCC GGACCGGTAC CTGACGGCGT 2520
ACGAGC

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Seq ID NO: B10 Protein sequence
Protein Accession #: CAC35071.1

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55     1      11      21      31      41      51
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MENMLLLWLF FTPGWTLLDG SEMEWDFMWH LRKVPRIVSE RTFHLTSPAF EADAKMMVNT 60
VQIEQCQKEL PTPSLSELED YLSYETVFEN GTRTLTRVKV QDLVLEPTQN IITKGVSRR 120
KRQVYGTDSR FSLDKRFLT NFFPSTAVKL STGCSGILIS PQHVLTAHC VHDGKDYVK 180
30     SKGLRVGLLK MNKSGGKRR RSKRSRREA SGGDQREGTR EHLRERAKGG RRRKKSGRGQ 240
RIABGRPSFQ WTRVKNTHIP KGWARGMGMD ATLDDYDALL ELKRAHKKKY MELGISPTIK 300
KNPGGMIFPS GFDNDRADQL VYRFSVSDE SNDLLYQYCD ABSGSTSGSV YLRKDPDKK 360
NWKRIIAVY SGHQVVDVHG VQKDYNAVVR ITPLKTAQIC LWHGNDANC AYG

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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002035.1
Coding sequence: 108..1106

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70     1      11      21      31      41      51
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CGCGCGCGCC CGCGCGCGCC GCTCGCGGCC CCTGGCCCGG CGGAGCGATG CTGCTGCTGG 120
CTGCGCGCCTT CCTCGTGGCC TTGCTGCTGC TGCCTGACAT GGTGTCTCCG CTCATCAGCC 180
CCAAGCCCTT CGCCCTGCCC GGGCGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
75     GGAAGTGCAAT TGCTATCGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGACAGAA 300
ATGAGGATAA GCTGCTGAG GCAAGAAAG AAATGGAAT GCACCTCTAT AATGACAAAC 360
AGGTGCTGCT TTGCATATCA GTTGATGTAT CTCAGACTA TAACCAAGTA GAGATGTCA 420
TAAACACAGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAAATTGT GCAGGAATGG 480
CAGTGTGAGG AAAATTGAA GATCTTGAAG TTAGTACCTT TGAAGGTTA ATGAGCATCA 540
80     ATTACCTGGG CAGCGGTGAC CCCAGCCGGG CCGTGATCAC CACCATGAAG GAGCGCGGG 600
TGGGAGGAT CGTGTGTTG TCCCTCCAGG CAGGACAGTT GGGATTATTC GGTTCACAG 660
CCTACTCTGC ATCAAGTTT GCCATAAGGG GATTGCGAGA AGCTTTGCGA ATGGAGGTGA 720
AGCCATATAA TGCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGGCTTGT 780
CGAAGAAAAA CAGAACAAAG CCTTTGGAGA CTCGACTTAT TTCAGAGACC ACATCTGTGT 840
GCAAAACCAG ACAGGTGGCC AAACAAATTG TTAAGATGTC CATACAAGGA AATTTCACAA 900

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5 GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960
CTTCTATTAC TGAGGGGCTC CAGCAGGTGG TCACCATGGG CCTTTTCCGC ACTATTGCTT 1020
TGTTTTACCT TGAAGTTTT GCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTITCCAAA 1140
CTGAAAATGC AGACAAAACCT GCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTITCCAAA 1200
TAATTTGAAC AGCTTGTCTG TAAATGGGAC CCAATTTTTG GCCTATAGAC ACTTATGTAT 1260
TGTTTTCGAA TAGCTCAGAT TGGACCAAGT CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG 1320
CTAGAAGTTC ACCTCCTGAC AGTATTATTA ATACTATGCA AATATGGAAAT AGGAGACCAT 1380
TTGATTTTCT AGGCTTTTGT GTAGAGAGGT GAAGGTATGA GAATTAATAG CGTGTGAACA 1440
AAGTAAAGAA CAGGATTCCA GAATGATCAT TAAATTTTGT TCTATTTTAT CTTTTTTGCC 1500
CCCTTAGAGA TTAAGTCCAG AAATGTACTT TCTGGCACAT AAAGAAATCT TGAGGACTTT 1560
GTTTAAACCT TCCATAAAAA AACAAATTTT GGTITCTCGG GTTCTCTCTC TCTGTCTCTC 1620
TGCTCTCTG TCTCTCTGTC TCTCTCTCTC TCTCTCTCTC TCTCTCTCTC TCTTTGTGTA 1680
TTTTATTCAA GATGAGTTGG ACCCATTTGCC AGTGAGTCTG AATGTCACGT ACAGCCCTGT 1740
GTTGTGCTCA GGACTCACTC TGCTGCTGGT GGAACACTCAT GGCTTCTCTC TCTCTTTGAT 1800
CCCTAAAGC TAGCAGGGGG ACGGGAGAGG GCAGTGCAAT GGGAAAGTAA GAGATATTTT 1860
CCAGTAGAAT AAGCAATGCT TTTTGTCTT TAGACTCAAA TGCTTAGGGA ACGTTTCATT 1920
TCTCATTCAT GGGGAAAGGC AGCCTCCTTA AATGTTTCTT GAAGAGCGGT AAAATCTAGA 1980
AGCTTAAGAA TTTACAGTTC CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCAT 2040
TAGCATCTA CTTGTTTTTC CCATCTCTTC CTTTCCAATT TTGCTTATAC TGCTGTAATA 2100
TTTTTTGAAA AAAAAAAGAA AAGGAAAAAA AAGACCAGCT AAAATTTTCG ACTTGACTTT 2160
TTAACTTAAC TCAATGAATTA ATTAAGCAA ATGAAAAAAT TAAAGAGTGT GACTTTTTCT 2220
CGGAGCATAT ATGTAGCTTT TAGGAAAGGC TGATGATGGT ATAAAGTTTG CTCATTAAGA
AAAAAGACA AGGCTGATTT TGAAGAGAGT TGCTTTTGAA ATAAATGAT CA

25 Seq ID NO: B12 Protein sequence
Protein Accession #: NP_002026.1

30 1 11 21 31 41 51
| | | | |
MLLLAAAPLV AFVLLLYMVS PLISPKPLAL PGAHVVTGG SSGIGKCAI ECKYKQGAFIT 60
LVARNEKLL QAKKEIEMHS INDKQVLCI SVDVSQDYNQ VENVIKQAE KLGFPVDMLVN 120
CAGMAVSGKP EDLEVSTFER LMSINYLSV YPSRAVITM KERRVGRIV VSSQAGQLGL 180
FGFTAYSASK FAIRGLAEAL QMEVKPYNVY ITVAYPPDTD TPGFAENRT KPLETRLISE 240
TTSVCKPEQV AKQIVKDAIQ GNFNSSLGSD GYMLSALTG MAPVTSITEG LQQUVTMGLF 300
35 RTIALFVLGS FDSIVRRMM QREKSENADK TA

Seq ID NO: B13 DNA sequence
Nucleic Acid Accession #: CAT Cluster

40 1 11 21 31 41 51
| | | | |
CTTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTTAA TTTTAAAT 60
CGGCAAAATA TTGGTGCCCT TCCCGAAATT TGTCGCCGGG CTCCCTTATA GGATAATTGG 120
TTTGATTTGG TTAAGTCCAA TTATTAAATG CTGCGGTTTC AAATTTCCAG CTGGAAGGAC 180
45 CACCCATTTA AAAACCTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAATAAT 240
CCAGGCATTG GTTTGACATA TTTCCAGAGC TCAAACTGCG AGTGTCCAC ATGCACATAC 300
AAGATCCAGA GTCTCATGTT AAAATCACTT ACATACCCAG AAAGACCACC ACTTTGCAGG 360
TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
AAGAACAATC AAGATGCCTT CTCCATCAA ATGCACCTGC TTGTGAATTA ATGGACTTGT 480
50 AAATGAACA ATGCAATCAG TCTTTTATAA TGCACTGTTC AATTGAGAT TCAAGTATTT 540
CTATTTCTTG GAAAAAATTT TAAGATCAA AATAAAGAA AATAAAAGT GCATACAGTT 600
AAACATTCCA AAAAAAATAA AA

55 Seq ID NO: B14 DNA sequence
Nucleic Acid Accession #: XM_086767.1
Coding sequence: 276..611

60 1 11 21 31 41 51
| | | | |
CTGTGTCATG GCATCTTTAG AAACAAACTG CAATTTTATT TCATTTCCCT GTGTTTCATA 60
CAAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC 120
TCGGCTGGGT TATCAAGCCA AGCTATTTAA AGGTGTTTTA AAAGAAAGGA TGGAAAGGAG 180
65 ACCTCTTAGG ACCACTGTGT TTTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240
ATTTTGTCT CAGTATAATT GTTCCAGATA AAACATATGAT GGATGGCTCG TTTTCATTTA 300
AATTATTAAA TCAGCTTGGG ATGATTGAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT 360
TTTATAAATC TCAAGAAAGT AAGATTCTTG CTCAATTTTA TAATGACITT GTAAATATTT 420
CAAGCATTTG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCACA TGCACATACA 480
70 AGATCCAGAG ACTCATGTTA AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540
ATAATATTGT ACTTAAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCAA 600
AGAACACATA AGATGCCCTT TTCCATCAAA TGCACTGTCT TGTGAATTA TGGACTTGTA 660
AATGAACAA TGCAATCAGT CTTTATATAA GCACGTGTCA ATTTGAGATT CAAGTATTTT 720
TATTTCTTGG AAAAAATTTT AAGATCAAA AATAAAGAAA ATAAAAATG CATACAGTTA 780
AACATTCC

75 Seq ID NO: B15 Protein sequence
Protein Accession #: XP_086767.1

80 1 11 21 31 41 51
| | | | |
MMDGFSFKL LNQLGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNISS IGLTYFQSSN 60
LQCSTCTYKI QRLMLKSLTY PERPPLCRYN IVLKDREEVF LNPNTCTPKN T

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

	1	11	21	31	41	51	
5	TTTTTTTTT	TTTTTTTTT	TAAATGCAA	AGGAGCAACA	AAATTTATTG	ACTGAATTAA	60
	ACACAACAGT	AAAATGGCAG	TGTTGTAATT	TCATTTTCAG	ATGTTTGAAT	GGAACAAGAA	120
	AAGTGTCTATT	AGCCCAAGCT	TCCTACATT	ATTAAAGAG	TGACTATCAA	AAACAGCAAC	180
	ATGCACAATG	GTACATATGC	ACAAAATGGA	ATTATATCAA	CAAATATACA	AAATACCCAA	240
10	AATAAAATAT	TTACAGGTTT	AAAAATATAA	ACATTGATT	CTCTATCCCA	TTAAACCATT	300
	GGAGTGGAGA	AAGGAGGAAA	GACCCTATTG	CTATTTAGAA	TCCTTTTAA	AACAAGTTTT	360
	TAAACATGAT	AATTAAGTCT	AGGAGACAAT	TTTGTATGTT	TTTCAGGGGT	TTAACATTCT	420
	ATTATAAAAA	TAACATCTAT	AAACCTACTA	ACAATTTTCC	TCCTGTGCAC	AAAAATAATA	480
	CTGCCAAAC	CTGTCTCTAA	AGACATGCCT	GACTTTTCAG	AAAGCTAATT	ATGGAAATGG	540
15	AGTTTCTCGT	TTGGGTATC	TTTGTACTA	TTTTCAAATA	ACCAGCAACT	CCCTATATTA	600
	CAGTGAAGTA	CTTTATATAA	ATAACGTGGG	CGAAACCTGA	AGTTCACAAT	GAGCCTGCTA	660
	GGTAGCTGGT	GTCAAGTACA	AATGATAGGA	ATTGACTTTG	CCAACAACAT	CAAAAGCATT	720
	TTCCCTGATA	TTCTGATAG	ACCTACCACT	ATCAGATCCT	CCATATTCAA	TAAGATTAT	780
	CTGTGAAGCA	ATGAAATGT	TAAATATTAC	TTTGCTAGAG	TTTCTCTCC	TTTATTAGA	840
20	AATAAATGTG	TAGTGGGGAC	CAGTGGTGT	AATGTAGATA	CTTGAGAAGT	TTTATTGATT	900
	CCTTCAGACC	CATGCCG					

Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM_022898.1

Coding sequence: 268..2739

25	1	11	21	31	41	51	
	TTTTCTTGCT	TTTCTTCCCT	TTTTTTTCTT	TTTGCAACA	AAACAAAAA	CAGCATAGAA	60
30	GAAAGAGCAA	AATAAAGAAG	AAGAAGAGGA	GGAAGAGAGG	GAAAGAGAGG	AAGGGAAAAA	120
	AAACACCAC	CCGGGACAGG	GAGGAGGTGC	GGCGGCGCGG	GGCGGCGCGG	CAGCGGCGGC	180
	AGCGGCGG	CGGCGGCTCG	GACCCCTCC	CCCGGCTCCC	CCCATCAGTG	CAGCTCTCCG	240
	GGCGATGCCA	GAATAGATGC	CGGGGCAATG	TCCGCGCGCA	AACAGGGCAA	CCCGCAGCAC	300
	TTGTCCACGA	GGGAGCTCAT	CACCCACAG	GCTGACCATG	TGGAGGCCGC	CATCTCTGAA	360
35	GAAGACGAGG	GTCTGGAGAT	AGAGGAGCCA	AGTGGCCTGG	GGCTGATGGT	GGGTGGCCCC	420
	GACCCCTGAC	TGCTCACTCG	TGGCCAGTGT	CAAAATGAAT	TCCCTCTGGG	GGACATCTCT	480
	GTTTTATAG	AGCAAAAG	GAAGCAGTGT	GGCGCAGCT	TGGGTGCTGT	CTATGACAA	540
	GCCCTGGACA	AGGACAGCCC	GCCACCTCC	TCACGCTCCG	AGCTCAGGAA	AGTGTCCGAG	600
	CCGGTGGAGA	TCGGGATCCA	AGTCACCCCC	GACGAAGATG	ACCACCTGCT	CTCACCCACG	660
40	AAAGGCATCT	GTCCCAAGCA	GGAGAACATT	GCAGGTAAG	ATGAGCCTTC	CAGCTACATT	720
	TGCACAACAT	GCAAGCAGCC	CTTCAACAGC	GGGTGGTTCC	TGCTGCAGCA	CGCGCAGAAC	780
	ACGCAAGCTG	GGCGCATCTA	CCTGGAGCCC	GGGCGGCGCA	GCAGCTCGCT	CACGCGCGCG	840
	CTCACCATCC	CGCCGCGGCT	CGGCGCGGAG	GGCGTGGGCG	AGTCCCGGCT	CATGAATTTC	900
	CTGGGCGACA	GCAACCCCTT	CAACCTGCTG	CGCATGACGG	GCCCCATCCT	CGGGGACCAC	960
45	CGGGGCTTGG	CGGAGGGCGG	CCTGCGGGCC	ACGCGGCTTC	TCTTCAGTCC	CCGCGCGCGC	1020
	CACCACTTGG	ACCGGACCGG	CCTCAGTGCC	GAGGAGATGG	GGCTCGTCCG	CCAGCACCCC	1080
	AGTGCCTTGG	ACCGAGTCA	GGCCTGAAC	CCCATGGCCA	TGAGCTCGCC	CGCCATGGAG	1140
	TTCTCGCGCG	GGCTCCGCGA	GCTGGCGGGC	AACAGCTCCA	CGCCGCGCGC	CGTGTCCCGG	1200
	GGCCGCGGCA	ACCTATGCA	CGGCTCTCTG	AACCCCTTCC	AGCCGAGCCC	CAAGTCCCGG	1260
50	TTCTTGAGCA	CGCGCGCGCT	GCOCGCCATG	CCCCCTGGCG	GCACGCGCGC	CCCGCAGCGG	1320
	CCAGCCAAGA	GCAAGTCTGT	CGAGTCTCTG	GGCAAGACCT	TCAAGTTCCA	GAGCAATCTC	1380
	ATCGTCACT	TGGAGAACGA	CACGGGCGAG	AAGCCCTACA	AGTGCCAGCT	GTGCGACCC	1440
	GCGTGTCTCG	AGGCCAGCAA	GCTCAAGCGC	CACATGAAGA	CGCATATGCA	CAAGGCGGCG	1500
	TCGCTGGCGG	CGCGCTCCGA	CGACGGGCTC	TCGGCGGCGA	GCTCCCCCGA	GCCCCGCACC	1560
55	AGCGAGCTGG	CGCGGAGGGG	CCTCAAGGCG	CGCGAGCGTG	ACTTCCGCGA	CCAGGAGAGC	1620
	GACCGGCTCG	TGGGCGACGA	GCGGAGGAGG	GAGGAGCAGG	AGGAGGAGGA	GGAGGAGGAG	1680
	GAGCTGCTAC	TGGAGAACGA	GAGCGGCGCC	GAGTCAGACT	TCAGCATGGA	CTCGGAGCTG	1740
	AGCGCAACC	CGGAGAACCG	CGGTGGTGGG	GTGCCCGGGG	TCCCGGGCGC	GGGGGGCGGC	1800
	CGCGGCAAGG	CGCTGGCTGA	CGAGAAAGGG	CTGGTGTCTG	GCAAGGTCTAT	GGAGAACGTG	1860
60	GGCTTAGGCG	CAGTGCAGCA	GTACGCGGAG	CTCTGGCGCG	ACAAGCAGAA	GCGCGGCGCC	1920
	TTCTTGAAGC	GTGCGGCGGG	CGCGGGGAC	CGCGGCGAGC	ACGACGAGCG	GGGCGGCTGC	1980
	GGGAGCGCGG	GCGCGGGCGG	CGCGGTCAAC	GGGCGCGGGG	GCGGCTTCGC	GCCAGGCACC	2040
	GAGCCCTTCC	CCGGGCTCTT	CCCGCGCAAG	CCCGCGCGCG	TGCCAGCCCG	CGGGCTCAAC	2100
	AGCGCGGCGA	AGCGCATCAA	GGTGGAGAG	GACCTGGAGC	TGCCGCGCGC	CGCGCTCATC	2160
65	CCGTCCGAGA	ACGTGTAATC	GCAGTGGCTG	GTGGGCTACG	CGGCGTGGCG	GCATTTCTATG	2220
	AAGGACCCCT	TCCTGGGCTT	CACGAGCGCA	CGACAGTCCG	CCTTCGCCAC	GTGCTCCGAG	2280
	CAGTGTCTCG	AGAACGCGAG	CCTGCGCTTC	TCCAAGCGCG	CCGGGGACCT	GCTGGAAGGC	2340
	GGCCTCTCGG	GCGCGAGCGG	CACGGCCAGC	GGAGGCAGCA	CCCGCACCT	GGGCGGCGCG	2400
	GGCCCGGGCG	GGCCAGCTC	CAAGGAGGGC	CGCGCGAGCG	ACAGTGGCGA	GTAATGCGGC	2460
70	AAGGTGTACA	AGAACTGCAG	CAACTTGACG	GTGCACCGCG	GGAGCCACAC	CGCGGAGCGG	2520
	CCTTACAAGT	GCGAGCTGTG	CAACTACGCG	TGCGCGCAGA	GCAGCAAGCT	CACGCGCCAC	2580
	ATGAAGACGC	ACGGGACAGT	CGGCAAGGAG	GTGTACCGCT	GCGACATCTG	CCAGATGCCC	2640
	TTCAGGCTCT	ACAGACCCCT	GGAGAAACAC	ATGAAAAAGT	GGCAGGCGGA	GCATTTGCTG	2700
	ACTAACGACG	TCAAAATCGA	GCAGGCGGAG	AGGAGCTAAG	CGCGCGGGCC	CGCGCGCCCC	2760
75	GCACCTGTAC	AGTGGAAACG	TTGCCAACCG	AGAGAATGCT	GACCTGACTT	GCTTCCGTGT	2820
	CACGCGCCAC	CCGCAACCGG	CGTGTCCCGG	GGGCGGAGGG	GAGGCGGCGC	TCCAACCTAA	2880
	CCTGTGTCTG	CGAAGTCCCTA	TGGAACCGG	AGGGTTGATT	AAGGCAGTAC	AAATTTGTTGA	2940
	GCCTTTTAAC	TGTGCAATAA	TTTCTGTATT	TATTGGGTTT	TGTAATTTT	TTGGCATGTG	3000
	CAGGTACTTT	TTTATTATTAT	TTTTTCTGTT	TGAATTCCTT	TAAAGATTTT	TGTTGGGTAT	3060
80	CCATCCCTTC	TTTGTTTTTT	TTTTAACCGG	GTAGTAGCCT	GAGCAATGAC	TGCAAGCAAA	3120
	TGTTAGAGGG	GAAAGCATATC	TTTTAAATTA	TAAATTTGGG	GGAGGGGTGG	TGCTGCTTTT	3180
	TGTAAATTTA	AGCTAAGCAT	GTGTAATTTT	TTGTGAAGAA	GCCAACTACT	AAATGACTTT	3240
	TAAAGTGTGT	TACTTTTTCA	TTCTTCTCTT	TTTTTTGTCC	TGAAATAAAA	AGTGGCATGC	3300
	AGTTTTTTTT	TTAATTTATT	TTTAAATTTT	TTTTTGGTTT	TTGTTTTTGG	GGTGGGGGGT	3360
	GTGGATGTAC	AGCGGATAAC	AATCTTTCAA	GTGCTAGCAC	TTTGTTCAG	AACTGGAATG	3420

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GAGATGTAGC ACTCATGTGC TCCCAGTCA AGCGGCCCTT TCTGTGTGA TTTCCGGCTTT 3480
 CATATTACAT AAGGGAAACC TTGAGTGGTG GTGCTGGGGG AGGCACCCCA CAGACTCAGC 3540
 GCCGCCAGAG ATAGGGTTTT TGGAGGGCTC CTCTGGGAAA TGGCCCGACA GCATTCTGAG 3600
 GTTGTGCATG ACCAGCAGAT ACTATCCTGT TGGTGTGCC TGGGGTGCCA TGGCTGCTAT 3660
 TCGCTGTAGA TTAGGCTACA TAAATGGGC TGAGGGTACC TTTTGGGGA GATGGGGTGG 3720
 CCTGCAGTGA CACGAAAGG AAGAACTAG CGGTGTCTT TTAGGGGTT TCTGGCTTGA 3780
 CGGCTTCTCT CTTTTTTTAA ATCACCCECA CCACATAAAT CTCAAATCT ATGTTGCTAC 3840
 AAGGGGTCAT CCATCATTTT CCAAGCAGAC GAATGCCCTA ATTAATTGAA GTTAGTGTTC 3900
 TCTCATTTAA TGCACACTGA TGATATTGTA GGGATGGGTG GGGTGGGGAT CTTGCAAAAT 3960
 TCTATTCTCT TTTACTGAAA AAGCAGGGGA TGAGTTCAT CAGAAGGTGC CCAGCGCTAC 4020
 TTCCCAGGTT TTTATTTTTT TTTTCTATC TCATTAGGTT GGAAGGTACT AAATATTGAA 4080
 CTGTTAAGAT TAGACATTGT AATTCTGTG ACCCGCACTT TAAAGCTTT GTTTGCAATT 4140
 AAATTAATG GCTTCTAAAC AAGAAATGTC AGCATATTCT TCTCTTTGGC CCAGAGGTGG 4200
 GTTAACTGT AAGGGACAGC TGAGATTGAG TGTCAGTATT GCTAAGCGTG GCATTCACAA 4260
 TACTGGCACT ATAAAGAACA AAATAAATA ATAATTATA GGACAGTTT TCTACTGCCA 4320
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 GAAGCAGATG ATCCCGAGAG AGAGGCTCT AGCATGGGTG ACCCAGCCGA CCTCAGSCG 6960
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 TAAGGAAATC AGCTTTTAT CCGGCTCTA AGTAACCGT AGCCGARGT CTOGTGGAAC 7140
 ACAGGCAAC CCGTATTTT GGTGCTCTT GTAACCTAG CCTGCAAGC AAAGTCCCAT 7200
 TGATTTAAGT TGTTCGATT TGTACTGGCA AGGCAAAATA TTTTATTAC CTTTCTATT 7260
 ACTTATTGTA TGAGCTTTG TTGTTACTT GGAGGTTTG TCTTTACTA CAAGTTTGA 7320
 ACTATTATT ATTGCTTGT ATTGTGCTC TGTITAAGAA ACAGGCACCT TTTTATTATA 7380
 TGGATAAAAT GTTGATGTA CAGGAGGTCA TTTCAATAT GCTTAGTAAA ATATTATTG 7440
 TTCTTTATT CTCTGTACAA GATTTTGGGC CTCTTTTTT CCTTAAGTC ACAATGTTGA 7500
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 TCAAGTTATA AAATAAAT GGACATTTA CTGTATCTC AAA

Seq ID NO: B18 Protein sequence
 Protein Accession #: NP_075049.1

75
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1 11 21 31 41 51
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 PEEDHLLSP TKGICPKQEN IAGKDEPSSY ICTCKQPPN SAWPLLQHAQ NTHGFRIYLE 180
 PGPASSSLTP RLTIPLPLGP EAVAQSPLMN FLGDSNPFNL LRMTGPILRD HPGFGEGRLP 240
 GTPPLFSPPP RHHLDPHRLS AEEMGLVAQH PSAFDRVMRL NPMALDSPAM DFRRLRELA 300
 GNSSTPPPVV PGRGNPMHRL LNPFQSPSKS PFLSTPPLPP MPFGTTPPPQ PPAKSKSCEF 360
 CGKTFKQSN LIVHRRSHTG EKPVKQLCD HACSQASKLK RHMKTHMKA GSLAGRSDDG 420
 LSAASSPEPG TSELAGEGLK AADGDFRHHB SDPSLGHEPE EEDEEEEEEE EELLLENESR 480

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PESSFSMDSE LSRNRENGGG GVPGVPGAGG GAAKALADEK ALVLGKVMEN VGLGALPQYG 540
 ELLADKQKRG AFLKRAAGGG DAGDDDDAGG CGDAGAGGAV NGRGGGFAPG TEPPFGLFPR 600
 KPAPLSPGGL NSAAKRIKVE KDLELPPAAL IPSENVYSQW LVGYAASRHF MKDPFLGFTD 660
 ARQSPFATSS EHSSENGSLR FSTPPGDLDD GGLSGRSGTA SGGSTPHLGG PGPGRPSSKE 720
 GRRSDTCEYC GKVFKNCSNL TVHRRSHTGE RPYKCELCNY ACAQSSKLTR HMKTHGQIGK 780
 EVYRCIDQCM PFSVYSTLEK HMKKWHGEHL LTNDVKIEQA ERS

Seq ID NO: B19 DNA sequence
 Nucleic Acid Accession #: NM_000399.2
 Coding sequence: 339..1769

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 TTGACCATAT GAACGAGATG GCCCGAGATG GCATGATCAA CATTGACATG ACTGGAGAGA 540
 AGAGGTGCTT GGATCTCCCA TATCCAGCA GCTTTGCTCC CGTCTCTGCA CCTAGAAACC 600
 AGACCTTCAC TTACATGGGC AAGTTCTCCA TTGACCTCA GTACCTGGT GCCAGCTGCT 660
 ACCCAGAAAG CATATCAAT ATTGTGAGTG CAGGCATCTT GCAAGGGGTC ACTTCCCAG 720
 CTTCAACAC AGCCTCATCT CGCCTCACCT CTGCTCCCC CAACCCACTG GCCACAGGAC 780
 CCCTGGGTGT GTGCACCATG TCCAGACCC AGCCTGACCT GGACCACTGT TACTCTCCGC 840
 CACGCGCTCC TCCTCCTTAT TCTGGCTGTG CAGGAGACCT CTACCAGGAC CCTTCTGCGT 900
 TCCTGTGAGC AGCCACACAC TCACCTCTT CTCTCTGGC CTACCCACCA CCTCCTTCTC 960
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 GATTCTTCC ATCTCAGTGG CAGAGAGACC TACATGGTAC AGCTGGCCCA GACCGTAAGC 1080
 CCTTTCCTCG CCCACTGGAC ACCCTGCGGG TGCCCTCCCT ACTCACTCCA CTCTCTACAA 1140
 TCCGTAACTT TACCCTGGGG GGCCCCAGTG CTGGGGTGAC CGGACCAGGG GCCAGTGGAG 1200
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 AGCCCTTCCA GGTCTGGATC TGCATGCGCA ACTTCAGCCG CAGTGACCC CTACCCACCC 1500
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 ATTTGAGATA AGAATGTACA TAATGTTACC GGAGCTGAT TGTGTGGTCA TTAGCTCTTA 2880
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Seq ID NO: B20 Protein sequence
 Protein Accession #: NP_000390.2

1 11 21 31 41 51
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 LQGVTSFASP TASSSVTSAS PNPLATGPLG VCTMSQTQPD LDHLYSPPPP PPYPGSCAGD 180
 LYQDPSAFLS AATTSTSSSL AYPPPPSYPS PKPATDPGLE PMIPDYPGPF PSQCQDLHG 240
 TAGPDRKPPF CPLDTLRVPP PLTPLSTIRN FTLGGPSAGV TGPAGSGGSE GPRLPSSSA 300
 AAAAAAAYY NPHEHLPLRI LRPRKYPNRP SKTPVHERPY PCPAEGCDRR FSRSDDELTRH 360
 IRIHTGKRF QCRICMRNFS RSDHLTTHIR THTGEKPFAC DYCGRKPARS DERKHKTHI 420
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Seq ID NO: B21 DNA sequence
 Nucleic Acid Accession #: NM_004962.2
 Coding sequence: 457..1893

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CACACACGGG CGCACGCACA CGGCAGCCGG GCCAGGGACG ACCCTGTGAG CTGCAGCCCC 60
 AGAGGTCCCGG GCGCGCGCAGC CGGGTCCCTT CGAGGGGCGCA GCGGGGCGCC CCGCCCCCGCC 120
 CCTCGAAGCA GCGGGGCGCG GCGCGCAGTG GGCTACAAAC TTTCGCGACG CGAGTCCCGCC 180
 AAGCCAGCGC GCGGACTCGG GCTCGGCTCG GCTCTGCGCT GCTCCGGACG GGTGTGACCG 240
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 AAGCCCTCGG CCGCGCGCGG ACCTCGGTAT CCAGCGCCCT GCTGCCCGGG CTCTCCCGGC 360
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 GGCTCGCAGG GGCACAGGGA TCTCCAGCGG CACCCTGGGG ACGCGGCGC CACGTTGGGC 660
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 CAGGGCGCGC GCGCGGGAGG GGGCAACACG GTCCGCGAGT TCAGGGCCAG GCTGGAAGTG 780
 GTGACACAGA AGGCGGTGTA TTCTTCAAC CTGACTTCCA TGCAAGACTC GGAAATGATC 840
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 AGGGAGGGCG TTGACACCAT TCCCCACAGA GATAGTCATG CTGAGTGTGG GTTGTTTTAA 2520
 CATGCATATT GAAATAACAC ATATAGTAAC GTGGGAATAC TAAAAAATAA CCAAGATTIT 2580
 ATATTTTTGT AAATTATACT TTCTATACTG TAGATTGTGT ATGTTATGTG TTTTATGGA 2640
 AAGCTAATAA ATTAAAGTGA CAGTGTATC TTGA

Seq ID NO: B22 Protein sequence
 Protein Accession #: NP_004953.1

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1 11 21 31 41 51
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 GDAATLGPSS AQMDVAHVHMH RLYEKYSRQG ARPGGGNTVR SFRARLEVD QRAVYFFNLT 120
 SMQDSEMLTT ATHFYSEEP RWPRALEVLK KPRAKNASGR PLPLGPPTPQ HLLPRSLSQN 180
 TATQGLLRGA MALAPPFRLG WQAKDISPIV KAARRDGELL LSAQLDSEER DPGVPRPSPY 240
 APYLIVYAND LATSEPNVA VTLQRYDPPF AGDPEPRAAP NNSADPRVRR AAQATGPLED 300
 NELPGLDERP PRAHAQHFK HQLWPSPPFA LKPRPGRKDR RKXGQEVFMA ASQVLDFDEK 360
 TMQKARRKQW DEPRVCSRRY LKVDPAIDGW NEWIISPKEF DAYYCAGACE FPMPIKIVRPS 420
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Seq ID NO: B23 DNA sequence
 Nucleic Acid Accession #: AK026322.1

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 TCCATCATCT GTCACTTTTG CATCTGTTTT TATTGACTAA CTTTCTTCTT CATCATGGTC 120
 ACATATCCTT GCTTCTTCCC ATATTTAGTA AAGTTTAGTT GGATGCTGGA TTGTTTTAAT 180
 TTAGCATTTT GGAGTGACTG CTTTGTCACT TGCCTTTAAA AGTATTGGAC TTGCTTTTGA 240
 TAGTTGAATT ACTTGCAAAAT CAGCTTGATC ATTCTGAGAC TTGTTTTTAA CTTTGTGCGA 300
 AAAGGCTATG CTACTTCAAG TATAATAAAA CCTAGTTTGA GTTTTATCCT ATAACATAAG 360
 CATGTGTTCA ATTTGAATGT CTCCAACCTT GTGTGAACCT TGAAAATTGT TCAGCTCCCA 420
 ATTTGCGAGT AATTTTTTTT GTTCAGCCTT GCAGTCTCAT CCTACTCAAG TGTGGCTCTG 480
 TATCCAACAA CAGTCTTGGA GATCTCATGA AGATTCTGGA AACTTTTGCT CTCGAGGATA 540
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 CTACTATAGG ATAAATTGTG TTTTATAGAG CAATTCTCA TGGGTACAGA GGGATAGTAC 1140

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GATTGTGAAA AAAAAAAAAA AAAA

5 Seq ID NO: B24 DNA sequence
Nucleic Acid Accession #: cat cluster

1 11 21 31 41 51
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CTTTCCCACT CTGATGATTT GTGCTCTTAT TTTTCTTAGA TTTACCTCAT CTAGGGCATA 180
TTCTTTTCCC TCCTCTCTTT TACCTTTTCT GGTCTGTATC CCTCTGTACT CAGTTCCCTC 240
15 AAATATTGG ACTACAACT AATATACTAG AAAAGCATAC ACTTATTTTA TTTGAATGCA 300
GAAATGCTAT CTATCAGTAT ATATACATAA GAATGTATAT TACAGTATAT CTATATATAC 360
TTAACACTGT AACTTTTCACT ATTCCTCCAGT TAGCGTACCT AACTCTCCTG TGGGTTATGT 420
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20 TGCCCATATA GTAATAAGTA TAGCCACATT CTGAACATAT CAAAAGTACA AACTTAGGAG 600
GAGTGTATGT ACAAATATGT AAAATTTTAT GAAATGAAC ATGTTTTTAT GATGTTATTT 660
CTAGTTCATA AGAATGTGAT GACTGCTTTG CTTCATTTAT GTACGTTTCC ATTATATTCT 720
TGCTGTCAAT CAATCACAAA TTTATATCAG ATTAGGATAA ACTAAGCCAT TTTATGTATT 780
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25 AATTACAGC GTATTACAAA ACATAGAAAT GTATTGTAGC TACAAAGACA ACCAAGCATT 900
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30 AACATTCAT TTGATTTTAA GCAAAATGTA TGTAAAGCA TGTTTTTACA TCAGTAAAGT 1260
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TAACAATCAT ATTTGTCAAT GTTGTTTTCT GCAACAAAA ATGTTTATGG GCTTCATGTA 1380
GGCTTAAGAT TGTAGGCAAA AATGGACTGA GTTCAGGACC CTTCAGCAG TAGGCATTCA 1440
35 GTTACAGAGC AGTTGGTACT TTGTAACCCA GACTTACAGT TTAAAAATAT CAAGTTAGCT 1500
GATGTTTCAT TATAATAAAA ATACTATTTT GCTTAAGAGT TGTATTACAA ATATTGTGTC 1560
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GCATGGTTTA TTTTAAATAA TGAAATAGAG AACATAATAC GTAATGTTCA GTATAACAGC 1680
TGAGTTAAAA CATCTGCCAG GATTAACTC AGTGCCTTTT TGCCAAATGA TAGAGGCATT 1740
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TACAAGTAAC TAGTGGGTGA TATGTTTCAC TCCAAGGGT GTATTAATTC TGAATGCTAA 1860
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Seq ID NO: B25 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..1144

1 11 21 31 41 51
50 ATGAGAGCGG GGATGCACCT CGGTGCAGCG GCGCGCGGCG AGGACGACCT CTTCTGTCAC 60
AAGAGCCTGA GCGCCTCCAC CTCCAAGCGC TTGGAAGCGG CTTTCCGCTC CACGCCCCCG 120
GGCATGAGAC TGTCCTCTGGC GCGCGCGGCT CGGGAACGCC CGCGCTCCTC CTCCTGCTCG 180
CCCTTGGGCT GCTTCGAGCC GGCTGACCCC GAGGGGGCAG GGTCTGTGTT GCGCGCGGCT 240
GGAGGAGGCG GCGCGGCGAG CGCGGGAGT GCGCGCGGCG GCGCGCGGCG GGTGGGTGTC 300
55 CCGGGCTGCG TAGTAGGTTT AGCCGCGGCTT GGGGGCGAGC CTAGCCTAAG CAGCCTGCCG 360
GCGCGGCGCG CCCTTTGGCT CAAGTACGCG GAAAGCGCGA GCGCGGCGCT GGTGGCCGAG 420
AGCAGCGGCG GCGAGCAGAG CCCCGACGAC GACAGCGAGC GTGCTGCGA GCTCGTGTG 480
CGGGCGGAG TAGCCGACCC GCGGGCTCC CCGGAGCGG GAGGTGCTGG CGCGAAGGCA 540
GCGAGGGGCT GCTCCAATGC CCACCTCCAC GCGCGCGCCA GCGTCCCTCC GGGGGGCTG 600
60 GCGCGGCGCG GCGCGGCGG TAGCAGCAGC GGTAGCAGT GCGGCGGTGG CGGTAGCGGT 660
AGCGGCGAG GCGCGAGCAG CAGCAGCAGC AGCAGCAGCA GCAAGAAATC CAAAGAGCAA 720
AAGCGCTGCG GCGTTAATAT CAATGCCCGA GAGCGCGGCG GATGCAAGC CCGTGAAGCA 780
GCGCTGAGCG AGCTGCGCGC GGTGATCCCC TACGCGCACA GCCCTCGGT GCGAAGGCTC 840
TCCAAGATCG CCACGCTGCT GCTGCGCAAG AACTACATCC TCATGCAGGC GCAGGCCCTG 900
65 GAGGAGATGC GCGGCTAGT CGCCTACCTC AACCAGGSCC AGGCCATCTC GGTGCTCTCC 960
CTGCCAGCT GCGGCGGCTG AGCGGCGAGC GCTGCTGCC TGCAACCGGC GCTCGGCGCC 1020
TACGAGCAGC CAGCGCGCTA CCCGTTTACG GCGGAGCTGC CCGCGGCTGC CTCCTGCCCG 1080
GAGAAGTGCG CCCTGTTTAA CAGCGTCTCC TCCAGCTCTC GCAACAGTGC CACCGAGAAG 1140
CCTT

70 Seq ID NO: B26 Protein sequence
Protein Accession #: FGENESH predicted

1 11 21 31 41 51
75 MERGMILGAA AAGEDDLFLH KSLASASTSKR LEAARSTPP GMDLSLAPPP RERPASSSSS 60
PLGCFEPADP EGAGLLLP PP GGGGGGSAGS GGGGGGGVGV PGLLVGSAGV GGDPLSLSLP 120
AGAALCLKYG ESASRGSVAE SSGGEGSPDD DSDGRCELVL RAGVADPRAS PGAGGGGAKA 180
AEGCSNAHLH GGASVPPGGL GGGGGGGSSS GSGGGGGSGS SSGSGSSSSS SSSSKSKSEQ 240
KALRLNINAR ERRRMHDLND ALDELRAVIP YAHSPSVRKL SKIATLLAK NYILMQAQL 300
80 EEMRLVAVL NQGQAIASAS LPSSAAAAA AALHPALGA YEQAAGYPFS AGLPPAASCP 360
EKCALFNSVS SSLCKQCTEK P

Seq ID NO: B27 DNA sequence
Nucleic Acid Accession #: cat cluster

Seq ID NO: B28 DNA sequence
Nucleic Acid Accession #: NM_002581.2
Coding sequence: 368..5251

808

5 GTACCAATAT TGGGTCATAA CTATTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT 3180
 CACATACATC CATGACCGTG GGTACTGTGG CGATGGCATT ATACAAAAG ACCAAGGTGA 3240
 ACAATGCGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTTCT GCCGACAAGA 3300
 AGTCTGCTTC AATTGTATTG ATGAACCCAG CCGGTGCTAT TTCCATGATG GTGATGGGGT 3360
 ATGTGAGGAG TTGTAAACAA AAACCAAGCAT TAAGGACTGT GGTGTCTACA CGCCCCAGGG 3420
 ATTCCTGGAT CAGTGGGCAT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCCAGG 3480
 CTGGGTCAAT ATCGGACAGC CAGCAGCATC CCAGGTGTGT CGAACCAAGG TGATAGATCT 3540
 CAGTGAAGGC ATTTCCAGC ATGCCTGGTA CCCTTGCAAC ATCAGCTACC CATATTCCCA 3600
 10 GCTGCTCAG ACCACTTTT GGCTCGGGC GTATTTTCT CAACCAATGG TTGCGGCAGC 3660
 TGTCAATTGC CACCTGGTGA CGATGGGAC ATATTATGGG GACCAAAAGC AGGAGACCAT 3720
 CAGGCTGAGC CTGCTTGATA CCAAGATCA GAGCCAGAT CTAGGCCTCC ATGTCTTGAG 3780
 CTGCAGGAAC AATCCCCTGA TTATCCCTGT GGTCCATGAC CTCAGCCAGC CCTTCTACCA 3840
 CAGCCAGGCG GTACGTGTGA GCTTCAGTTC GCCCCTGGT GCCATCTCGG GGGTGGCCCT 3900
 15 CCGTTCTTTC GACAACTTTG ACCCGGTCAC CCTGAGCAGC TGCCAGAGAG GGGAGACCTA 3960
 CAGCCCTGCC GAGCAGAGCT GCGTGCACTT CGCATGTGAG AAAAAGTACT GTCCAGAGCT 4020
 GGCTGTGAG AATGCTTCT TCAATTGCTC CAGCAGGAGC CGCTACCAAG GTGCCAGTG 4080
 TACTGTGAGC TGCCGGACAG GCTACGTGCT CCAGATACGG CGGATGATG AGCTGATCAA 4140
 GAGCCAGAGC GGACCCAGCG TCACAGTGAC CTGTACAGAG GGCAAGTGA ATAAGCAGGT 4200
 20 GGCCTGTGAG CCAATGCTCT GAGCATCCG AGATCACCAT CAAGTCTATG CTGCCCTCTT 4260
 CTCTGCCCT GAGGGCACCA CCTTGGCAG TCAATGTTC TTCCAGTGCC GTCAACCTGC 4320
 ACAATGAAA TCCATGCTT TCCCTCTGAC CTGCATGGAG GATGGCTGT GGTCTTCCC 4380
 AGAGGCCCTG TGTGAGCTCA TGTGCTCTGC TCCACCCCTT GTGCCCAATG CAGACCTCCA 4440
 GACCGCCCGG TGCCGAGAGA ATAAGCACAA GGTGGGCTCC TTCTGCAAA ACAAATGCAA 4500
 25 GCTGTGATAC CAGTGCCTG GATCCTCTCG GAAGTCAAAG AAACGGGCTT TCAAGACTCA 4560
 GTGTACCCAG GATGGCAGCT GGCAGGAGGG AGCTTGTGTT CCTGTGACCT GTGACCCACC 4620
 TCCACCAAAA TTCCATGGG TCTACAGTG TACTAATGGC TTCCAGTTCA ACAGTGAGTG 4680
 TAGGATCAAG TGTGAAGACA GTGATGCCCT CCAGGACTT GGGAGCAATG TCATTCAITG 4740
 CCGGAAAGAT GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGAGATGC AAGGCCAGTG 4800
 30 CTGGTTCCA AACAGCTCA ACAGCAACCT CAACTGACG TGCCCTGATG GCTATGCCAT 4860
 AGGGTCGAG TGTGCCACCT GGTGCTGGA CCAACAAGC GAGTCCATCA TCCTGCCAAT 4920
 GAAAGTGACC GTGGGTGACA TCCCCACTG GCTGAACCCC ACACGGGTAG AGAGAGTTGT 4980
 CTGCACTGCT GGTCTCAAGT GGTATCTCA CCCTGCTCTG ATCACTGTG TCAAGGCTG 5040
 TGAGCCCTTC ATGGGAGACA ATTATTGTGA TGCCATCAAC AACCGAGCTT TTTGCAACTA 5100
 35 TGAGGCTGGG GATGTGCTCA CCTCCAGT GAAGACCAAA AAGGTACACC CATTCCTAT 5160
 GTCTGTGAG CTACAAGGTG ACTGTGCTG TCGGAGCCCC CAGGCCCAAG AACACAGCCG 5220
 GAAGACCTC CGGGGATACA GCCATGGCTA AGGAAGGACA AGAAGTTGTC AAAGAATTCC 5280
 CAAGCCAGG ACCCATATCC CTTTGGTATT GATTTCACAG TCAGCTGCTC AACGGAATGG 5340
 CCTCTCCACA CCAGGGATCC TTAGCACCCA ACCGGTCTGC CTTTAAATTT ACCCAGGAAG 5400
 40 GACTCATT GGGCGAATG AACCAAGTT CGCCATGCTG GATGATGAAA TGGATTCCCA 5460
 TCCCAAAGTC TGAGATGGAT TGCAATACA GTGTGCAGTC CCAGAGCCTC CTAAAATTCT 5520
 AGCCATTGT CACACAACCA CAGCAAAAA AAA

Seq ID NO: B29 Protein sequence
Protein Accession #: NP_002572.1

45 1 11 21 31 41 51
 | | | | |
 MRLWSWVHL GLLSALGCG LAERPRRRR DPRAGRPPRP AAGPATCATR GPRPPRLAAA 60
 AAAAGRAWEA VRVPRRRQR EARGATEEPS PPSRALYFSG RGEQLRVLRA DLELPDRAFT 120
 50 LQVWLRAEGG QRSFAVITGL YDKCSYISRD RGVVVGIIHTI SDQDNKDPY FFSLKTDRA 180
 QVTTINAHRS YLPGQWVLA ATYDQFMKL YVNGAQVATS GEQVGGIFSP LTQKCKVLM 240
 GGSALNHNRY GYIEHFSWLK VARTQREILS DMETHGAHTA LPQLLLQENW DNVKHAWSPM 300
 KDGSPPKVEP SNAHGFLDIT SLEPPLCGQT LCDNTEVIAS YNQLSSFRQP KVVRYRVVNL 360
 55 YEDDHKNPTV TREQVDFQHH QLAFAFKQYN ISWELDLVLEV SNSSLRRRLI LANCDISKIG 420
 DENCDPECNH TLTHGHDGDC RHLRHPAFVK KQHNVCMDM CNYERFNPDG GECCDPEITN 480
 VITQCFDPS PHRAYLDVNE LKNILKLDGS THLNIFFAKS SEELAGVAT WPDKEALMH 540
 LGGIVLNPSF YGMPGHHTM IHEIGHSLGL YHVFRGISBI QSCSDPCMET BPSFETGDL 600
 NDTNPAPHK SCGDGPGND TCGFHSFPNT PYNNFMSYAD DDCTDSFTPN QVAMHCYLD 660
 60 LVYQWQPSR KPAPVALAQ VLGHITDSVT LEWFPPIIDGH FFERELGSAC HLCLEGRILV 720
 QYASNASSEM PCSPSGHWSF REAEGHPDVE QPCKSSVRTM SPNSAVNPHT VPPACPEPQ 780
 CYLELEFLYP LVPESLTIW TFVSTDWDS GAVNDIKLLA VSGKNISLGP QNVFCDVPLT 840
 IRLWDVGEV YGIQYITLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVVR DPPLQMDVAS 900
 ILHLNKRFPD MDLNLGSVYQ YWVITISGTE ESEFSPAVTY IHGRGYCGDG IYQDKQGEQC 960
 65 DDNKNKINGDG CSFLCRQEVF FNCIDBPSRC YFHGDGVCB EPEQKTSIKD QGVYTPQGL 1020
 DQWASNASVS HQDQCPGWV IIGQPAASQV CRTKVIDLSE GISQHWYPC TISYPYSQLA 1080
 QTTFWLRAVF SQPMVAAWI VHLVTDGTY GDQKQETISV QLLDTKDQSH DLGLHVLSCR 1140
 NNPLIIPVH DLSQPFYHSQ AVRVSFSSPL VAISGVALRS FDNFDPVTL SQRGETYSP 1200
 AEQSCVHPAC EKTDCPELAV ENASLNCSSS DRYHGAQCTV SCRTGYVLQI RRDELIKSQ 1260
 70 TGPSVTVTCT EGKWNKQVAC EPVDCSIPDH HQVYAASFSC PBGTTFGSQ SFQCRHPAQL 1320
 KGNLSLLTC EDGLWSPFA LCELMCLAPP PVPNADLQTA RCRENKHVG SFQKYKCKPG 1380
 YHVPSSSRKS KKRAFKTQCT QDGSWQEGAC VPVTCDPPPP KFHGLYQCTN GFQFNSECR 1440
 KCEDSDASQG LGSNVHICRK DGTWNGSFHV CQEMQGCQSV PMSLNSNLKL QCPDGYAIGS 1500
 ECATSCLDHN SESIILPMIV TVRDIPHLN PTRVERVCT AGLKWYHPA LHCVKGCPE 1560
 75 FMGDNYCDAI NNRAFCNYDG GDCCTSTVKT KKVTPPFMSC DLQGDCACRD PQAQHSRSD 1620
 LRYSHG

Seq ID NO: B30 DNA sequence
Nucleic Acid Accession #: NM_032808.1
Coding sequence: 61..1008

80 1 11 21 31 41 51
 | | | | |
 CTAGTCTATC TCCGCTTCTT CAACCTCTCC TACAACCCCA TCAGCACCAT TGAGGGCTCC 60
 ATGTTGCATG AGCTGCTCCG GCTGCAGGAG ATCCAGCTGG TGGGCGGSCA GCTGCCCGTG 120

5 GTGGAGCCCT ATGCTTCCG CGGCTCAAC TACCTGCGG TGCTCAATGT CTCTGGCAAC 180
 CAGCTGACCA CACTGGAGGA ATTAGTCTTC CACTCGGTGG GCAACCTGGA GACACTCATC 240
 CTGGACTCCA ACCCGCTGGC CTGCGACTGT CGGCTCCTGT GGGTGTTCG GCGCGCTGG 300
 CGGCTCAACT TCAACCGGCA GCAGCCACG TGCGCCACG CCGAGTTTGT CCAGGGCAAG 360
 GAGTTCAAGG ACTTCCCTGA TGTGCTACT CCCAACTACT TCACCTGCGG CCGCGCCGCG 420
 ATCCGGGACC GCAAGGCCCA GCAGGTGTTT GTGGACGAG GCCACACGGT GCAGTTTGTG 480
 TGCGGGGCGG ATGGGACCC GCGGCCCGCC ATCTCTGGC TCTCACCCTG AAGCACCTG 540
 GTCTCAGCCA AGAGCAATGG GCGGCTCACA GTCTTCCCTG ATGSCACGCT GGAGGTGCGC 600
 TACGCCCAGG TACAGGACAA CGGCACGTAC CTGTGCATCG CGSCCAACGC GGGCGGCAAC 660
 GACTCCATGC CGGCCACCT GCATGTGCGC AGCTACTCGC CCGACTGGCC CCATCAGCCC 720
 AACAGACCT TCGCTTTCAT CTCCAACCAG CCGGGCGAGG GAGAGGCCAA CAGCACCCCG 780
 GCCACTGTGC CTTTCCCTTT CGACATCAAG ACCCTCATCA TCGCCACCA CATGGGCTTC 840
 ATCTCTTCC TGGGCGTGT CTCTTCTGCG CTGGTGTGCG TGTTCCTCTG GAGCCGGGCG 900
 AAGGGCAACA CAAGGACAA CATCGAGATC GAGTATGTGC CCGAAAAGTC GGACGCAGGC 960
 15 ATCAGCTCCG CCGACGCGCC CCGCAAGTTC AACATGAAGA TGATATGAGG CCGGGCGCGG 1020
 GGGCAGGAGC CCGCGGCGG CCGGCGAGG GAAGGGGCTT GCGCGCACCT TGCTCACTCT 1080
 CCAGTCTTCC CCACCTCTCT CCTACCTTTC TACACAAGTT CTCTTCTTCC CTCCGCGCTC 1140
 CGTCCCTTGC TGCCCGCCGC CAGCCCTCAC CACTGCGCTT CCTTCTACCA GGACCTCAGA 1200
 AGCCGAGAGC TGGGAGCCGC ACCTACACAG GGGCATTGAC AGACTGGAGT TGAAAGCCGA 1260
 20 CGAACCCGACA CCGGCAGAG TCAATAATTC AATAAAAAAG TTACGAACTT TCTCTGTAAC 1320
 TTGGGTTTCA ATAAATTATG ATTTTATGTA AAACCTGAAA TAATAAAAAG AGAAAAAAG 1380
 TATTTCTAT AGCTAGTCGG AATGCAAACT TTTGACGTCC TGATTGCTCC AGGCCCTCT 1440
 TCCAACCTAG TTCTTGTGTT TTCTCTTCTT CCTCTCTCTT TTCTTCTCTT TTCTCTTCTT 1500
 25 CTCCCCAGT GGGGAGGAT CACTCAGGAA AACAGGAAAG GAGGTTCAGG CCCCACCCAC 1560
 CTGCCACCC CCGCCAGGCG ACCATCAGGA GCAGGCTAGG GGGCAGGCTT GGGCCACGCT 1620
 CCGGCTGGC TTTTGTGAGG GCGCAGGTGG AGGGGACAGG TCTGCGATG GGGTGGGAG 1680
 CCTGTCTGCT GGGCTGCCAG CCGGCACCC TGAAGGGGT GGGAGCCTGG CTGGGTGTG 1740
 GCTGAGACTC TGGACAGAGG CTGGGCTCCT CTGGGGGAC AGCAGCTCA GTGGAGAGAG 1800
 CCAGGGGCTG GAGGTGGGGC CCACCCAGC CTCTGTGCTC AGCTCTGCTG CTCACTTGCT 1860
 30 GTGTGGCTC AGCAGGTCA CTGGCTCTC TGGGCTCAG TCTCCACATC GTACAAATG 1920
 GGAACTATAC CCGCTGCCCT GCCTACCTCA CAGGCTGTT GTGAGGAATT GATGAGATGA 1980
 TGTATGTGAA ACACCTTTGA ACCTGTAAG CGCTGTGCAC ACGTG

Seq ID NO: B31 Protein sequence
 Protein Accession #: NP_116197.1

1 11 21 31 41 51
 MLHELLRLQE IQLVGGQLAV VEPYAFRGLN YLRVLNVSNG QLTLEELVF HSVGNNLETLI 60
 40 LDSNPLACDC RLNVFRRRW RLNFNRQOPT CATPEFVQKG EFKDFPDVLL PNYFTCRER 120
 IRRKQAQVF VDEGHTVQFV CRADGPPPA ILWLSPRKHL VSAKSNRGLT VFPDGTLEVR 180
 YAQVQDNGTY LCIAANAGWN DSMFAHLHVR SYSPDWFHQP NKTAPFISNQ PGEGEANSTR 240
 ATVPFFPDIK TLIITATMGF ISPLGVLFPC LVLLFLWSRG KGNTKHNIEI EYVPRKSDAG 300
 ISSADAPRFK NMRMI

Seq ID NO: B32 DNA sequence
 Nucleic Acid Accession #: CAT cluster

1 11 21 31 41 51
 CAGCACATAC AAGAAACATA CAGTGTACCT CAAAAGGGGC CCTTGAAATG TCATCAAGG 60
 GTAATAACCT AGTGAGTGAG TTGTGATGTC ATCTGGAACA TAGGAAATGG GGCTCTTAGC 120
 GTATTGCGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAATGATA ATCTTTGGGA 180
 55 AACGAGGACC CTGCTCCCA GCGCAGAGGT GGAGGAGGGC GGTGAGGGTG GGGTCTACAG 240
 TGGCAGCAGA CTGACAAAGG TAGAGGGAAA TGAATAGCA CATCTACGCT GCAGTCTGGT 300
 GAAAGTGGCC GGGGTGCTCC TTGGAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360
 AGCCTTTCCG TCACGGGCGG GGACGCTTG ATTTAAAAA AATAAATAA TAAACGTCT 420
 GGGTATAGAA A

Seq ID NO: B33 DNA sequence
 Nucleic Acid Accession #: NM_006174.1
 Coding sequence: 71..1408

1 11 21 31 41 51
 GAAAGGCTAT CGGTAACAAC TGACCTGCCA CAAAGTTAGA AGAAAGGATT GATTCAAGAA 60
 AGACTATAAT ATGATTTAG AGCTCGACGA GTATTATAAC AAGACACITG CCACAGAGAA 120
 TAATACTGCT GCCACTCGGA ATTCTGATTT CCCAGTCTGG GATGACTATA AAGCAGTGT 180
 70 AGATGACTTA CAGTATTTTC TGATTGGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT 240
 GGGGAATCTA CTTATTTTAA TGGCTCTCAT GAAAAGCGT AATCAGAAGA CTACGCTAAA 300
 TCTCTCATTA GGCAATCTGG CCTTTCTGTA TATCTTGGTT GTGCTGTTT GCTCACCTTT 360
 CACACTGACG TCTGTCTTGC TGGATCAGTG GATGTTGGC AAGTCAATGT GCCATATTAT 420
 GCTTTTCTT CAATGTGTGT CAGTTTGTGT TTCAACTTTA ATTTTAATAT CAATTGCCAT 480
 75 TGTCAAGTAT CATATGATAA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540
 CTTTCTGATA GCTACTGTCT GGACACTAGG TTTTGCCATC TGTCTCCCC TTCCAGTGTT 600
 TCACAGTCTT GTGGAACCTT AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATT 660
 ATGTGTTGAG TCATGGCCAT CTGATTCATA CAGAATTGCC TTTACTATCT CTTTATTGCT 720
 AGTTCAGTAT ATTCTGCCCT TAGTTTGTCT TACTGTAAAT CATACAAGTG TCTGCAGAAG 780
 TATAAGCTGT GGATTGTCCA ACAAAGAAAA CAGACTTGAA GAAAATGAGA TGATCAACTT 840
 80 AACTCTTCAAT CCATCCAAAA AGAGTGGGCC TCAGGTGAAA CTCTCTGGCA GCCATAAATG 900
 GAGTTATCAT TCACTCAAAA AACACAGAG AAGATATAGC AAGAAGACAG CATGTGTGTT 960
 ACCTGCTCCA GAAAGACCTT CTCAGAGAA CCACCTCAGA ATACTTCCAG AAAACTTTGG 1020
 CTCTGTAAAG AGTCAGCTCT CTTCATCCAG TAAGTTTATA CCAGGGGTCC CCACTTGCTT 1080
 TGAGATAAAA CTGAAGAAA ATTCAGATGT TCATGAATTG AGAGTAAAAA GTTCTGTTAC 1140

AAGAATAAAA AAGAGATCTC GAAGTGTTTT CTACAGACTG ACCATACTGA TATTAGTATT 1200
 TGCTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTFTA ATGACAATCT 1260
 TATTTCAAAT AGGCATTTC AATGTTGGTA TTGCATTGTG CATTGTGTGG GCATGATGTC 1320
 CTGTGTCTT AATCCAAATC TATATGGGTT TCTTAATAAT GGGATTAAAG CTGATTTAGT 1380
 GTCCCTTATA CACTGTCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence
 Protein Accession #: NP_006165.1

1 11 21 31 41 51
 MDLELDEYYN KTLATENNTA ATRNSDFPVM DDYKSSVDDL QVFLIGLYTF VSLLGFMGNL 60
 LILMALMKKR NQKTTVNFLI GNLAFFSDILV VLFCSPTTLT SVLLDQNMFG KVMCHIMPFL 120
 QCVSVLVSTL ILISIAIVRY HMIKHPISNN LTANHGYFLI ATVMTLGFAL CSPLPVFHSN 180
 VLQBTFGSA LLSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240
 GLSNKENRLE ENEMINLTILH PSKKSGPQVK LSGSHKWSYS FIKKHRRRYS KKTACVLPAP 300
 ERPSQENHSR ILPENFGSVR SQLSSSSKFI PGVPTCFEIK PEENSVDHEL RVKRSVTRIK 360
 KRSRSVFYRL TIILVFAVS WMLHLFHV TDFNDNLISN RHFLKLYCIC HLLGMSCCL 420
 NPILYGLFNN GIKADLVSLI HCLHM

Seq ID NO: B35 DNA sequence
 Nucleic Acid Accession #: NM_014279.1
 Coding sequence: 286..1689

1 11 21 31 41 51
 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCGCG CCAGCCCAGC 60
 CCTGCCGAGC CCTGCCGCGA GGCAGAGCGG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
 CGGAGGCTTC GCGCAGCAGA GCGCGCGCGC CGCCGCTCC GGTGTCTGAA TCCAGGCGTG 180
 GGGACACGAG CCAGGCGCGG CCGCGCGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
 TCCGCGTACA CCGAGCGCGC GCGCGCGCAG CACCCAGGGC CCGTGCATCC AGGTCTGTGG 300
 AGGTGCGCAG GAGACATGCA CCGGCGCGCG AAGCTCCTCA GCCTCCTCTT CCTCATCTCG 360
 ATGGGCACTG AACTCACTCA AGTGTCTGCC ACCAACCTCG AGGAGAGCTG GCAGGTGTAC 420
 AGCTCTGCCG AGGACACGGA GGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480
 ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
 ATGTCTCAAT CCATAGAGGT CTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAAGTCA AACAGGTGGA GGAGAGTCAT 660
 AAGCAACACC TGGCCAGGCA GTTTAAGGCG ATAAAAGCGA AAATGGATGA ACTTAGGCCT 720
 TTGATACCTG TGTGGAAGA GTACAAGGCC GATGCCAAT TGGTATTGCA GTTTAAAGAG 780
 GAGGTCCAGA ATCTGACGTC AGTGCTTAAC GAGCTGCAAG AGGAAATGCG CGCCTATGAC 840
 TACGATCAAT TCCAGAGGAG AGTGTCCAAT CTTGAAGAAA GGCTCCGTGC ATGCATGCAA 900
 AAACAGCTTT GCGGGAAGTT GACGGGCATC AGTGACCCCG TGACTGTCAA GACCTCCGGC 960
 TCGAGGTTCG GATCTGGAT GACAGACCTT CTGCGCCCTG AAGGCGATAA CCGGGTGTGG 1020
 TACATGGAGC TGTAGGCCAA CAACCGCTTC GTACGTGAGT ACAAGTCCAT GGTGACTTTC 1080
 ATGAACACCG ACAATTTTAC CTCCCAACGT CTCCCCACCC CCTGGTGGGG CACGGGGCAG 1140
 GTGTCTTACA ACGGTTCTAT CTACTTCAAC AAGTTCAGGA GCCACATCAT CATCAGGTTT 1200
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC 1260
 ATGTACCATC ACGCTGGGG TGGCCACTCG GACATCGACC TCATGGTGA CGAGAGCGGG 1320
 CTGTGGCGCG TGTAGGCCAC CAACCCAGAAC GCTGGCAACA TCGTGTGTCAG TAGGCTGGAG 1380
 CCGGTGTCCC TGCAGACCTT CGAGACCTGG AACACGAGCT ACCCAAGCG CAGCGCGCGG 1440
 GAGGCGCTCA TCATCTGCGG CACGCTGTAC GTCAACCAAG GCTACTCAGG GGGTACCAAG 1500
 GTCCACTATG CATACAGAC CAATGCCTCC ACCTATGAAT ACATCGACAT CCAATTCCAG 1560
 AACAAATATC CCCACATCTC CATGCTGGAG TACAACCCCA AGGACCGGGC CCTGTATGCC 1620
 TGGAAACACG GCGACACAGT CCTCTACAC GTGACCTCTT TCCACGTCTT CCGCTCCGAC 1680
 GAGTTGTAGC TCCCTCTCTC TGGAGGCCAA GGGGCCACGT CCTCACCACA AAGGAGCTCC 1740
 TGTGAACACT GCGCAAAAAA GATACCAATA ACCTAACCAA TACCGATCTT GAAAAATCAT 1800
 CAGCAGTGGC GATTCTGACA TCGAGGGATG GCATTACCTC CGTGTTCCTC CCTTTCGAGC 1860
 CCGCGGGCCA CAGAGCTGGG AAGAACTCC CGTATTGCA GCTGGAATCG CAGCCACCGG 1920
 CGCCCGGTTT TTCCTCCCGG CCTGTCCCTT CTCTGGTCAA ACAACATACT AAAGAGCGGA 1980
 GGCATGACT GTTGCCAGT TCTCACCGGG GAAAAACCCA CTGTAGGAT GGCATGAACA 2040
 TTCTCTAGA TCGTGTGAG CTCCGAGGAA TGTGGCGTCC AGGCTCTTTG AGAGCCATGG 2100
 GCTGCACCGG CCGTAGGCT AGTGTAACTC GCATCCCATT GCATGCGCTT TCTTGTACTG 2160
 TGTGTCTGTC TCTTAGATTA ACCGTGCTGA GGCTCCACAT AGCTCCTGGA CCTGTGCTTA 2220
 GTACATAGTG AAGCGATGTT CAGAGTGTGT AGAGTGAAAT TGTGTGCCCC ACATTGTTT 2280
 AACTCGCGTA CCGCGTAGAT ACATTGTGCA ACGTCTTCTT GTTATTCCCT TGAGGTGGTA 2340
 ACTTGTATG TTAGTTTAT GCGATGATTG TTGTAAATGC AATGCCGTAG TTTGGATTAA 2400
 TAAGTGGATG GTTTTGTGTT CTAATAAGAA AAAAAAATC AGTGTTCACC CTTATAGAGA 2460
 CATAGTCAAG TTCATGTTGA TAATAATCAA AGGAATTACT CTCTTCTTGT TAAATTAGCT 2520
 AAATCATGTA ACCGCAGATA GGAAGGGCTC ACCTGGGGAA ACTCTGTTT CCGATGGGAC 2580
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTTAAGTAA AAAAAAAGG 2640
 CAAACTTTGT ACTATCCAGT TATCTAAGGA ACAATAAAAA CATTAGGAGA AAAAAAAGG 2700
 AAAAAAAGG AAAAAAAGG AAAAAAAGG AAAAAAAGG A

Seq ID NO: B36 Protein sequence
 Protein Accession #: NP_055094.1

1 11 21 31 41 51
 MPGRWRQRD MHPARKLLSL LFLILMGTEL TQVLPTNPBE SQVYSSAQD SEGRICITVV 60
 APQQTMCSDR ARTKQLRQLL EKVQNMSSSI EVLDRRTQRD LQYVEKMENQ MKGLESKFQK 120
 VBSHHQHLA RQFKAKAKM DELRPLIPVL EYKADAKLV LQFKEEVQNL TSVLNELOEE 180
 IGAYDYDELQ SRVSNLEERL RACMQKLACG KLTGISDPVT VRTSGSRFGS WMTDPLAFEG 240
 DNRVWYMDGY HNNRFVREYK SMVDFMNTDN FTSRLPHPW SGTGQVYVNG SIYFNKPFQSH 300
 IIRFDLKTE TILKTRSLDY AGYNNMTHYA WGGHSDIDL M VDESGLWAVY ATNQNAAGNIV 360

VSRLDPVSLQ TLQTWNTSYP KRSAGEAFII CGTLVVTNGY SGGTKVHYAY QTNASTYEYI 420
DIPFQNKYSH ISMLDYNPKD RALYAWNNGH QILYNVTLFH VIRSEDL

Seq ID NO: B37 DNA sequence
Nucleic Acid Accession #: NM_006334.1
Coding sequence: 286..693

1 11 21 31 41 51
10 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
CCTGCCACGC CTGCCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
CGGAGGCTTC GCGCAGCAGA GCCCGCGGCG CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
GGGACACGAG CCAGGCGCGG CCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
TCGCGTCCA CGCAGCGCGC GCGCGGCGC CACCCAGGGC CCTGCATGCC AGGTCTGTGG 300
15 AGGTGGCAGC GAGACATGCA CCGGCGCCCG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
ATGGGCACTG AACTCACTCA AGTCTGCCCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
AGCTCTGCCC AGGACAGCGA GGGCAGGTGT ATCTGCACAG TGGTCGCCCC ACAGCAGACC 480
ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTTGAGAA GGTGCAGAAC 540
ATGTCTCAAT CCATAGAGGT CTTGGACAGG CGGACCCAGA GAGACTTGCA GTACGTGGAG 600
20 AAGATGGAGA ACCAAATGAA AGGACTGGAG TCCAAGTTCA AACAGGTGGA GGAGAGTCAT 660
AAGCAACACC TGGCCAGGCA GTTTAAGGGC TAACTTAAAG GAGTTTTTTC AATGCTGCAG 720
TGACTGAAGA AGCAGTCCAC TCCCATGTAA CCAATGAAAG GAGCCAGAGA GCTTTTTCAG 780
CCATGCAATT TTAATATTAT TTTCCAATAC TTAGCACCAT TTCCTAAGG AACCTTGAAT 840
ACAAACGAGA TCCTCTTTTG CATCGGACTG TAGCTGCATT TCATGAATAG TTTGAACCTT 900
25 TGTCATGCA TTTTGTGAAA AAGAAAGAAA AAAAAAATT CGTGTATGTG ACTCAAAGCA 960
TGTAACCTTA AGATGTTGCA TTCTAAACTG ACAATAAGA CCTTTCCTCC

Seq ID NO: B38 Protein sequence
Protein Accession #: NP_006325.1

1 11 21 31 41 51
30 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TQVLPTNPBE SQVYSSAQD SEGRICITVV 60
APQQTMCSDR ARTKQLRQLL EKVQNMSSQSI EVLDRRTQRD LQYVEKMENQ MRGLESKFQK 120
35 VEESHKQHLA RQPKG

Seq ID NO: B39 DNA sequence
Nucleic Acid Accession #: NM_058199.1
Coding sequence: 286..795

1 11 21 31 41 51
40 GCGCGGGGGA GCCATTAGGA GCGGAGGAGA GAGGAGGGCG CAGCTCCCGC CCAGCCCAGC 60
CCTGCCACGC CTGCCCCGGA GGCAGACGCG CCGGAACCGG GACGCGATAA ATATGCAGAG 120
45 CGGAGGCTTC GCGCAGCAGA GCCCGCGGCG CGCCCGCTCC GGGTGCTGAA TCCAGGCGTG 180
GGGACACGAG CCAGGCGCGG CCGCGGAGC CAGCGGAGCC GGGGCCAGAG CCGGAGCGCG 240
TCGCGTCCA CGCAGCGCGC GCGCGGCGC CACCCAGGGC CCTGCATGCC AGGTCTGTGG 300
AGGTGGCAGC GAGACATGCA CCGGCGCCCG AAGCTCCTCA GCCTCCTCTT CCTCATCCTG 360
ATGGGCACTG AACTCACTCA AAATAAAAGA GAAAACAAAG CAGAGAAGAT GGGAGGGCCA 420
50 GAGAGCGAGA GGAAGACAC AGGAGAGAAG ACACTGAACG AGCTTCCCTT GTTTTGCTG 480
GAAGCCACG CTGGCTCCCT GGCTCTGCCC AGGATGTGCA GTCCAAATCC CAATCCAGCA 540
GTGGGTTTAT GTCTGCCGCG TTACCTCTAG AGCCCTTCTC CTGGTCTGTC CCAGAAGATC 600
AGCCAGTCCC TCTCTGAGAG GTTCTGTCAT GCCTCTAGGA GAGAAGTTT CTGGGCCCA 660
GGAAGGCTG GTGGAGGGTG GTGGTTGTGC ACTGTTGCTG GACAGATGCA TTCATTGATG 720
55 TGACACACAC CACACACACA TGACACACA GGGGAGCAGA TACCTGCAGA GAAGAGCCAA 780
CCAGGTCTCT ATTAGTGGCA AGCTGCCCCA CAAAGGGCTA TGCTGTGTTC TTATTGAGAC 840
ACCTTGGCAA AGAGATGGCT GATTCTGGGT GGTCTGTGAC ATGGCCGAC CCAAGGGCCC 900
TCCAAGCCTT AATGGCACC TGAAGCCTCC ATGCCAGGC CAAAGATGC TTTTCTCTCC 960
TAAAAAATAA AAAAAAATAA

Seq ID NO: B40 Protein sequence
Protein Accession #: NP_478106.1

1 11 21 31 41 51
65 MPGRWRWQRD MHPARKLLSL LFLILMGTEL TONKRENKAB KMGPESEK TTEKTLNEL 60
PLFCLAHAG SLALPRMCSF NPNPAVGLCR PAYPQSPSPG AAQTISQSL ERFCMASRRE 120
VFLAPGRPG GWNLCTVAGQ MHSFMCTHTH THAHTGBQIP AEKSPQPGD

Seq ID NO: B41 DNA sequence
Nucleic Acid Accession #: AY038071.1
Coding sequence: 1..1686

1 11 21 31 41 51
75 ATGAGCAATC AGTACCAGGA GGAGGGCTGC TCCGAGAGGC CCGAGTGCAA AAGTAAATCT 60
CCAACTTTGC TCTCCTCCTA CTGCATCGAC AGCATCTCGG GCGGAGGAG CCCGTGCAAA 120
ATGCGGTTGC TGGGAGCCCG GCAGAGCTTG CCTGCTCCG TGACAGCCCG CGCCGACCCG 180
80 GAAAAGGCCG TGCAAGGCTC CCCTAAGAGC AGCAGCGCCC CGTTGAGGC CGAGCTGCAC 240
CTGCCGCCCA AGCTGCGCGG CCTGTACGGC CCGGCGGGGG GCGGCTCCTT TCAGGGTGGC 300
GCAGCGCGCG GCGCGCGCGG GCGGCGCGCG CCGCCACGGC CACGGCGGGT 360
CCAGCGGGGG AGGCCCTCTC GCCGCCACCG CCAACCGCGC GCGCGGGGA ACGGCGGGAC 420
GGCGCGGGGG CCGCGCGCGG AGCGCGGGCC GCGCGCGCGG CGGCTGGGA CACGCTCAAG 480
ATCAGCCAGG CGCGCGAGGT GAGCATCAGC CGCAGCAAGT CGTACCGCGA GAACGGGGCG 540

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CCCTTCGTGC CGCCGCGGCC CGCGCTGGAC GAGCTGGGCG GCCCGGGGGG CGTCACGCAC 600
CCGAGGAGGC GCCTTCGGGCT GGCCGCGCGC CGGGGCGAGC CCCCAGGCTG GGGTGGTGGC 660
ACCGGCACCG AGGACGACGA GGAGGAGCTG CTGGAGGACG AAGAAGATGA GGACGAGGAA 720
GAGGAATCGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACGAGCCTCG CGCGCTGCTC 780
AAGGAGCCCC GCGCTGTGCT TGTGGCCGCC ACTGGCGCCG TGGCCGCAGC AGCTGCCGCT 840
GCAGTGGCCA CAGAGGGCGG GGAGCTGTCA CCCAAGGAGG AGCTGCTGCT GCACCCGGAA 900
GACGCTGAGG GCAAGGACGG CGAGGACAGC GTGTGCCTCT CTGCGGGCAG CCACTCGGAG 960
GAGGGGCTGC TGAACGCAA ACAGAGGCGC TACCGCACA CGTTACCCAG CTACCAGCTG 1020
GAGGAATCGC AGCGGGCCTT CCAGAAGACG CACTACCCGG ACCTCTTAC CAGGGAGGAA 1080
CTGGCCATGA GGCTGGACTT GACCGAGGCC CGAGTCCAGG TCTGTTCCA GAACCGTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGCAGGC GCGCAGACC ACCCCCTGG GCTGCCCTTC 1200
CCGGGGCGCG TCTCCGCCAC CCACCCGCTC AGCCCTTACC TGGACGCCAG CCCCTTCCTT 1260
CCGCACCAAC CGCGCTCGA CTCCGCTTGG ACTGCGCTG CCGCGCGCGC CGCGCGCGCT 1320
TTCCGAGGCC TACCTCCGCC TCCGGGCTCG GCCAGCCTGC CGCCAGCGG GCGCGCGCTG 1380
GGCTGAGCA CTTCCTCGG AGCGGCGAGT TTCGACACC CAGCTTTCAT CAGCCCGGCA 1440
TTCGCGAGG TCTTTTCCAC AATGGCCCC CTGACCAGCG CGTCGACCG GCGCGCGCTG 1500
CTGAGACAGC CCACACCCGC CGTGGAGGGC GCAGTGGCAT CCGCGCGCTT GCGCGACCG 1560
GCCACGCGCG CCGCAGACAG ACGCGCTCT AGCATAGCG CGCTGAGGCT CAAGGCCAAG 1620
GAGCACGCGG CGCAGCTCAC GCAGCTCAAC ATCTGCGCG GCACCAGCAC GGGCAAGGAG 1680
GTGTGC

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Seq ID NO: B42 Protein sequence
Protein Accession #: AAK93901.1

25
30
35

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1 11 21 31 41 51
| | | | |
MSNQYQEEGC SERPECKSKS PTLSSSYCID SILGRRSPCK MRLLGAAQSL PAPTSTRADP 60
EKAVQGSFKS SSAPFEAEHL LPPKLRLRYG PGGRLLQGA AAAAAAAAAA AAAAATATAG 120
PRGEAPPPFP PTARPGERPD GAGAAAAAAA AAAAAMDTLK ISQAPQVSIS RSKSYRENGA 180
PFVPPPPALD ELGGPGGVTH PEERLVAGVG PGSAPAAAGG TGTEDEEEL LEDEDEDEE 240
EBLLEDEEE LLEDDARALL KEPRRCFVAA TGAVAAAAAA AVATEGGEELS PKEELLHPE 300
DAEGKDGDS VCLSAGSDSE EGLLRKQRR YRTFTSYQL BELERAFQKT HYPDVFTREE 360
LAMRLDLTEA RVQVWFQNR AKNRKREKAG AQTHPPGLPF PGPLSATHPL SPYLDASFPF 420
PHHPALDSAW TAAAAA AAAA FPLPPPPGS ASLPPSGAPL GLSTFLGA AV FRHPAFISPA 480
FGRLFTMAP LTSASTAAL LRQPTPAVEG AVASGALADP ATAAADRRAS SIAALRLKAK 540
EHAAQLTQLN ILPGTSTGKE VC

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Seq ID NO: B43 DNA sequence
Nucleic Acid Accession #: CAT cluster

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45
50
55
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1 11 21 31 41 51
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TTCCGCGCGT TCCGTGCGCC CTCTCTGCGC TTCCGCTTCA CCTCCGCTT GCGTGTGCT 120
CTGCTCTCCT CCGCTCTCAT GCCCTTTTCA GCTCTACTCT TGCTGTGCTC CCGCTCCCTC 180
GCTCGTTTCT CTGTGTCTTC TCTTCCCGG TTGCTGTCT GCTCTCTCT GTTCCCTCTC 240
GTCTGTGTTT GTGGGTGCTC CTCTGCGTCC TGCTCTTTT TCTTGCGTTT CCGCGCGCTT 300
CCTGTGTTTG TCCCTCTGCT TCTGCGCGCG TTCTGTGTGC GCGGGCGGCC CGGTCTTTT 360
TTGGTGTCTT GCTCTGCTCT TCTGTCTGCT GTTCTCTGCG GTCTGTGCTT TCTCTCTTT 420
ATCTCTGTT TTCTCTTTT CTGTGTTCTT CTGTGTTT TTGTCTTTT TTTCTCTTA 480
GCTGAGGTTG GGGAGAGATA ACGCTGTAAA CTTTATTTT TCAGGAATC TGAAGACCTA 540
CAGTCTCCAT GCTGCTCTAG CCAAGAAGGA GCTCACTGTG GGCACCAGAG ACAGGGACCC 600
AATGTGGAGA CCTGTAGACC TGTGTCCGCG CCTGAATCT CAAGCACAGG GCAGGCTTCC 660
TGAGCATTTA AGAGATATAG TGGGAGAAC AACAAGAAAT TGAAGAAAT TGAAGGTGT 720
CTTCTTGA TGTATTCCA TGATAGATAG TAGGGGAGG AGTAGAGAG GCTGACTAGG 780
TCTGGACATG GAGGCTGGAA GAGTCAGGT GTGATTGGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GGTGGAAT CTGAGGGTCA GTGTGCAAG TCACTCAGAG ACAGAAATC 900
AGCATAGCCC TTGCTGATGG CAA

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Seq ID NO: B44 DNA sequence
Nucleic Acid Accession #: NM_014421.1
Coding sequence: 718..1497

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75
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GCGCTGGCAG CGATTGCGTG TCTCTTGTA GTACGGGAC AACGCTTCGG GGCACATGTG 120
AGTGCGCGTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCGTC OGGGGACGTC 180
TCCTGATCCC TACTATAAGC GCGTGTAAAC TTTGAAAAGG AGCACTGTGT CCGTCAAAAT 240
TTGACACATA AAGGATAGGA AAAGAGAGGA GAGAAAAGCA ACTGAGTTGA AGGAGAAGGA 300
GCTGATCGCG GCCTCTGAT CAATTAAGAG GAGAGTTAAA CCGCGAGAT CCGCGCGGA 360
CCAAGGAGGT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTTCT 420
TGACCTTGG GTACGCGCTC CTGTGCGAGA AAGCGCTCG CATTTGATTG CTTCAGTTA 480
TTGAGAACT TCTGTCTCTG GTGGAGAGGC GGTCTCTGCT TGGGTTCCCG TAATTTCTGT 540
CCTGAGCGCT GAGACTGAGT TCATAGGGTC CTGGTCCCC GAACAGGAA GGGTTGAGGG 600
AACACAATCT GCAAGCCCC GCGACCCAAG TGAGGGGCC CGTGTGGGG TCTCTCTCC 660
CTTTGCATT CCACCCCTCC GGGCTTTGCG TCTTCTTGGG GACCCCTCG CCGGAGATG 720
GCGCGTGA TGCGAGCAA GGATTGCTCC TGCTGCTGCT TCTACTGCG CCGGTGCTG 780
ATGGTGGAGA GCTCAGATG CGGCAGTTC GCGGCCAAC TCAACTCCAT CAAGTCTCT 840
CTGGCGCGGG AGACGCTGG TCAGGCGGCC AATCGATCT GCGGCATGTA CCAAGGACTG 900
GCATTGCGCG CGAGTAAGAA GGGCAAAAAC CTGGGGCAGG CTAACCTTG TAGCAGTGT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCCAC AGTCCCAACC AAGGATCATC GGCCTGCATG 1020
GTGTGTGCGA GAAAAAGAA GCGCTGCCAC CGAGATGGCA TGTGCTGCC CAGTACCCGC 1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCGCT 1140

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5 CTGGATGGTA CTGGGCACAG AGATCGAAAC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200
 TGGCAGAATC TAGGAAGACC ACACACTAAG ATGTACATA TAAAGGGCA TGAAGGAGAC 1260
 CCTCTGCTAC GATCATCAGA CTGCAITGAA GGGTTTTGCT GTGCTCGTCA TTTCTGGACC 1320
 AAAAACTGCA AACCAATGCT CCATCAGGGG GAAGTCTGTA CCAACAACG CAAGAAGGGT 1380
 TTCTATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAAGTA 1440
 TGGAAAGATG CCACCTACTC CTCCAAGCC AGACTCCATG TGTGTAGAA AATTGTATCA 1500
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATTATAGCAT 1560
 GGTGGAAAAAT AAGGTTTCAGA TGCAGAGAA TGGCTAAAAAT AAGAAACGTG ATAAGAATAT 1620
 10 AGATGATCAC AAAAAGGGAG AAAGAAAACA TGAACCTGAAT AGATTAGAAT GGGTGACAAA 1680
 TGCAGTGCAG CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740
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 TACAAATAAC CTACATGCCA GATTTCATAT CAACGTTAGA GTTTAACAAA ATACTCTAG 1920
 15 AATAACTTGT TATACATAG GTTCTAAAAA TAAATGTCT AAACAAGAAA TGAACAACATG 1980
 GAGCATTTGT AATTACACAG AGAAAATTAC CTTTGTATTT GTAACTATC TTCTGCTGTT 2040
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 TAATGGCCAG TTGTTTAGGA AGGCCTTTAG GAAGACAAAT AAATAACAAA CAAACAGCCA 2160
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 20 AAAAACTGTT CCTTCAGATT CTACGGAATG ACAGTATATC TCTCTTATC CTATGTGATT 2280
 CCTGCTCTGA ATGCATTATA TTTTCCAAAG TATACCCATA AATTGTGACT AGTAAAAATC 2340
 TTACACAGAG CAGAAATTTT ACAGATGGCA AAAAAATTTA AAGATGTCCA ATATATGTGG 2400
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 AGAATTAGAT TGGTAAATAC ATGTATTTCAT ACATACTCTG TGGTAAATAGA GACTTGAGCT 2520
 25 GGATCTGTAC TGTAGAGGAG TAAGCAAGAA AATTGGGAAA ACTTTTCTGT TTGTTCAAGT 2580
 TTTGGCAACA CATAGATCAT ATGTCTGAGG CACAAGTTGG CTGTCTATCT TTGAAACAGC 2640
 GGGATGCACA GTCTAAATGA ATATCTGCAT GGGATTGTCT ATCATAATNT TTCCTATGCN 2700
 GNTGAATTCT GTGTGAGGTC CTGTGTCCGT CCTATCTCTA AATTATTAT TTTATAGTGC 2760
 TGAGATCCTC AAATAATCTC AATTTCGGAG GTTTCACAAA ATGGACTCCT GAAGTAGACA 2820
 30 GAGTAGTGAG GTTTCATTGC CCTCTATAAG CTCTGACTA GCCAATGGCA TCATCCAATT 2880
 TTCTTCCCAA ACCTCTGACG CATCTGCTTT ATTGCCAAAG GGCTAGTTTC GGTTTTCTGC 2940
 CAGCCATTGC GGTAAAAAAA TATAAGTAGG ATAACCTGTA AAACCTGCAT ATTGCTAATC 3000
 TATAGACACC ACAGTTTCTA AATTCTTTGA AACCCTTTTA CTACTTTTTT TAACTTAAC 3060
 TCAGTTCTAA ATACTTTGTC TGGAGCACAA AACAATAAAA GGTATCTTTA TAGTTGTGAC 3120
 35 TTTAAACTTT TGTAGACCAC AATTCACTTT TTAGTTTTCT TTTACTTAAA TCCCATCTGC 3180
 AGTCTCAAT TTAAGTTCTC CCAGTAGAGA TTGAGTTTGA GCCTGTATAT CTATTAATAA 3240
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 40 TTATATTGAT AATTGTTTCT CTGCAATATT TTTCTTATGT CCACCTTTT AAAAAATTAT 3480
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 AAAAAAAAAA A

45 Seq ID NO: B45 Protein sequence
 Protein Accession #: NP_055236.1

50 1 11 21 31 41 51
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 MAALMRKSDS SCCLLLLAAY LMVSSQIGS SRKLNSIKS SLGGETPGQA ANRSAGMYQG 60
 LAFGSGSKGK NLQAYPCSS DKECEVGRYC HSPHQSSAC MVRKKRKRK HRDGMCCPST 120
 RCNNGICIPV TESILTPHIP ALDGTNRHRD NEGHYSNHD L GWQNLGRPRT KMSHIKHEG 180
 DPLRSLSDCI EGFCCARHFV TKICKFVLHQ GEVCTKQRKK GSHGLEIFQR CDCAKGLSCK 240
 VWKDATYSSK ARLHVQCQKI

55 Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_019885.1
 Coding sequence: 1..1539

60 1 11 21 31 41 51
 | | | | |
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 65 CGCGACAAGA GCTGCAAGCT GCCCATCCCC AAGGGATCCA TGGGCTTCCC GCTCATCGGA 180
 GAGACCGGCC ACTGGCTGCT GCAGGGTTCT GGCTTCCAGT CGTCCGCGAG GAGAAAGTAT 240
 GGCAAGGTGT TCAAGACGCA TTTGTTGGGG CGCGCGCTGA TACGCTGAC CGGCGCGGAG 300
 AACGTGCGCA AGATCCTCAT GGGCGAGCAC CACTCTGTGA GCACCGAGTG GCCTCGCAGC 360
 ACCCGCATGT TGCTGGGCCC CAACACGGTG TCCAATTCCA TTGGCGACAT CCACCGCAAC 420
 70 AAGCGCAAGG TCTTCTCCAA GATCTTCAGC CACGAGGCC TGGAGAGTTA CCTGCCCAAG 480
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 TGCCCTGGCA AGCACCTGGC CAAGCTGTTC CTGAAGGTGC TGGCGGTGGA GCTGGCTAGC 1380

5 ACCAGCCGCT TTGAGCTGGC TACACGGACC TTCCCCCGCA TCACCTTGGT CCCCCTCCTG 1440
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 10 GAACTGCTCC CTTCCTTCG TTCCCTTTAG ACCCTTTTGG CTGGGGTTGG GGGACGGGAA 1920
 GAGCGGTGCC CCCTTGGGGG CACTCTTCAG CGTCTCCTCC TCGTGGCCCC CACTGCGTTC 1980
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 15 GCCCCAGGCC CTGTCTCCCC AGCATCCTCC CTGGTGGCCC TGGGCAAGTG CACTGACACC 2220
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 20 ACTTCTGTGA GTGAAGAGGA AGGGGTCTCT GGTCAAACCC AGCCCCAGG GCCTAGGGTT 2460
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 35 GCCACCTGA AGATAGACTA TAGGAACGG CCCATACCAC ACAGACTGCT CTCAATCCC 3360
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 45 GTTCTTACT TATCATCCCT AACTATTGCA ACTTGACCTT AAAAAGACAA AACCCACAA 4020
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 TTTTITTTCA TAAATGTTAT AATTITGTGT CTGTCTTTAT AAACATTAT AAGTACTATT 4200
 TTTGTTATAA TTCAAATAG ATATTAGTA TAAAGTTTT GCTGTTAAAT ATTTGTTATT 4260
 50 TAGTAAATAA TGAATTTTGC TCTATTGTA ACATGGTTGA AAATAITTAAT ATGTTTTTAT 4320
 CACAGTCGTT TTAATATTGA AAAAGCACTT GTGTGTTTT TTTTGATATG AAACCTGTAC 4380
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 AAAAA

Seq ID NO: B47 Protein sequence
 Protein Accession #: NP_063938.1

1 11 21 31 41 51
 60 MLPEGLDLVS ALATLAACLV SVTILLAVSQ QLNQLRWAAT RDKSKCLPIP KSGMGFPLIG 60
 ETGHWLQGS GFQSSRRREKY GNVFKTHLLG RPLIRVTGAE NVKILMGEH HLVSTEWPRS 120
 TRMLLGENIV SNSIGDIHRN KRKVFSSKIFS HEALESYLPK IQLVIQDTLR AWSSHPBAIN 180
 VYQEAQKLT RMAIRVLLGF SIPEEDLGHF FEVYQFVDN VFSLEVDLPF SGYRRGIQAR 240
 QILQKLEKA IREKLQCTQG KDYLDAIDL L IESSKEHCKE MTMBELKDTG LELIFAAYAT 300
 65 TASASTSLIM QLLKHPTVLE KLRDELRAHG ILHSGGPCPE GTLRDLTSLG LRYLDCVIKE 360
 VMRLFTPISS GYRTVLQTFE LDGFQIPKGV SVMYSIRDTH DTAPEVKDVN VFDPRPSQA 420
 RSEDKDRFPH YLPFGGVRT CLGKHLAKLF LKVLAVELAS TSRFELATRT FPRITLVFVL 480
 HPVDGLSVKP PGLDSQNEI LPETBAMLSA TV

Seq ID NO: B48 DNA sequence
 Nucleic Acid Accession #: AB040527.1; AL136582.1
 Coding sequence: 94..2319

1 11 21 31 41 51
 75 GCGGCTCGCG GGTCTCTGGT GCTGAGGACG GACGCCATTG GAGTTCCTCGA GAAGCATGGC 60
 TGAGGGAAGC TTCAGCGTGC AATCGGAAAG CTACAGTGTG GAAGACATGG ATGAGGGTAG 120
 CACGAAATGC GGGGAGGAG AGATGGTTGA AGGCAACGAC TATGAAGAAT TCGGTGCGTT 180
 TGGTGGCTAT GGCACCTTCA CCAGCTTTGA CATCCATATC CTCAGAGCCT TCGGAAGCTT 240
 80 GGGTCCAGGC CTTGCGATCT TATCGAATGA GCCCTGGGAA CTGGAAGGCT CTGTGCTGGC 300
 CCAGACCTTG GTGGAGGCAT TGCAGCTGGA TCCGGAACA CTGCGCAATG AGACGCGCGC 360
 CGTGTCTGCC AACGTAGCCC GCGCGCGCGC CTCACACCGT GCGGCTCGGG CCGCTGCGCG 420
 CGCTGCGCGT ACCGCTTCA GTCAAGTGGT CGTAGCCAC CGGGTGGCCA CGCGCAGGT 480
 CTCAGGAGAG GATACCCAGC CCAAGACCTA CGCCGCGAG GCTCAGGGGC CACCCCTGA 540
 GCCACCCCTT GCTTCTCGC AGACCTCCA GATGTTAGTC ACCAGTAAGA TGGCTGCCCC 600

5 CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CCGGCCCCAGG AGGCTGCTAC 660
 TGAGGGCCCT AGTAGCGCCT GTGCTTTCTC TCAGGCTCCG TGTGCCAGGG AGGTGGACGC 720
 CAAACCGGCC AGCACAGCCT TCCTGGGCCA GAATGATGTC TTGATTTCA CTCAGCCGCG 780
 AGGTGTCACT GGCATGGCCT TCCCGCGCCC CAAGAGACCT GCCCCAGCCC AAGAGGCTGC 840
 CACAGAGGGC CCCAGTGCCT CCTCTGGTGT GCCCCAGAGC GGACCTGGCA GGGAGGTGGC 900
 AGCCACCCCG CCCAAGACCA CCAAGTCGGG GAAGGCGCTG GCCAAGACTC GGTGGGTGGA 960
 GCCTCAGAA GTTGTGGCAG CAGCTGCTGC CAAGGCCAAG ATGGCCACGA GCATCCCTGA 1020
 GCGGAGGGT GCAGCTGCTG CCACTGCTCA GCACAGTGCT GAGCCCTGGG CCAGGATGGG 1080
 10 AGGCAAGAGG ACCAAGAAGT CCAAGCACCT GGATGATGAG TATGAGAGCA GCGAGGAGGA 1140
 GAGAGAGACT CCCGCGTCC CACCCACCTG GAGAGCATCA CAGCCCTCAT TGACGGTGGG 1200
 GGCTCAGTGT CCGCTCGGC CCCGATGGC CCCGAGTCC CAGATACCT CAAGGCCAGT 1260
 ACTGTGCTG CCCCCCGCA AGGTGACCTC TCTGAGGAG AGGCAAAATA AGTTGGTGAA 1320
 ATACCTGATG ATTAAGGACT ACAAGAAGT CCCCATCAAG CGCGCAGACA TGCTGAAGGA 1380
 15 TGTATCAGA GAATATGATG AACATTTCCC TGAGATCAIT GAACGAGCAA CGTACACCCT 1440
 GGAAAGAGG TTTGGGATCC ACCTGAAGGA GATCGACAAG GAAGAACACC TGTATATTCT 1500
 TGTCTGCACA CCGCTCGCT CAGCTCGCCT CCTTGGAAAA ACCAAGGACA CTCGCCGCT 1560
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 TGTCTCTGG GAGGCACTAC GCAAGATGGG ACTGCGCCTT GGGGTGAGGC ACCCATCTCT 1680
 20 CGGCGATCTG AGGAAGCTCA TCACAGATGA CTTTGTGAAG CAGAAGTACC TGGAAATACAA 1740
 GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTC TGGGGCTGCG GAGCCCGCCA 1800
 TGAGACCAAG AAGATGAGGG TCCTGAGATT CATGCCCAAG AATCAGAAAC GAGACCCCGC 1860
 GGAATGGAAG GCTCATTTCT TGGAGGCTGT GGATGATGCT TTCAAGACAA TGGATGTGGA 1920
 TATGGCCGAG GAACATGCCA GGGCCAGAT GAGGCCCAAG ATGAATATCG GGGATGAAGC 1980
 25 GCTGATTGGA CGGTGGAGCT GGGATGACAT ACAAGTCGAG CTCCTGACCT GGGATGAGGA 2040
 CGGAGATTTT GGGATGCTC GGGCCAGGAT CCCCCTTGCT TTCTGGGCCA GATACCATCA 2100
 GTACATTTCTG AATAGCAACC GTGCCAACAG GAGGCCACAG TGGAGAGCTG GGTCAAGCAG 2160
 TGGCACCATG GAGGGGCCCA GCACGAGCT CTTAGATGCG CCCAGCACCA GCTCCACCAT 2220
 CCGGACCAGA AATGCTGCCA GAGCTGGGCG CAGCTTCTCT TCCTGGATCC AGCACCGTTG 2280
 30 ACGAACTGCA GCGATCTTAC TGGCCAAGCC AGAGCGCCTC CTCTCAGATT CCTTCTCGAC 2340
 ACAGACCCCT AGGCGGCTTC TTCTCTGTAG TCGGAGGTGG CATGCAAGAT GAAGCTCTCT 2400
 TTGCTCTTCC TGCTTTCAAT TTGTGCTTTT CCTTGTGTTT TCATGTTTGG GGTATCAGTG 2460
 TTACATTAAA GTTGCAAAAT TAAA

Seq ID NO: B49 Protein sequence
 Protein Accession #: BAB33378.1; CAB66517.1

1 11 21 31 41 51
 40 MAEGSFSVQS ESYSVEDMDE GSDEVGEEEM VEGNDYEEFG AFGGYGTITS FDIHILRAFG 60
 SLGPGILRLS NEPELENPV LAQTLVREALD LDPETLANET AARAANVARA AASNRAARAA 120
 AAAARTAFSQ VVASHRVATP QVSGEDTQPT TYAAEAQOPT PEPPLASQPT SQMLVTSKMA 180
 APEAPATSAQ SQTGSPAQEA ATEGPSSACA FSQAPCAREV DANRPSTAFI GQNDVDFDTQ 240
 PAGVSGMAFP RPKRPAPAE AATEGPSAAS GVPQTGPGRE VAATRPKTKK SGKALAKTRW 300
 45 VEPQNVVAAA AAKAKMATSI PEPEGAAAAT AQHSAEPWAR MGGKRTKKSK HLDDEYESSSE 360
 EERETPAVPP TWASQPSLT VRAQLAPRPP MAPRSQIPSR HVLCLPPRNV TLLQERANKL 420
 VKYLMKIDYK KIPKIRADML KDVIREDYDEH FPBIIRATY TLEKRFGIHL KEIDKEEHL 480
 ILVCTDRSSA RLLGKTKDTP RLSLLLVILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540
 FLGDLRLKIT DDFVKQKYLE YKKIPNSNPP EYEFWGLRA RHETSKMRVL RFIAQONQNRD 600
 PREWKAFPLE AVDDAFKTM DMAEBEHARA QMRAQMNIGD EALIGRWSWD DIQVELLTWD 660
 50 EDGDFGDWA RPPAFWARY HQYILNSNRA NRRATWRAGV SSGTNGGAST SVLDGPSTSS 720
 TIRTRNAARA GASFFSNIQH R

Seq ID NO: B50 DNA sequence
 Nucleic Acid Accession #: XM_084965.1
 Coding sequence: 356..2014

1 11 21 31 41 51
 60 GACCTAGCGT GTGCTCAGCT CTGGACAAGA CATGGATGTA GGCAGACATG CTTCTGCTCT 60
 GCTGGGCTTA GTGCACCAAT GCTAAGGACA GACATGAAGG GCTTGGGAAA GGCATGAAGA 120
 TGCAGGGAGT CTAGGAGAGA GGATAAGAAA AACAAACATT TTGTGGTGGG TTGAATTGCG 180
 TTGTGCTTTT TAGAGGCATT TCGTGATCCA TGGTTGCGCT CCGGTGAAGA GCGAGTCTAG 240
 AGAAGGAATC CSAAGCGGCG GCGGCGAGCG CCGCTCAGGT TGATTTAGAA TACGGGTGAC 300
 65 AGTGGCCTGG CCGAGCCCA CTGCTGACGA AAGCGGCTTA TCCCGCGCGG TTTCCATGGA 360
 GACGAGCCGG AGCCGCGGCG GCGGCGGGGC TGTCAGCGAG CCGGCGGAGG CTGGCGGCTC 420
 CGTGGGGGTC TGCAGGAGGA AGGCGGAGGC CCGGCGGGGG ACCGGGACCC TCGCGGCAGA 480
 CATGACATTG CATTGTGACT GTGCCGCCGA AACGCCCGCC GCGGAGCCGC CGTGGGGGAA 540
 GATTAATAAA GCTGCTTCA AATTATTCAA GAAGAGGAAA TCGGGTGGCA CCAATGCCAG 600
 70 CATTTTGGGG GTCAAAAACA AAGGGGACGG GAAAGCTCG GGTCCGACGG GGCTGGTGGAG 660
 GAGCAGGACC CAGCAGGAC TTGCCGAGGT GCTGTGCTG GAGAGCGGCA GGAAGGAGGA 720
 GCGGCGCGGC GGGGCGGACA GCGGCGGGGG CCGGCGGGGG CCGCGGAACC CCGGCGCCCC 780
 CAGAGCCGCA GGGCCCGGCG GGGGCTCCCT CGCCAGCAGC TCGGTGGCCA AGTCCGACAG 840
 CTTCTTCTCG CTGCTGAAGA AGAACGGGCG CTGGAAGAAC GGCAAGGGAG AGCCTGTGGA 900
 75 CCGAGGCAAG GCGGCGGCGA AACAAAGCG GGGGCTGCGG GGGCTGTTCA GCGGCATGCG 960
 CTGGCAGAGC AAAGCAAGC GGGCCAAGGC GAGAGCCCGG GAGGGGCGCG GCGCCGGGGG 1020
 CCGCTTGATC CTACCGGCT CGCTCACCGC CAGCTTGGAG TGCGTCAAGG AGGAGACGCC 1080
 CAGAGCCGCG CCGAGCGCG AGGAGCCCGC CAGGAGCCCG CCGGAGAGCC CAGCAGGCTG 1140
 TGGAGATATT ATTGCGAGC AAGAGGAAGA GGCAGGTCCC AGCTGTGACA AGCATGTGCC 1200
 80 CCGGCCAGGC AAGCCGCTC TGTCTAAAAA GAACCCCGCG GTGGTGGCCT ACCAAGGAGG 1260
 CCGGGGAAGC ATGGCCAGCC CGGACGAGGT GAGCAGACCC TATCTACAGG AGTTCTGGGA 1320
 CATGCTCTCC CAGACCGAGC AGCAGGGACC CAGGCCCGCG GAGGGCGCGG CTAAGGTGGC 1380
 AGCTGCGCTG GAACCAAGG TGTGTCGCGA GACCCCAAAA GACACCAAGT GTGTGGAAGC 1440
 GGCACAGGAC GCGTCTCTCG TCAAGCGCAG GAGGCTCAAC CGGATTCCCA TCGAGCCCCA 1500
 TCCTAAGGAG GAGCCCAAGC ACCCGGAGAA GGAGCAGCAG GAAGGCGTCC CCAACAGCGA 1560

CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620
 GAAGGGGGGC ATCCCCCGGG ATAGCTACAG CGGGGACGGC CTCTATGATC TCTATGCTGA 1680
 CCCGGACGGA AGTCCAGCAA CCTTCCTGG AGGGAAGGAC AACGAGGAGA CGTCTCCCT 1740
 GTCCCGGTTA AAGCCCGTAT CTCCAGGCAC CATCACCTGT CCACTGCGAA CACCAGGCAG 1800
 CTTGCTGAAG GACTCTAAGA TCCCTATTAG CATCAAGCAC CTGACCAACC TTCCATCTAG 1860
 CCATCCCGTG GTGCACCAGC AACCTCCAG GAGTGAGATG CCCAGAACAA AAATCCCGGT 1920
 TTCCAAAGTG CTGGTCCGCA GAGTCAGCAA CCGGGGCTTG GCTGGGACCA CCATCAGAGC 1980
 AACGGCTGCG CACGACAGTG CCAAAAAGTT GTGAGGTCTT CCAGGCCAAG GTGGATGGGC 2040
 CCATGCGCAA GGAATACAAC TTTTCCCTGG AAACCACTAA AGTAAGTTTT GCTTTTCCTA 2100
 AAGAAAGTCT TTTAGGACAC CACCCGTCCT CCGCCTGCT CCAGAGCGTG GACCGAGGAG 2160
 GTCTTTGTGC CCTGAGCAGG GACCGGATAA CACCAGAAAG AGGGATGCTA CACGGGGGTT 2220
 TCTCTCTCA AGATAAGTCC CTGAGAATTA TTTTCAAGCA CTTTTTCTT TTTTACCTTT 2280
 AAGTTTTTCT TCCTTTTGCT TTAATATACT GAACACTTGG AAGTCACCTT TACTTGCCTT 2340
 TGCAAGAAAC AGAAGTTAGC CAAACCTAAG TAAGAGTCAT GCGTGATAT TGGGATAAGC 2400
 CAGTGCTAG AGGCCTGAAG GAACCGCTGA AGAACAGAG GAGATCTCCT CTTCACAGAC 2460
 ACGTTTCCCT CCTTCCCTT TTTCTCTTT CTTTCCAGT T

Seq ID NO: B51 Protein sequence
 Protein Accession #: XP_084965.1

1 11 21 31 41 51
 METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
 GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
 EEPGGGDSG GGGGGRPNFG PPRAAGPGG SLASSSVAKS HSFFSLKKK GRSENGKGEP 180
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGLLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDPG GCGDIIADQE EEAGPSCDKH VPGPGKPLS KKNPGVVAYQ 300
 GGGEEAMSPD EVDITYLQEF WDMLSQTEEQ GPEPQEGAAK VAALETKVY PETPKDTRCV 360
 EAAKDASSVK RRRLLNRPIE PHPKEBPKEP EKEQBGVFN SDEGYWSTT PGPEEDSSSS 420
 GKAGIPRDS YSGDALYDLY ADPDGSPATL PGGKDNEETS SLRLKVPSP GTITCPLRTP 480
 GSLKDKSIP ISIKHLNLNLP SSHPVVHQFP SRSEMPRTKI FVSKVLVRRV SNRGLAGTTI 540
 RATACHDSAK KL

Seq ID NO: B52 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2016

1 11 21 31 41 51
 ATGGAGACGA GCCGGAGCCG CGGCGGCGGC GGGGCTGTCA GCGAGCGCGG CGGAGCTGGC 60
 GGGTCCGTGG GGGTCTGCAG GAGGAAGGCG GAGGCGGGG CCGGACCGG GACCTCGCG 120
 GCAGACATGG ACTTGCAATG TGACTGTGCC GCCGAAACGC CGGCCGCGGA GCCGCCGTG 180
 GGGAAAGATT ATAAAGCTGC CTTCAAATTA TTCAAGAAGA GGAATCCGG TGGCACCATG 240
 CCGACATT TTGGGGTCAA AAACAAAGGG GACGGGAAAG GCTCGGTTCC GACGGGGCTG 300
 GTGAGGAGCA GGAACCAAGA CGGACTTGCC GAGGTGCTGG TGCTGGAGAG CGGCAGGAAG 360
 GAGGACCGCG CGCGCGGGGG CGACAGCGCG GGGGCGGGG GGGGCGGGC GAACCGGGG 420
 CCCCCAGAG CCGCAGGGCC CGCGCGGGG TCCCTCGCCA GCAGCTCGGT GGCCAAGTCG 480
 CACAGCTTCT TCTGCTGCT GAAGAAGAAC GGGCGCTCGG AAAACCGCAA GGGAGAGCCT 540
 GTGACGCGGA GCAAGGCGCG CGGCAACCAA AAGCGGGGG TGCGGGGCT GTTCAGCGGC 600
 ATGCGCTGGC ACAGGAAGCA CAAGCGGGCC AAGCGGAGG CCGCGAGGG GCGCGCGCCC 660
 GGGGCGGCT TGATCTTACC CGGCTGCTC ACCCGAGCC TGAGTTCGT CAAGGAGGAG 720
 ACGCCAGAG CCGCGCGCGA GCGGAGGAG CCCAGCCAG ACGCCCGCG AGACCCAGCA 780
 GGTGAGCCCG CAGGGGAGGA GGAGGTGCCG GCCCGCGCG ACCCGCGCCC AGCGCGGAGC 840
 TGCCGAGAG CAGAGGGGCT CGCGCACCCC GCGGACACCG GCGCCGCGGG AGAGGAAGCC 900
 GCGGGGCATC GCGCGCGCGA GCGGGGCGCC GGGGAGGTCC GCACGGCAGA GGAAGCTTCC 960
 AGGAGCGGGG CCGTTCCCGT AAAGACGGTC CCCCTTGTG ACTCGAAGG CGGCAGCGGC 1020
 CGGGCGCCC CGGCCCCAGA CCTGCTCTCT GTGATCCAC CCTCAGACC GTCCGCGAGT 1080
 CGTATTGTGT TGATGTTTTT TGACGTGACT TCACTGAAA GCTTTGACT TCTTACAGGC 1140
 TGTGAGATA TTATTGCGA CCAAGAGGAA GAGGAGGTC CCAGCTGTGA CAAGCATGTC 1200
 CCGCGGCCAG GCAAGCCGCG TCTGTCTAAA AAGAACCCCG GCGTGGTGGC CTACCAAGGA 1260
 GCGGGGAAG AGATGGCCAG CCGGAGCAG GTGGACGACA CCTATCTACA GAGTTCTTGG 1320
 GACATGCTCT CCCAGACCGA GGAGCAGCGA CCGAGCCCC AGGAGGGGCG GGTAAAGGTG 1380
 GCAGCTGCGC TGGAAACCAA GGTGGTGCCC GAGACCCCA AAGACACCAG GTGTGTGGA 1440
 GCGGCCAAGG ACGGCTCCTC GTTCAAGCG AGGAGGCTCA ACCGGATTCC CATCGAGCCC 1500
 CATCCTAAGG AGGAGCCCAA GCACCGGAG AAGGAGCAGC AGGAAGCGCT CCCCAACAGC 1560
 GACGAGGGCT ACTGGGACT CACCAAGCCA GCGCAGAGG AAGACAGCTC GAGCAGCGGG 1620
 AAGAAGGCGG GCATCCCGCG GGATAGCTAC AGCGGGGAG CGCTCTATGA TCTCTATGCT 1680
 GACCCGAGCG GAAGTCCAGC AACCTTCTCT GGAGGGAAGG ACAACGAGGA GACGTCTCTC 1740
 CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGGG AACACAGGC 1800
 AGCTTGCTGA AGGACTCTAA GATCCCTATT AGCATCAAGC ACCTGACCAA CCTTCCATCT 1860
 AGCATCCCG TGGTGACCA GCAACCTCTC AGGAGTGAGA TGCCAGAAC AAAAATCCCG 1920
 GTTTCCAAAG TGCTGGTCCG CAGAGTCAGC AACCGGGCT TGGCTGGAC CACCATCAGA 1980
 GCAACGGCCT GCCACGACAG TGCCAAAAG TTGTGA

Seq ID NO: B53 Protein sequence
 Protein Accession #: FGENESH predicted

1 11 21 31 41 51
 METSRSRGGG GAVSERGGAG ASVGVCRRKA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
 GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
 EEPGGGDSG GGGGGRPNFG PPRAAGPGG SLASSSVAKS HSFFSLKKK GRSENGKGEP 180
 VDASKAGGKQ KRGLRGLFSG MRWHRKDKRA KAEAAEGRAP GGLLILPGSL TASLECVKEE 240
 TPRAAREPEE PSQDAPRDPG GEPAGGEEVP APADRAPARS CREAEGLAHP GDTGARGEDA 300

5 AGHRRRAEPGP GEVVRTAEDAS RTGAVPVKTV PLVDSEGGSG RAPAAPDPAS VDPSPDPSAD 360
 RICLMFSDVT SLKSFDSLITG CGDIADQEE BAGPSCDKHV PGPGKPALSK KNPGVVAYQG 420
 GGEEMASSPDE VDDTYLQEPWF DMLSQTEEQG PEQDEGAARV AALETQVVP ETPKIDTRCVR 480
 AAKDASSVVR RRLNRIPIEP HPKEEPKHP EQQEGVPMN DEGYWDSTTP GPEDSSSSSG 540
 KKAGIPRDSY SGDALYDLYA DPGDSPATLP GGDNEETSS LSRLKPVSPG TITCPLRTPG 600
 SLKDSKIP I SIKHLTNLPS SHPVVHQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660
 ATACHDSAKK L

10 Seq ID NO: B54 DNA sequence
 Nucleic Acid Accession #: NM_014138.1
 Coding sequence: 60..854

15 1 11 21 31 41 51
 CTGCAGAGAC TTCCCAGGAA GGTCCAGCGC CCTCTCAGCC TTCGTACTCA GAACAGCCGA 60
 TGATGGGCTT CATTAACCTG AGCCCCGCTC CTGGCCCCAG CCAGGCCGTG CCTCTCCCAG 120
 AGGGGCTGCT CCCCCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA 180
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCGCG 240
 ATCACATGGC CCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCCTCATTA GGTGACAGAA 300
 20 GTCAAGATCG ATTCGATGT GAATGTCTG ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360
 GGATCCCTGG GAGAGATTAAC AGGGCCCCAC ATCCTCTCTC CTGGGAGACG CTGGTGACGG 420
 GGCTCAGTGG CTTCAGCTCTC AGCCTAGGCA CCAACCAGCC CGGCCCTCTG CCTGAAGCGG 480
 CACTCCAGCC ACAGGAGACA GAGGAGAAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCATG 600
 25 GGATGAGAC CCGAAGGAGC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGTGTGGGC 660
 CCATTTTGGG GACCAACACG CAAGCTGTGG TCGGATGAGT GCCAGGACCT GTGTACCGGG 720
 ACAGTGGA GAATCTCCAG CATGATGCTT GACTGACCGG AGGAAGGTCC TCATGTTTCG 780
 TGCTGTGCTT TCTCGATGG CTGTGAGGCA TTCCTTGGCA AGGGACGCTC CGTACCAGCG 840
 GTCTCACCG CACTCACAT GGCTCCTGTG ATGCATGTTG TGCTTTCTCC ACCCGGGATC 900
 30 TCCATCTCTC TTCCCTCTCT GCTGTCTAGT AGAGATCACA TGCTGTGTA GTGTGAATGC 960
 CTGTGCTCTG TCCTGTGCTT TTGCACCAT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020
 GCCTGTTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAAATGGG AGGTAAACGC 1080
 AGTGTGGGAA AGGAATGTGG AATGAGAATC TGGTGGTTCA CCGCTGTACT ATTTGTGTAA 1140
 ATGTTTACGT ATGTGATAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200
 35 TAGTAGTCTC CCTTACAGGA ATTTTGAAG GGGTTCCTCA TCATCAATAC CAAATAAATA 1260
 TATGTAGGAA TGGAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1320
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA

40 Seq ID NO: B55 Protein sequence
 Protein Accession #: NP_054857.1

45 1 11 21 31 41 51
 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRWE RLEFLQRKKA FLRHVRRRHR 60
 DEMAPYAVGR EARISPLGDR SQNRFRBCSR YCQSHRPNLS GIPGESNRAP HPSSWETLVQ 120
 GLSGITLSLG TNQPGPLPEA ALQPQSTEEK RQRERQQESK IMPQRLKQW LEEN

50 Seq ID NO: B56 DNA sequence
 Nucleic Acid Accession #: NM_000025.1
 Coding sequence: 198..1424

55 1 11 21 31 41 51
 GCTACTCTCT CCCCAAGAGC GGTGGCACCG AGGGAGTTGG GGTGGGGGGA GGCTGAGCGC 60
 TCTGTGCTGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTGCCTCTC ATGCCCTGCT 120
 GTCCCCCTCC CTGAGCCAGG TGATTTGGGA GACCCCTCTC TTCCTTCTTT CCCTACCGCC 180
 CCAAGCGGGA CCGCGGAGTG GCTCCGTGGC CTCACAGAAA CAGCTCTCTT GCCCCATGGC 240
 CGGACCTCCC CACCCTGGCG CCCAATACCG CCAACACCA GGGGCTGCCA GGGGTTCCGT 300
 60 GGGAGGCGGC CCGAGCCGGG GCCCTGCTGG CGCTGGGGGT GCTGGCCACC GTGGGAGGCA 360
 ACCTGCTGGT CATGCTGGCC ATCGCTGGA CTCGAGACT CCAGACCATG ACCAACGTGT 420
 TCGTGACTTC GCTGCGCGCA GCCGACCTGG TGATGGGACT CCTGGTGGTG CCGCGGCGG 480
 CCACCTTGGC GCTGACTGGC CACTGGCCGT TGGGCGCCAC TGGCTGCGAG CTGTGACCT 540
 CGGTGGAAGT GCTGTGTGT ACCGCCAGCA TCGAAACCT GTGCGCCCTG GCCGTGGACC 600
 65 GCTACCTGGC TGTGACCAAC CCGCTGGGTT ACGGCGCACT GGTCAACCA GCTGCGGCC 660
 GGACAGCTGT GGTCTGGTG TGGGTGTTG CGGCGCGGTT GTGTTTGGG CCCATCATGA 720
 GCCAGTGGTG GCGGTAGGG GCCGACCGCG AGGCGCAGCG CTGCCACTCC AACCGCGCT 780
 GCTGTGCTTT CGCTCCCAAC ATGCCCTACG TGCTGTCTGT CTCCTCCGTC TCCTTCTACC 840
 TTCTCTCTCT CGTGATGCTC TTCTGTCTAG CGCGGGTTT CGTGTGGCTC ACGCGCCAGC 900
 70 TGCGCTGCTC GCGCGGGGAG CTGGGCGGCT TTCCGCCCGA GGAGTCTCCG CCGCGCGCT 960
 CGCGCTCTCT GCGCCCGGCC CCGGTGGGGA CGTGGCTCC GCCCGAAGGG GTGCGCGCT 1020
 GCGGCGGGCG GCGCGCGGCG CTCCTGCTCT TCCGGGAACA CCGGCGCTG TGCACTTGG 1080
 GTCTCATCAT GGGCACCTTC ACTCTCTGCT GGTGTGCCCT CTTTCTGGCC AACGTGCTGC 1140
 GCGCCCTGGG GGGCCCTCTC CTAGTCCCGG GCGCGGCTTT CCTTGCCTTG AACTGGCTAG 1200
 75 GTTATGCCAA TTCTGCTCTC AACCCGCTCA TCTACTGCGG CAGCCCGGAC TTTGCGAGCG 1260
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 CCGCGCGGCG CCGCTTCCCG TCGGCGGCTC CTGCGCGCGG GAGCAGCCCA GCGCAGCCCA 1380
 GCGTTTGGCA ACGGCTCGAG GGGGCTTCTT GGGGAGTTTC TTAGGCTTGA AGGACAGAAA 1440
 80 GCAACAATCT GTTGTATCAG AACCTGTGGA AACCTCTGG CCTCTGTTCA GAATGAGTCC 1500
 CATGGGATTC CCGCGCTGTC AACTCTACC CTCAGAACCC TGACGACTGG GCCATGTGAC 1560
 CCAAGGAGGG ATCTTACCA AGTGGGTTT CACCATCTCT TTGCTCTCTG TCTGAGAGAT 1620
 GTTTTCTAAA CCCCAGCCTT GAACTTCACT CCTCCCTCAG TGGTAGTGTG CAGGTGCGGT 1680
 GGAGCAGCAG GCTGCTTTG GTAGGGGCGC CCATCACCGG GCTTGCCTGT GCAGTCAGTG 1740
 AGTGCTTAGG GCAAGAGAG CTCCCTGGT TCATTCCTT CTGCCACCA AACCTGATG 1800

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTGGGG GTTTTATCTC TGGTTCCTCT ATTACTGCTC TCAAGCAGTG GCCTCTCTCA 1920
CTTTAGCCAT GGAATGGCTC CGATCTACCT CACAGCAGTG TCAGAAGGAC TTGGCCAGGG 1980
TTTGGGAGC TCCAGGGTTC ATAAGAAGGT GAACCATTAG AACAGATCCC TTCITTTCTC 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TGCAGTTCAT CCTCGGCCCA CTTTCCCTCC 2100
GTTTGTTCCT TTTCATAAT CCACCTTACT CCTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCAGT AAATTAGGCC TAATCCTCAC TCTTTTCTTC CTAATCTTCA TCAACAAAAA 2220
AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCCCTCCTG AAACCTCTGA AATCCAGTTG CCATGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400
GCATTTGTCC CTTCAATGCT ATAATCCAGT GGTGCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGCGTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGSCA CAAAGCAITG CTTGGGTTGG 2520
TCAAATGTCT TGTGTCAATA ATATATTCTG ATGTTTCCCA GCCTTTCCAC AACCTCTACC 2580
TTCCCACTCA CCTTCCCGAG CTACAAAAAT CTGTATTATC CTCTTAAAGT AAAACTGGAG 2640
TTAC

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Seq ID NO: B57 Protein sequence
Protein Accession #: NP_000016.1

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30

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1 11 21 31 41 51
MAPWPHENSS LAPWFDLPTL APNTANTSGL PGVPWEAALA GALLALAVLA TVGGNLLVIV 60
AIANTPRLQT MTNVFVTSIA AADLVMGLLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
VTASIELTCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VWVSAAVSF APIMSQNHRV 180
GADAEQQRCH SNPRCCAFAS NMPYVLLSSS VSFYLFLLVM LFVYARVFWV ATRQLRLLRG 240
ELGRFPPEES PPAPRSRLAP APVGTCAPE GVPACGRRPA RLLPLREHRA LCTLGLIMGT 300
FTLCWLPFFL ANVLRALGGP SLVPGPAFLA LNWLGYSANSA FNPLIYCRSP DFRSAFRRL 360
CRGRRRLPFB PCAAARPALF PSQVPAARSS PAQPRLCQRL DGASWGV

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Seq ID NO: B58 DNA sequence
Nucleic Acid Accession #: NM_032553.1
Coding sequence: 37..1038

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ATTCTTGTGC CAGGTCTCAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180
AAAGAAACAA AACGAGCTGT GATATTTATG ATAAACTTAG CCATTGCTGA CTTACTACAA 240
GTCTTTCTCT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300
GGTCTCTGCA TGTTCGTGTT CTACCTGAAG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGCTCTGCA TCASTGTGCG ACGATTTTGG TTCTCTCATG ACCCTTTTGG CTTCCATGAC 420
TGCAACAGCA AATATGACCT GTACATCAGC ATTGCTGGCT GGTGATCAT CTGCCITGCC 480
TGTGTACTCT TTCCACTCCT CAGAACCACT GATGATACCT CTGGCAATAG GACCAATGC 540
TTTGTGGATC TTCTTACCAG GAATGTCAAC CTGGCCCACT CCGTTGTTAT GATGACCAAT 600
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GTTTTATATC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
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CAGAACATAT CTGCAATACC CAAGCCACAG GGAAGAACTT GCAAAACAAC ACAGCTTTTC 1140
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Seq ID NO: B59 Protein sequence
Protein Accession #: NP_115942.1

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MYFPRFHDCK QKYDLYISIA GWLIICLACV LPPLRLTSDS TSGNRTKCPV DLPTRNVNLA 180
QSVVMTIGE LIGFVTEPLLI VLYCTWKTIV SLQDKYPMAQ DLGEKQKALK MILTCAGVFL 240
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Seq ID NO: B60 DNA sequence
Nucleic Acid Accession #: CAT cluster

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	CACATAATTAA	CAGAGTGTCA	ATTATGCTAA	CATCTCATTT	ACTGATTTTA	ATTAAAAACA	720
	GTITTTGTGA	ACATGCTATG	TTAGGGTTGG	CTTCTTAATA	ATTCTCTCTT	CCTCTCTCTT	780
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	CAGAAAACAG	GCAGATGATA	ATGATGAAGA	AAAGAAAAAA	GAAGAAGAAG	CATTCCCCCTA	3480
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10 Seq ID NO: B62 Protein sequence
 Protein Accession #: NP_055337.1

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 LAKDNGVPPV TSNVTVFVSI IDQNDNSPVF THNEYNFYVP ENLPRHGTVG LITVIDPDY 600
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35 Seq ID NO: B63 DNA sequence
 Nucleic Acid Accession #: XM_059180.2
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	ATATATTGTT	TCTGTACAAA	AATGACTGTA	TTCTCTCACC	AGTAGGACTT	AAACTTTGTT	4320
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	AGCCTACATC	ACCAAGGTCT	CTGTGTCAAA	CCTGTGGCCA	CTCTATATGC	ACTTTGTTTA	5040
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Seq ID NO: B64 Protein sequence
Protein Accession #: A39577

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50	DNEQSVNRHS	PKKQNGYBK	KKIPDATPLL	DASSLEYLFA	QGGYDLVKCL	APIRDPKTEQ	180
	DGHDIEENCL	GMVLAISHY	AMMKMKQLPE	LPKDISYKRY	IPETLNKISR	QRNLLTRMRI	240
	NNVFDPLKE	PNKLTICDSS	VSTHDLKVYK	LATLETLTKH	YGAEIFPESM	LLISSEENEMN	300
	WEHSDNGGVN	LYEVMVTGN	LGIQWRHKPN	VVSVEKEKNK	LKKKLEKNK	KKDEEKNKIR	360
	BEWNNSFFPP	EITHIVIKES	VVSINKQDNK	KMELKLSHE	EALSFVSLVD	GYFRLTADAR	420
55	HYLCTDVAPP	LIVHNIQNGC	HGPICTEYAI	NKLRQEGSEE	GMVVLNWSCT	DFDNILMTVT	480
	CFEKSQVQGG	AQKQFNFQI	EVQKGRYSLH	GSDRSFPLSG	DLMHLKKQI	LRTDNISFML	540
	KRCQPKPRE	ISNLLVATKK	AQEQPVVYPM	SQLSFDRILK	KDLVQGEHLG	RGRTRHIYSG	600
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	VENIMVEEFP	EGGPLDLFMH	RKSDVLTTFW	KPKVAKQLAS	ALSYLEDKDL	VHGNVCTKNL	720
60	LLAREGIDSE	CGPFIKLSDP	GIPITVLSRQ	ECTERIPWIA	PECVEDSKNL	SVAADKWSFG	780
	TTLWEICVNG	EIPLDKTLI	EKERFYESRC	RPVTPSCKEL	ADLMTRCMNY	DPNQRPFYRA	840
	IMRDINKLEE	QNPDIVSRRK	NQPTFVDPHT	FEKRFLLKIR	DLGEGHFGKV	ELCRYDPEDN	900
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65	SGSLKEYLPK	NKNKNLKKQ	LKYAVQICKG	MDYLGSRQYV	HRDLAARNVL	VESEHQVKIG	1020
	DFGLTKAIET	DKEYYTVKDD	RDSPVFWYAP	ECLMQSKFYI	ASDVWSFGVT	LHELLTYCDS	1080
	DSSPMALFLK	MIGPTHGQMT	VTRLVNTLKE	GKRLPCPPNC	PDEVYQLMRK	CNEFPQSNRT	1140
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Seq ID NO: B65 DNA sequence
Nucleic Acid Accession #: NM_004867.1
Coding sequence: 140..931

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	CGCAGCCCGA	AGATTCACTA	TGGTGAAAT	CGCCTTCAAT	ACCCCTACCG	CCGTGCAAAA	180
	GGAGGAGGCG	CGGCAAGACG	TGGAGGCCCT	CCTGAGCCGC	ACGGTCAGAA	CTCAGATACT	240
	GACCGGCAAG	GAGCTCCGAG	TTGCCACCCA	GGAAAAAGAG	GGCTCCTCTG	GGAGATGTAT	300
80	GCTTACTCTC	TTAGGCTTTT	CATTATCTT	GGCAGGACTT	ATTGTTGGTG	GAGCCTGCAT	360
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	TGAGGATCCT	GCAAAATCCC	TTGCTGGAGG	AGAGCCTAAC	TTCTGCTGCT	TGACTGAGGA	480
	GGCTGACATT	CGTGAGGATG	ACAACATTGC	AATCATTGAT	GTGCTGTGCC	CCAGTTTCTC	540
	TGATAGTGAC	CCTGCAGCAA	TTATTATGTA	CTTTGAAAAG	GGAATGACTG	CTTACCTGGA	600
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Seq ID NO: B66 Protein sequence
 Protein Accession #: NP_004858.1

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Seq ID NO: B67 DNA sequence
 Nucleic Acid Accession #: XM_083862.1
 Coding sequence: 121..813

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Seq ID NO: B70 Protein sequence
Protein Accession #: NP_002966.1

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RGDENPAGTV EGKEDWEMEE DQEEEEEEEA TPTPSSGSPS SPTPEDIVTY ILGRLAGLDA 120
10    GLHQLHVRHL ALDTRVVELT QGLRQLRNAA GDTRDAVQAL QEAQGRAERE HGRLEGCLKG 180
      LRLGHKCFLL SRDFFEAQAAA QARCTARGGS LAQPADRQQM EALTRYLRAA LAPYNWPVWL 240
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      SDDGSWWHDH CQRRLYVCE FPF

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Seq ID NO: B71 DNA sequence
Nucleic Acid Accession #: BC000839.1

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25    GAGAGCTCTG TGTGTGCAAT GTTCAGCCCA CAAGAGCTTA CTGGTGAAGG AATGGGACAA 360
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      GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTTGCT 840
      GTGTATCACA TTTCTGTATT TTATCACCCC CTTCCTGCAA CATTATTAT CTGGAATCTA 900
35    CTGCCCCTTT TGTTTTTTAG ATACAAGGGC TTGTTTTTGT TACCCAGGCT GGTTCAGAG 960
      CCATAGCTTT AAGAGATCTT CTCACCACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
      TTCATGGCAC CGCAGCTTTG CTGCCCTTCT TACATGATCC AGGCCACGAA CCCAACTCAA 1080
      GGCACCTGAT AGATGACCAC TTTCGTAAAC TACTGACCTA GCTTGTGTCC AATGTGTGAT 1140
      TGAACCTCCC ATAACCTCAC TTCGTGCTGT TTCCTCTGTA TACAGCCACC TTCGTGTCCC 1200
40    GTCATGAGCC TTATGCTCTC CATTTGCATA TTGCAAAATC TATGTTCCAT GTAGGTAGCT 1260
      CATTGAGGGC CTGCTCTTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCAATTTG 1320
      TGTGCTGTGT TTGTTGTGTG ATGAAAAATA TAAATGATT GATTACATAA AAAAAAATAA 1380
      AAAAAA

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Seq ID NO: B72 DNA sequence
Nucleic Acid Accession #: CAT cluster

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45      1      11      21      31      41      51
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TGCTAGTAGG GCCTGGGTTA ATGGGCCGAG GGTGGCTTGG TGGTCTTTAT AGCTGTACT 60
50    CTTTGTACTT GTCTTTTTCT TTTATTTTCT TTTGAGCGAT TGTGCGAACA TAGCATAGCA 120
      CGCACTATGG CACGAGGCTC GTGCTGCCCT GCCAGGGCGA CTGGCGGATA AGGTCTTGTG 180
      CGTGCCCTCG AGGCTTAAAA GTAGCAGTGG GGCCTTTGTA AGGACAAAAT GCGCATGGCG 240
      GGCCGTGTAG GTCCCCCTTC CTATGATGAG GACCTTTTCA CAGACCTGTA CTGAGCTCG 300
55    TGAGGATAAA TAACTCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC CGTCTGTCA 360
      GAAAAATAGC TTTTCGAAAT GCCCTGAGTT GACCTAATGT CTATTTGGG TCCTGTCTGC 420
      AGGATTTAGC OGCAGCTTGG AACCGAAGAG AGCTCTGTGG TTGCAATGTT CAGCCACAA 480
      GAGCTTACTG GTGAAGGAAT GGGACAAGAC CCATCTTTAT GCRAAGCCAG CGTTACAGTA 540
      ATGTTCCAGC ATCTCATAAT CTATCCTGGG GAATTCAGCT GCCTCCGAG GTGAATACAG 600
      GTATTCTGTA TGACAGTCTG CCTCTATCTT ACAGAGCAGC TTGTTGCTAT ATACCATTGA 660
60    AAAGCCCTCA GAGCTGAGAG GTACTACTAA CCAATAACCT GCTTGGCTCA AAGGGCCAGC 720
      ACCTTCTCTC TAAAGCCCAA GAGGAGTTTG AGGAAAACTA GGTGTCTGTG TTCCTCCAG 780
      GCTGAAGTTA CAGGTCTGAG CAAATAAGGT GTATAAAAAA TGGAACTCTG CTGGAAGGAC 840
      ATCAGAAGGT GAATTTTCCA AGTTCTTGGG CAACCTAGCT GTTGAAGAGC TTTCTGGGTT 900
65    TGGGGGGTAT TTCAGATGTA CCTTAAAGTG TTAGCAGACA CAGATTAGA CACTGGGAGC 960
      CAATGAACA GCAGTTGAGG GTTTGCTGTG TATCACATT CTGTATTTTA TCACCCCTT 1020
      CCTGCAACAT TATTATCTG GAATCTACCT GCCCTTTTGT TTTTATAGATA CAAGGGCTTG 1080
      GTTTTGTATC CCAGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGATT 1140
      TCCAAAGTGC TGGGATTTGA GGTGTGATTG ATGGCACCCA GACITTTGCTG CCTTCTTAC 1200
70    ATGATCCAGG CCCAGAACCC AAACCTCAGG ACTGTATAGA TGACCACTTT CGTAAACTAC 1260
      TGACCTAGCT TGTGTCCCAT TGTGATTGTA ACTTCCCAT ACTCCACTTC GTGTCTGTTC 1320
      CTCTGTATAC AGCCACCTTC TGTTCCTGTC ATGAGCCCTT AGGTCTCCAT TTGCATATTG 1380
      CAAATACTAT GTTCCATGTA GGTAGCTCAT TCAGGGCCTT GCTCTTCACT TCAAAAAAGG 1440
      TTCCCTTGAG GACTGGCTGT CAATTTGTGT TGCTGTGTGG GTTGTGTATG AAAATAATAA 1500
      AATGATTGAT TACATAAAAA AAAAAAATAA AAAAAAATAA CAAAAAATAA 1560
75    GCGCGGCTTT TTTCCCGGGC GCACAAAGTT ATAAACGCC GTCCATC

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Seq ID NO: B73 sequence
Nucleic Acid Accession #: NM_000222.1
Coding sequence: 22..2952

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80      1      11      21      31      41      51
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GATCCCATCG CAGCTACCGC GATGAGAGGC GCTCGCGCGG CCTGGGATTT TCTCTGCGTT 60
      CTGCTCCTAC TGCTTCGCGT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120

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	CCGCTCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGCACTGA	TCCGGGCTTT	GTCAAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGG	CAGAAGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACACGCGCTA	AGCAATTTCA	TTTATGTGTT	TGTTAGAGAT	360
	CTTGCCAAAGC	TTTTCTCTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTC	CTCTCACAGA	CCCAGAAAGT	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGGCGGGCAT	CATGATCAAA	540
	AGTGTGAAAC	GCGCTTACCA	TCCGCTCTGT	CTGCATTGTT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGCTGT	CGGAAAAATT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAAGC	TGTGCTGTGT	660
	GTGTCTGTGT	CCAAAGCAAG	CTATCTTCTT	AGGGAAAGGG	AAGAATTTCAC	AGTGACGTGC	720
	ACAAATAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAACGTGGA	AAAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGCTGACT	TCAATTATGA	ACGTGAGGCA	840
	ACGTTGACTA	TCAGTTACGC	GAGAGTTAAT	GATTCCTGGAG	TGTTTATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACAACA	ACCTTGGAAG	TAGTAGATAA	AGGATTCATT	960
	AAATATCTCC	CCATGATAAA	CACCTACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTGT	1020
	ATTGTTAAAG	ATGAAGCATT	CCCCAAACCT	GAACACCAGC	AGTGGAATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAAGTAA	TATCAGATAC	1140
	GTAAGTGAAC	TTCACTTAAC	GAGATTAAAA	GGCACCGAAG	GAGGCACCTA	CACATTCTTA	1200
20	GTGTCCAATT	CTGACGTCAA	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAATCCTGA	CTTACGACAG	GCTCGTGAAT	GGCATGTCTC	AATGTGTGGC	AGCAGGATTC	1320
	CCAGAGGCGA	CAATAGATTG	GTATTTTGTG	CCAGGAACCT	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGGATGTGCA	GACACTAAAC	TCATCTGGGC	CACGCTTTGG	AAAGCTAGTG	1440
	GTTCCAGATT	CTATAGATTG	TAGTGCATT	AAGCACAAAT	GCACGTTTGA	ATGTAAGGCT	1500
25	TACAACGATG	TGGCAAGAC	TTCTGCCTAT	TTTAACTTTG	CATTTAAAGG	TAACAAACAA	1560
	GAGCAAAATC	ATCCCCACAC	CCTGTTCACT	CCTTTGTCTG	TTGGTTTCGT	AATCGTAGCT	1620
	GGCATGATGT	GCAATGATTG	GATGATTCTG	ACCTACAAAT	ATTTACAGAA	ACCCATGTAT	1680
	GAAGTACAGT	GGAAAGTTGT	TGAGGAGATA	AATGGAAACA	ATTATGTTTA	CATAGACCCA	1740
	ACACAACCTC	CTTATGATCA	CAAAATGGAG	TTTCCAGAA	ACAGGCTGAG	TTTTGGGAAA	1800
30	ACCTCGGGTG	CTGGAGCTTT	CGGGAAGGTT	GTGAGGCCAA	CTGCTTATGG	CTTAATTAAG	1860
	TCAGATCGCG	CCATGACTGT	CGCTGTAAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGGAAGCCG	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TTGGTAATCA	CATGAATATT	1980
	GTGAATCTAC	TTGGAGCCTG	CACCATTTGA	GGGCCCAACC	TGGTCATTAC	AGAATATTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTGAGA	AGAAAACGTG	ATTCAATTAT	TGTTTCAAAG	2100
35	CAGGAAGATC	ATGCAGAAGC	TGCACCTTAT	AAGAATCTTC	TGCATTCAAA	GGAGCTCTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGCCCG	ACAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCCCGCATCA	TGGAGGATGA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAGGTGG	CAAAGGGCAT	GGCTTTCCTC	GCCTCCAAGA	ATTGTATTCA	CAGAGACTTG	2400
40	GCAGCCAGAA	ATATCCTCCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTTGTGCTA	2460
	GCAGAGACAA	TCAAGAAATGA	TTCTAATATT	GTGGTTAAAG	GAAACGCTCG	ACTACCTGTG	2520
	AAGTGTGATG	CACCTGAAAG	CATTTTCAAC	TGTGTATACA	CGTTTGAAGG	TGACGTCTGG	2580
	TCCTATGGGA	TTTTTCTTTG	GGAGCTGTTC	TCTTTAGGAA	GCAGCCCTCA	TCTTGGAATG	2640
	CCGGTCGATT	CTAAGTTCTA	CAAGATGATC	AAGGAAGGCT	TCCGATGCTC	CAGCCCTGAA	2700
45	CACGCACTCG	CTGAAATGTA	TGACATAATG	AAGACTTGCT	GGGATGCAGA	TCCCCTAAAA	2760
	AGACCAACAT	CTAAGCAAAAT	TGTTCAAGCTA	ATTGAGAAGC	AGATTTTACA	GAGCACCATT	2820
	CATATTACTT	CAACCTTAGC	AAACTGCAGC	CCCAACCGAC	AGAAGCCCGT	GGTAGACCAT	2880
	TCGTGTGGGA	TCAATTTCTG	CGGCAGCACC	GCTTCTCTCT	CCAGCCTCTC	GCTTGTGCAC	2940
	GACGATGTCT	GAGCAGAATC	AGTGTTTGGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCTTCCATGA	TGGTTATTTT	CTTTTCTTTC	AACTTGCACT	CAACTCCAGG	ATAGTGGGCA	3060
	CCCCACTGCA	ATCCTGTCTT	TCTGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTCATCAGC	3120
	CACCACTCTA	TTGCAAAAGT	TCCAACCTGA	TATATTCCCA	ATAGCAACGT	AGCTTCTACC	3180
	ATGAACAGAA	AACTTTCTGA	TTTGGAAAAA	GAGAGGGAGG	TATGACTGCG	GGGCCAGAGT	3240
	CCTTTCCAG	GCTTCTCCAA	TTCTGCCCAA	AAATATGGTT	GATAGTTTAC	CTGAATAAAT	3300
55	GGTAGTAATC	ACAGTTGGCC	TTCAGAACCA	TCCATAGTAG	TATGATGATA	CAAGATTAGA	3360
	AGCTGAAAC	CTAAGTCTCT	TATGTGAAAG	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAAG	AATCTAGTAT	TTCACTGCTG	GAATGAGACA	TAGGCCATGA	3480
	AAAAATGAT	CCCCAAGTGT	GAACAAAGAA	TGCTCTTCTG	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGCTTTT	TAAATAGAGT	TTGCTATTAG	AGCATTTAAT	TGGAGAGAAG	3600
60	GCCTCCCTAG	CCAGCACTAG	TATATACGCA	TCTATAAATT	GTCCGTGTTT	ATACATTGTA	3660
	GGGGAACAA	CCATAAGGTT	TGTTTCTGT	ATACAAACCT	GGCATTATGT	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACACG	TAAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAAGCA	CAGTTTGAAC	AAAACTCTCT	CTTTTAGCTG	ATGAACCTAT	3840
	TCGTAGATT	CTGTGGAACA	AGCCTATCAG	CTTCAGAAAT	GCAATGTACT	CAATGGATT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCACT	GCAATGCTCC	CACAGGAGTG	GGAAAACACT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAAATAAAGT	ATAGGTTTAG	CCTCCTTGGC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTAAGTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGGCCC	TGAGTCCAA	AGGGTCTCTT	AGTACCTGAA	4140
	AAGTAACCTG	GCCTTCTATTA	TTAGTACTGC	TCTTGTCTCT	TTTACATAG	CTGTCTAGAG	4200
70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGAGTTTC	ACCTGCACTT	AAGGCACTCT	GTATTTTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATAATGC	TACTGTCTCA	CTGAAACATT	TAAATTTTAC	CCTTAGACT	4380
	GTAGCCTGGA	TATTTATTCT	GTAGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
	AACTCCCTTT	CCTCACTGCC	CAATATAAAA	GGCAAATGTG	TACATGGCAG	AGTTTGTGTG	4500
75	TTGTCTTGAA	AGATTGAGGT	ATGTTGCTTT	TATGTTTCCC	CCCTTCTACA	TTTCTTAGAC	4560
	TACATTTAGA	GAATCTGGGC	CGTTATCTGG	AAGTAACCAT	TTGCACCTGGA	GTCTTATGCT	4620
	CTGCACTTTT	TCCAAGTTGA	ACAGATTTTG	GGGTTGTGTT	GTACCCCAAG	AGATTGTGTG	4680
	TTGCCATACT	TTGCTGGAAG	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGTGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4800
	TTGCCATACT	TTGCTGGAAG	AATTCCTTTG	TGTTTCTATT	GACTTCAATG	ATAGTAAGAA	4860
80	AAGTGTGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4920
	AATGTCTTTT	GAATATTCCC	AAGCCCATGA	GTCCCTGAAA	ATATTTTFTA	TATATACAGT	4980
	AACCTTATGT	GTAAATACAT	AAGCGCGGTA	AGTTTAAAGG	ATGTTGGTGT	TCCACGTGTT	5040
	TTATTCCTGT	ATGTTGTC	ATTGTTGACA	GTTCTGAAGA	ATTC		

Seq ID NO: B74 protein sequence
Protein Accession #: NP_000213.1

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5      1      11      21      31      41      51
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PGFVKWTFEI LDETNNENKQ EWITEKAEAT NTGKYTCTNK HGLSNSIYVF VRDPAKLFLV 120
DRSLYKGEDN DTLVRCPLTD PEVTNYSLKG CQKPLPKDL RFIPDPKAGI MIKSVKRAYH 180
RLCLHCSVDQ EGKSVLSEKF ILKVRPAPKA VPVSVSKAS YLLREGEEPT VTCTIKDVSS 240
10     SVYSTNKRKN SQTKLQEKYN SWHHGDFNFE RQATLTISSA RVNDSGVFMC YANNTPGSAN 300
VTTLLEVVDK GFNIFPMIN TTVFVNDGEN VDLIVEYEA FPKPEHQMWIY MNRTFTDKWE 360
DYPKSENESE IRVYSELHLT RLKGTGGTGY TFLVSNSDVN AALAFNVYVN TKPEILTYDR 420
LVNGLQCVA AGFPEPTIDW YFCPGTEQRC SASVLPVDVQ TLNSSGPPFG KLVVQSSIDS 480
15     SAFKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPHT LFTPLLIGFV IVAGMMCIIV 540
MILTYKYLQK PMYEVQWKV EINGNNYVY IDPTQLPYDH KWEFPRNRLS FGKTLGAGAP 600
GKVVETAYG LIKSDAAMTV AVKMLKPSAH LTEREALMSE LKVLSYLGNH MNIVNLLGAC 660
TIGGFPLVIT EYCCYGDLIN FLRRKRDSFI CSKQEDHAEA ALYKNLLHSE ESSCSDSTNE 720
YMDMKPGVSY VVPTKADKRR SVRIGSYIER DVTAIMEDD ELALDLEDLL SFSYQVAKGM 780
20     AFLASKNCIH RDLAARNILL THGRITKIC FGLARDIKND SNYVVKGNAR LPVKKMAPES 840
IFNCVYTFES DVWSYGIFFW ELFSLGSSPY PGMPVDSKPY KMKIEGFRML SPEHAPAEY 900
DIMKTCDAD PLKRPTFKQI VQLIEKQISE STNHIYSNLA NCSFNRQKPV VDHSVRINSV 960
GSTASSQPL LVHDDV

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Seq ID NO: B75 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58..2298

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GGCCAGACTG GGAAGAAATC TGAGAAGGGA CCAATTGTGT GGCGGAAGCG TGTAAATCAT 120
GAGTACATGC GACTGAGACA GCTCAAGAGG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCA ATGTCAGAAA AATTTTGGAA AGAACGSAAG TCCTAAACCA AGAATGAAA 240
35     CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCTGTGA GCTCATTGCG CGGGACTAGG 300
GAGTGTTCGG TGACCAAGTA CTTGGATTTT CCAACACAAG TCATCCCATT AAAGACTCTG 360
AATGCAGTTG CTTCACTACC CATAATGTAT TCTTGGTCTC CCTACAGCA GAATTTTATG 420
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GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GAAAGTACA CGGGATAGA 540
40     GAATGTGGGT TTATAAATGA TGAATTTTIT GTGGAGTTGG TGAATGCCCT TGGTCAATAT 600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAAGAGAAGA AAAGCAGAAA 660
GATCTGGAGG ATCAGCGAGA TGATAAAGAA AGCCGCCCCC CTCGGAATTT TCCTTCTGAT 720
AAAAATTTGG AGGCCATTTC CTCAATGTGT CCAGATAAGG GCACAGCAGA AGAACTAAAG 780
GAAAAATATA AAGAACTCAC CGAACAGCAG CTCACAGGCG CACTTCCTCC TGAATGTACC 840
45     CCCAACATAG ATGACCAAAA TGCTAAATCT GTTCAGAGAG AGCAAAAGCTT ACACCTCTTT 900
CATAGCTTTT TCTGTAGCGG ATGTTTTAAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCAACCA CTTATAAGCG GAAGAACACA GAAACAGCTC TAGACAAACA ACCTTGTGGA 1020
CCACAGTGTT ACCAGCATTT GGAGGGAGCA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCACCAAAA ACGTCCAGGA GGCCGAGAAA GAGGACGGCT TCCCAATAAC 1140
50     AGTAGCAGCG CCAGCACCCC CACCATTAA TGTCTGGAAT CAAAGGATAC AGACAGTGAT 1200
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GATGAACCTT CGAGCTCCTC TGAAGCAAA TCTCGGTGTC AAACACCAAT AAGATGAAG 1320
CCAAATATTG AACCTCCTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAGA 1380
GTCCCTCATG GCACTTACTA TGACAATTTT TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
55     ACATGTAGAG AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
GCTGAGGATG TGGTACTCTC TCCAAGGAAA AAGAAGAGGA AACACCGGTT GTGGGCTGCA 1560
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CCCTGTGATC ATCCAGGCA GCCTTGTGAC AGTTCGTGCC CTGTGTGAT AGCAGAAAAT 1680
TTTTGTGAAA AGTTTGTGCA ATGTAGTTCA GAGTGTCAAA ACCGCTTTCC GGGATGCCGC 1740
60     TGCAAGACAG AGTGCAACAC CAAGCAGTGC CGTGCTTACC TGGCTGTCCG AGAGTGTGAC 1800
CCTGACCTCT GTCTTACTTG TGGAGCGGCT GACCATTGGG ACAGTAAAAA TGTGTCTGTC 1860
AAGAAGTGA GTATTACAG GGGCTCCAAA AAGCATCTAT TGCTGGCACC ATCTGAAGTG 1920
GCAGGCTGGG GGATTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
TGTGGAGAGA TTATTCTCA AGATGAAGCT GACAGAAGAG GGAAGTGTA TGATAAATAC 2040
65     ATGTGCAGCT TTCTGTTCRA CTGGAACAA TATTTTGTGG TGGATGCAAC CCGCAAGGGT 2100
AACAAAATTC GTTTTGCAAA TCATTGCGTA AATCCAAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCACAGGAT AGGTATTTT GCCAAGAGAG CCATCCAGAC TGGCGAAGAG 2220
CTGTTTGTGG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTCCG CATCGAAGA 2280
70     GAAATGAAA TCCCTTGACA TCTGCTACCT CTCCTCCCTC CTCTGAAAAC GCTGCCCTAG 2340
CTTCAGGAAC CTCGAGTACT GTGGGCAATT TAGAAAAAGA ACATGCAGTT TGAATTTCTG 2400
AATTGCAAA GTACTGTAG AATAATTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAGTGAATT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAAGTGA AAATAAAAAA AAAAAA

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Seq ID NO: B76 Protein sequence
Protein Accession #: NP_004447

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80     1      11      21      31      41      51
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QQRRIQPVHI LTVSSSLRGT RECSVTSLDL PPTQVPLPK LNAVASVPIM YSWSPQQNF 120
MVEDETVLHN IPYMGDEVLD QDGTIEBELI KNYDGKVHGD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDPEREERKQ KDLEDHRDDK ESRPPRKFPK DKILEAISSM FPDKGTAEEL 240
KEKYKELTEQ QLPALPPEC TPNIDGPNK SVQREQSLHS FHTLFCRCRF KYDCFLHPFH 300
ATPNTYKRKN TETALDNKPC GPQCYQHLEG AKBFAAALTA ERIKTPPKRP GGRRRGRLPN 360

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NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEBEK KDETSSSSSEA NSRCQTPIMK 420
KPNIEPPENV EWSGAEASMF RVLIGTYIDN FCAIARLIGT KTCRQVYEFR VKESSIIAPA 480
PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDHPRQPC DSSPCPVIAQ 540
NFCBKFCQCS SECQNRFPQC RCKAQNTKQ CPCYLAVREC DFDLCLTCGA ADHWDSDNVS 600
CKNCISQGRS KKHLLAPSD VAGWGIPIKD PVQKNEFISE YCSEIISQDE ADDRKGKYDK 660
YMCSPFLNIN NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
ELFVDYRYSQ ADALKVVGIE REMEIP

Seq ID NO: B77 DNA sequence
Nucleic Acid Accession #: NM_007015
Coding sequence: 1..1005

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AAGGTGGGAG CCGTGGTCTT CATTTGCGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGAGAGCC 300
TTTAAATGGG GAAGTGGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC 360
ACAGGAATTC GTTTTGTCTG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
ATTCTGAGGG TGGGCGCGGT GACCAACAG AGCATCTCCT CCAAACTGGA AGGCAAGATC 480
ATGCCAGTCA AATATGAAGA AAATTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
GACACACAGT TCTTGAGTTC TAAGGTGTTA GAACTCTGCG GTGACCTTCC TATTTTCTGG 600
CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGAAGAA GAGAAGTGGT AAGAAAAATT 660
GTTCCAACTA CCACAAAAG ACCACACAGT GGACCAACGA GCAACCCAGG CGCTGGAAGA 720
CTGAATTAATG AAACAGAGACC CAGTGTTCAG GAGGACTCAC AAGCCTTCAA TCCTGATAAT 780
CCTTATCATC AGCAGGAAGG GGAAGAGCATG ACATTGACC CTAGACTGGA TCAAGGAAGA 840
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GGGGGCTATT ACCCATGGCC TTATAATTAT CAAGGCTGCC GTTCGGCCCTG CAGAGTCATC 960
ATGCCAATGA GCTCGTGGGT GGCCCGTATC TTGGGCATGG TGTGAAATCA CTTTATATAT 1020
CAGTGTCTGT AAAATAAGAA CTAGCTGAAG AGACAACCAA AGAAGCATTG AGGCAGGTTG 1080
ATGCTGATGG GACCATAAAG TATTTTACA CGCAGCCTGA GCGGTATTTC TTGACACTCT 1140
TAACAGAATT TTTTAAATCG TTTTCCAGAA CTTTAGTATA TGCAATGCA CTGAAGGGT 1200
AGTTCAAGTC TAAATGCCA TAACCCCGTT ATTTGTTATT TTTTATTGCG ATTGATTGCG 1260
CATAAGTCTT CCCTTGCTTG CATCTTCCAA AGCTATTTCG AAATAAACAC GAAAAATTAC 1320
AGTTTGCC

Seq ID NO: B78 Protein sequence
Protein Accession #: NP_008946

1 11 21 31 41 51
45
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60
65
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75
80

MTNSDKVPI ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISG AVLLLFAGIG 60
AFYFWKGS DS HYNNVHYTMS INGLQDQSM EIDAGNNLET PKMGSGAEEA IAVNDFQNGI 120
TGIRFAGG EK CYIKAAQVKAR IPEVGAUTKQ SISKLEGGKI MPVKYEENSL IWVAVDQPVK 180
DNSFLSKVL ELCDLPIFW LKPTYPEIKI RERREVRVKI VPTTTKRPHS GPRSNPAGGR 240
LNNETRPSVQ EDSQAFNEDN FYHQQEGESM TFDPRLDHEG ICCIECRRSY THQKICEPL 300
GGYYPWPYNY QGCRSACRVI MPCSWWVARI LGMV

Seq ID NO: B79 DNA sequence
Nucleic Acid Accession #: NM_012449.1
Coding sequence: 66..1085

1 11 21 31 41 51
55
60
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70
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80

COGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
AATTAATGGA AAGCAGAAAA GACATCACA ACCAAGAAGA ACTTTGGAAG ATGAAGCCTA 120
GGAGAAATTT AGAAGAAGAC GATTATTTGC ATAAGGACAC GGGAGAGACC AGCATGCTAA 180
AAGACCTGT GCTTTTGCA TTTGACCAAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
CAGAACCTCA GCACACACAG GAACTCTTTC CACAGTGGCA CTTGCCAATT AAAATAGCTG 300
CTATTATAGC ATCTCTGACT TTTCTTTACA CTCTCTGAG GGAAGTAATT CACCCTTATG 360
CAACTTCCCA TCAACAATAT TTTTATAAAA TTCCAATCCT GGTCAATCAAC AAAGTCTTGC 420
CAATGGTTTC CATCACTCTC TTGGCATTGG TTTACCTGCC AGGTGTGATA GCAGCAATTG 480
TCCAACCTCA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
TAACAGAAAA GCAGTTTGGG CTCTCTAGTT TCTTTTTCG TGTACTGCAT GCAATTTATA 600
GTCTGTCTTA CCAATGAGG CGATCCTACA GATACAGAT GCTAAACTGG GCATATCAAC 660
AGGTCCAACA AAATAAGAA GATGCCTGGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720
ATGTGTCTCT GGAATTTGTG GGATTGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780
CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCATA TATTCAAGAG AAGCTAGGAA 840
TTGTTTCCCT TCTACTGGGC ACAATACAG CATTTGATTT TGCCCTGGAAT AAGTGGATAG 900
ATATAAAACA ATTTGTATGG TATACACCTC CAACTTTTAT GATAGCTGTT TTCCTTCCAA 960
TTGTTGTCTT GATATTTAAA AGCATACTAT TCCTGCCATG CTTGAGGAAG AAGATACTGA 1020
AGATTAGACA TGGTTGGGAA GACGTCACCA AAATTAACAA AACTGAGATA TGTTCACAGT 1080
TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
TCAAGTTTGT ATTTGTTAAT AAAATGATTA TTCAAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence
Protein Accession #: NP_036581.1

1 11 21 31 41 51
80

MESRKDITNQ EELWKMPPRR NLEEDDYLHK DTGETSMLKR FVLLHLHQTA HADEFDCPSE 60
LQHTQELFPQ WHLPKIAAI IASLTFLYTL LREVIHPLAT SHQQFYFKIP ILVINKVLP 120

VSITLLALVY LPGVIAAIQV LHNGTKYKKP PHWLDKNMLT RKQFGLLSFF FAVLHAIYSL 180
 SYPMRRSYRY KLLNWAYQQV QQNKEDAWIE HDVVRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 VSDSLTWREF HYQSKLGIIV SLLLGTIHAL IFANWKHIDI KQFVWYTPPT FMAVFLPIV 300
 VLIFKSILFL PCLRKILKI RHGWEDVTKI NKTEICSQL

Seq ID NO: B81 DNA sequence
 Nucleic Acid Accession #: NM_000684
 Coding sequence: 87..1520

10 1 11 21 31 41 51
 | | | | |
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 CCGGCCCCCG GCTCCGAG CTGGGCATGG GCGGGGGGT GCTGTCCTG GGCGCTCCG 120
 AGCCCGGTAA CCTGTCTCG GCCGCACCG TCCCGACGG CCGGCCACC GCGGCGCGG 180
 15 TGCTGTGTC CCGTCTCGG CCGGCTCTG TGCTGCTCC CGCCAGCGAA AGCCCGGAGC 240
 CGCTGTCTCA GCAGTGAGC GCGGGCATGG GTCTGCTGAT GCGCTCATC GTGCTGCTCA 300
 TCGTGGCGGG CAATGTCTG GTGATCTGG CCATCGCCAA GACGCGCGG CTGCAGACG 360
 TCACCAACCT TTCTATCAT TCCTTGCCA GCGCGACCT GGTCTGGGG CTGCTGGTGG 420
 TGCCGTTCCG GTCCACCATC GTGGTGTGG GCGCTGGGA GTACGCTCC TTCTTCTCG 480
 20 AGCTGTGGAC CTCAGTGGAC GTGCTGTGG TGACGGCCAG CATCGAGACC CTGTGTGTCA 540
 TTGCCCTGGA CCGCTACCT GGCATCACCT CGCCCTCCG CTACAGAGC CTGCTGACGC 600
 GCGGCGCGG GCGGGGCTC GTGTGACCG GTGGGGCAT CTCGCGCCG GTGTCTCTCC 660
 TGCCCATCT CATGCACTG TGGCGGGCG AGAGCGACGA GCGCGCGCG TGCTACAACG 720
 ACCCAAGTG CTGCGACTT GTCAACCAAC GGGCTACGC CATCGCTCG TCGTAGTCT 780
 25 CCTTCTACGT GCCCTGTGC ATCATGGCCT TCGTGTACT GCGGGTGTTC CGGAGGCGCC 840
 AGAAGCAGGT GAAGAAGAT GACAGCTCG AGCGCGTTT CCTCGCGGC CCAGCGCGG 900
 GCGCTCGCC CTCGCTCTG CCGCTCCCG CCGCGCGCC GCGCGCGGA CCGCGCGCC 960
 CCGCGCGCG CCGCGCGCC CCGCGCTGG CCAACGGCG TGCGGTAA GCGCGCGCT 1020
 CGCGCTCTG GCGCTACGC GAGCAGAGG CGCTCAAGC GCTGGGCATC ATCATGGCG 1080
 30 TCTTCAAGCT CTGCTGGCTG CCTTCTTCC TGSCCAAGT GGTGAAGGCC TTCCACCGCG 1140
 AGCTGGTGG CAGACGCTC TTCTCTTCT TCACTGGCT GGGCTACGC AACTCGGCT 1200
 TCAACCCAT CATCTACTG CCGACGCGG ACTTCCGCA GGCCTTCCG GAGTGTCT 1260
 GCTGCGCGG CAGGCTGCG CCGCGCGCC ACGGACCCA CGGAGACCG CCGCGCGCT 1320
 CGGGCTGTCT GCGCGCGCC GAGCCCGCG CATCGCCCG GCGCGCTCG GAGCAGCAG 1380
 35 ACGACAGTG CCGCGCGCC ACGCGCGCG CCGCGCTGCT GAGGCCCTG GCGCGCTGCA 1440
 ACGCGCGGG CAGCGCGGAC AGCGACTCG GCGTGAAGA GCGGTGCGC CCGCGCTCG 1500
 CCTCGGAAT CAGGTGTAG GCGCGCGCG GCGCGCGGA CTCGCGGAC GCGTCTCCAG 1560
 GGAACGAG AGATCTGTG TTACTTAAGA CCGATAGCA GTGAAGTCA AGCCCAAT 1620
 40 CTGCTCTGA ATCATCCG GCAAGAGAA AAGCCACGA CCGTTGCACA AAAAGGAAG 1680
 TTTGGGAAG GATGGGAG TGGCTGTCT ATGTTCTTG TTG

Seq ID NO: B82 Protein sequence
 Protein Accession #: NP_000675.1

45 1 11 21 31 41 51
 | | | | |
 MGAGVLVLA SEPGNLSSAA PLPDGAATAA RLLVPASPPA SLLPPASESP EPLSQWNTAG 60
 MGLLMALIVL LIVAGNLVLI VAIKTRPLQ TLNLFIMSL ASADLVMLGL VVPFGATIVV 120
 WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLL TRARARGLVC 180
 50 TWATISALVS FLPIIMHWR AESDEARRCY NDPKCCDFVT NRAYAIASS VSFYVPLCIM 240
 AFVYLRVRE AQRQVKIDS CERRFLGSPA RPPSPSPSPV PAPAPPPGPP RPAATAATAP 300
 LANGRAGRFR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVPRDLFV 360
 PFWNLGYS AFNPIIYCRS PDRKAFQGL LCCARRAARR RHATHGRPR ASGCLARPGP 420
 PPSPGAASDD DDDDVVGATP PARLLEFWAG CNGGAADSD SSLDEPCRPG FASESKV

Seq ID NO: B83 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence: 2..421

60 1 11 21 31 41 51
 | | | | |
 GGCTCAGCTG CCGGGCTGCT CCGGTTGGAA ACGCCAAGCC AGCTGCGGTC CTAATCCAAA 60
 AGCCATGAAC AGCGGCTGT GCTGTGCGT GCTGATGGG GTACTGGCGG CTGGGCGCT 120
 GACGACGCG GTGCTCCCG CAGATCCCG GCGCTCCGG CTGACGCGG CAGAGAGGC 180
 65 GCCCGTAGG CAGCTGAGG TATCGCAGAG AACGGATGGC GAGTCCCGG CCGACCTGG 240
 CGCCCTGCTG GCAAGATACA TCCAGCAGG CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300
 CGTTAAGAAC CTGCAGAAC TGGACCCAG CCACAGGATA AGTGACCGG ACTACATGG 360
 CTGGATGGAT TTTGGCGCT GCAGTGCGA GGAGTATGAG TACCCCTCT AGAGGACCA 420
 70 GCGCCATCA GCCCAACGA AGCAACCTCC CAACCCAGAG GAGGCAGAAT AAGACAACA 480
 TCACACTCAT AACTCATGT CTGTGGAGT TGACATTGAA TGTATCTATT TATTAAGTTC 540
 TCAATGTGAA AATTGTGTCT GTAAGATTGT CCAGTGCAAC CACACAGCT CACCAGAAGT 600
 TGTGCAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660
 TATGCTATTA AAGTATTTC ATTCTGCC

Seq ID NO: B84 Protein sequence
 Protein Accession #: NP_000720.1

80 1 11 21 31 41 51
 | | | | |
 MNSGVCLCVL MAVLAAGALT QPVPPADPAG SGLQRAEAP RRQLRVSQRT DGESEHLAGA 60
 LLARYIQQAR KAPSGRMSIV KNLQNLDP SH RISDRYMGW MDPGRRAAE YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5	A1 DNA SEQUENCE	
	Gene name:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
10	Nucleic Acid Accession #:	M31210
	Coding sequence:	251-1396
15	TCTAAAGTTC GGGGGCAGCA GCAAGATGCG AAGCGAGCCG TACAGATCCC GGGCTCTCCG 60 AACGCAACTT CGCCCTGCTT GAGCGAGGCT GCGGTTTCCG AGGCCCTCTC CAGCCAAGGA 120 AAAGCTACAC AAAAAGCCTG GATCACTCAT CGAACCACCC CTGAAGCCAG TGAAGGCTCT 180 CTCGCTCGC CCTCTAGCGT TCGTCTGGAG TAGCGCCACC CGGCTTCCTT GGGGACACAG 240 GGTTCGCACC ATCGGGGCCA CAGCGTCCG GCTGGTCAAG GCGCACGCA GCTCGGTCTC 300 TGACTAGTTC AACTATGATA TCATCGTCCG GCATTACAAC TACACGGGAA AGCTGAATAT 360 CAGCGCGGAC AAGCGAACA GCATTAACT GACCTCGGTG GTGTTTCATT TCATCTGCTG 420 CTTTATCATC CTGGAGAACA TCTTTGTCTT GCTGACCATT TGGAAAACCA AGAAATTCCA 480 CCGACCCATG TACTATTTTA TTGGCAATCT GGCCCTCTCA GACCTGTGG CAGGAGTAGC 540 CTACACAGCT AACCTGCTCT TGTCTGGGGC CACCACCTAC AAGCTCACTC CCGCCCACTG 600 GTTCTCGCG GAAGGGAGTA TGTTTGTGGC CCGTGTGAGC TCCGTGTTC GTCTCTCTGC 660 CATCGCCATT AAGCGCTATA TCACAATGCT GAAATGAAA GTCCACAACG GGAGCAATAA 720 CTTCCGCTCT TTCTGTCTAA TCAGCGCTCG CTGGGTCTAT TCCCTCATCC TGGGTGGCCT 780 GCCTATCATG GGCTGGAATC GCATCAGTGC GCTGTCCAGC TGCTCCACCG TGCTGCCGCT 840 CTACCAAGCT TACTATATCC TCTTCTGCAC CACGGTCTTC ACTCTGCTTC TGCTCTCCAT 900 CGTCACTCTG TACTGAGAAA TCTACTCTTT GGTCAAGACT CGGAGCGGCC GCCTGACGTT 960 CCGCAAGAAC ATTTCGAAGC CCAGCGCAG CTCTGAGAAT GTGGCGCTCG TCAAGACCGT 1020 AATTATCGTC CTGAGCGTCT TCATCGCTCG CTGGGCACCG CTCTCATCC TGCTCTCTGT 1080 GGATGTGGGG TGCAAGGTGA AGACCTGTGA CATCTCTTTC AGAGCGGAGT ACTTCTCTGT 1140 GTTAGCTGTC CACTATCCG GCACCAACCC CATCATTTAC ACTCTGACCA ACTAAGGAGAT 1200 GCGTGGGCCC TTCACTCCGA TCATGTCTCG CTGCAAGTGC CCGAGCGGAG ACTCTGCTGG 1260 CAAATTCAAG CGACCCATCA TCGCGGCAT GGAATTCAGC CGCAGCAAT CGGACAATTC 1320 CTCCCACCCC CAGAAAGACG AAGGGGACAA CCCAGAGACC ATTATGTCTT CTGGAACGCT 1380 CAACTCTTCT TCCTAGAATC GGAAGCTGTC CACCCACCGG AAGCGCTCTT TACTTGGTGC 1440 CTGGCCACCC CAGTGTCTGG AAAAAAATCT CTGGGCTTCG ACTGCTGCCA GGGAGGAGCT 1500 GCTGCAAGCC AGAGGGAGGA AGGGGGAGAA TACGAACAGC CTGGTGGTGT CGGTGTGTGG 1560 TGGGTAGAGT TAGTTCTCTG GAACAATGCA CTGGGAAGGG TGGAGATCAG GTCCCGGCTC 1620 GGAATATATA TTCTACCCCC CTGAGCTTTT GATTTTGCAC TGAGCCAAAG GTCTAGCATT 1680 GTCAAGCTCC TAAAGGGTTC ATTTGGCCCC TCCTCAAAGA CTAATGTCCC CATGTGAAAG 1740 CGTCTCTTGG TCTGGAGCTT TGAGGAGATG TTTTCTTCA CTTTGTGTTT AAACCCAAGT 1800 GAGTGTGTGC ACTTCTGCTT CTTTAGGGAT GCGCTGTACA TCCACACCC CACCTCTCTT 1860 TCCTTCTATA CCCTCTCTCA ACGTTCTTTT ACTTTTACT TTAACCTACT GAGAGTTATC 1920 AGAGCTGGGG TTGTGGAATG ATCGATCATC TATAGCAAT AGGCTATGTT GAGTACGTAG 1980 GCTGTGGGAA GATGAAGATG GTTTGGAGGT GTAAACAAT GTCCTTCGCT GAGGCCAAG 2040 TTTCCATGTA AGCGGGATCC GTTTTTTGA ATTGGTTGA AGTCACCTTG ATTTCTTTAA 2100 AAAACATCTT TCAATGAATA TGTTTACCA TTTTATATCC ATTGAAGCCG AAATCTGCAT 2160 AAGGAAGCCC ACTTTCTATT AATGATATTA GCCAGGATCC TTGGTGTCTT AGGAGAAACA 2220 GACAAGCAAA ACAAGTGAA AACCGAATGG ATTAACCTTT GCAACCAAG GGAGATTCTT 2280 TAGCAATGTA GTCTAACAAA TATGACATCC GTCTTTCCCA CTTTGTGTTA TGTTTATTTT 2340 AGAATCTTGT GTGATTCATT TCAAGCAACA ACATGTTGTA TTTTGTGTTG TTAAGAGTAC 2400 TTTTCTTGAT TTTTGAATGT ATTTGTTTCA GGAAGAAGTC ATTTTATGGA TTTTCTAAC 2460 CCGTGTAAAC TTTTCTAGAA TCCACCTCTT TGTGCCCTTA AGCATTACTT TAACGTGTAG 2520 GGAACGCCAG AACTTTTAAAG TCCAGCTATT CATTAGATAG TAATTGAAGA TATGTATAAA 2580 TATTACAAAG AATAAAATA TATTACTGTC TCTTTAGTAT GGTTTTCAGT GCAATTAAAC 2640 CGAGAGATCT GTGTTTTTTT TAAAAAGAA AGTATTTAAT AGGTTTCTGA CTTTGTGGA 2700 TCATTTTGCA CATAGCTTTA TCAACTTTTA AACATTAATA AACTGATTTT TTTAAAG	
60	A2 Protein sequence:	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	Gene name:	
	Unigene number:	Hs.154210
	Probeset Accession #:	M31210
65	Protein Accession #:	AAA52336
	Signal sequence:	none found
	Transmembrane domains:	50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301
	Cellular Localization:	plasma membrane
70	1 11 21 31 41 51 MGPTSVPLVK AHRSSVSDYV NYDIIVRHYN YTGKLNISAD KENSIKLTSV VFILICCFII 60 LENIFVLLTI WTKRKFERPM YFIGNLALS DLLAGVAYTA NLLLSGATTY KLTFAQWFLR 120 EGSMPVALSA SVFSLAIAI ERYITMLKMK LHNGSNFRL FLNISACNVI SLILGGLPIM 180 GWNCISALSS CSTVLPVLYHK HYILFCTTVP TLLLSIVIL YCRIYSLVRT RSRRLTFRKN 240 ISKASRSSEN VALLKTVIIV LSVFIACNAP LPILLLLDVG CKVKTDILF RABYFVLVAV 300 LNSGTNPIIY TLTNKMERRA FIRIMSCCKC PSGDSAGKFK RPIIAGMEFS RSKSDNSSHP 360 QKDEGDNPET IMSSGNVNSS S	
80	A3 DNA SEQUENCE	
	Gene name:	G protein-coupled receptor 51
	Unigene number:	Hs.198612
	Probeset Accession #:	AA452928
	Nucleic Acid Accession #:	NM_004624.1

1-2826 (underlined sequences correspond to start and stop codons)

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55  A4 Protein sequence:
Gene name: G protein-coupled receptor 51
Unigene number: Hs.198612
Probeset Accession #: AA452928
60 Protein Accession #: NP_005449.1
Signal sequence: 1-42
Pfam domains: 7tm_3 [481-754], ANF_receptor [130-204]
Transmembrane domains: 22-44, 477-499, 517-539, 552-574, 595-617, 653-675, 692-713, 722-744
Cellular Localization: plasma membrane

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65	1	11	21	31	41	51	
	MASPRRSQGP	GRPPPPPPPP	ARLLLLLLLL	LLPLPLAPGAW	GWARGAPRPP	PSSPPPLSIMG.	60
	LMPLTKEVAK	GSIGRGVLP	VELAEIQIRN	LSLLRPVYFD	LRLYDTBCDN	AKGLKAFYDA	120
70	IKYGFNHLAV	PGGVCPSTVS	IIAESLGQWN	VLDSFAAAT	PVLADKKKYP	YFPFTYPSDN	180
	AVNPAILKLL	KHYQWKRVGT	LTQDQWRQSE	VRNDLTGLVY	GEDIEISDTE	SPSNDPCTSV	240
	KKLGKNDVRI	ILQGQDNMA	AKVFCAYEE	NMYGSKYQWI	IPGHYEPSWN	PQVTHEANSS	300
	CLRLKNLLAA	MEGYIGVDPE	PLSSKKQIKTI	SGKTPQYQYR	EYNNKRSVG	PSKFGHAYD	360
	GIWVIAKTLQ	RAMELTHAS	RHQRIQDFNY	TLQDTHQILR	NAMNETNFGV	YQGVQVFRNG	420
75	ERMGTIKFTQ	QDSREKRVK	EYNVAADTLE	LINDTIRFQG	SEPPKQKTI	LEQIRKISLP	480
	LYSLISALTI	FGMNASAF	FNFIKNRKN	LKIMSSPYMN	NLIILGGLMS	YASIFLEGD	540
	GSFVSEKTFE	TLCTVTRWIL	TUGYTTAFGA	MPAKTRVHVA	IFKYNMKKKK	IKKQDKLLVI	600
	VGGMILLIDC	ILICQWAVDP	LRRTVEKYSN	BEDPADRGDI	IRPLEEHCN	TLTRTWIGIV	660
	YAYGGLMLP	CLFLQAWETR	VISIPALNDSK	YIGMSVYNVG	IMCIIGAAYS	FLTRDQPNVQ	720
	FCIVALVIIF	CSTIITCLVFP	VKPLITLRTN	PDAATQNRRF	QFTQNQKKED	SKTSDSVTSV	780
80	NQASTSRLEG	LQSENRHLRM	KITELDDKLE	EVTMLQDQTP	EKTTYIKQNH	QYSLDNLNL	840
	GNFTSTDDG	KAILKNHLD	NPQLQWNTTE	PSPTCKDPIE	DINSPEHQIR	RLSLQLPLIL	900
	HAYLPSIGVG	DASCSPCVS	PTASRRHRV	SPSRCSWVSE	L		

A5 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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10 1      11      21      31      41      51
    |      |      |      |      |      |
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    CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCC GGGAAACAAT TCACCAATGA 120
    GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCCTGGCA 180
    GTGTGACGGG CTGCTTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
15 GTCGAAATGT GGCCCAACCT TCTTCCCTTG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300
    CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
    AAACCCCTCTG CTTTGCTCCA CGCCCGCTA CCACTGCAAG AACGGCCTCT GTATTGACAA 420
    GAGCTTCATC TGCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
    AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
20 TTACCCCGAGC ATCACTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
    CCTGCTGGCA CTGCTCTTGC ACCACCGAG CGAAGCGAAC AACCTCATGA CGTGCCTCGT 660
    GCACCGGCTG CAGCACCCGT TGCTGCTGTC CCGCTCGTG GTCTTGAGCC ACCCCACCA 720
    CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
    GAATGCGTGG GAAGTAGGCT CCCCACCTC CTACTCCGAG GCCTTGCTGG ACCAGAGGCC 840
25 TGCGTGTGAT GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
    CGACCTGCCC AATGACGCT CCGGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
    CAGCAGCCTC CTGAGCGTGG AAGACACCA CCAAGCCCG GGGCAGCCTG GCCCCAGGA 1020
    GGGCACTGCT GAGCCAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
    AGTTATTCCA GGAGAGAGCA GGGTTAATCT GCTCTGACTT GTTGCCATT TCACCAATTG 1140
30 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
    AACTATCTCT CATGTTCCCT CCTCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
    TGACATGATC TGTGTGCGT CTTTCTGTC AGGTCACTCT TCCCTTGGGA CCGAGATCA 1320
    CACCCCTCAT TTTACATTA TTCTGTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380
    AAATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
35 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTGGGGTTAG 1500
    ATGATCTAAC CAGGAGGCCA TCACTGGAAT GTCAACCCCC CAAAAAAT CCATTTGAGC 1560
    ATCAAAACCT GCTTGCACA ATCCTATTG ATGCCCCAG TTACAGAGAG TCAGTGGCCA 1620
    AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTGGC AACGTTATTT TGGTTTGTG 1680
    AAGGACTCTG AAGCACTCTA CCCTGTATAA ATTCTGGCTT TAGAAATTG CCCAAGAATG 1740
40 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
    GAGCCCTCTC CATGATCTCT TCCAAGTTCT CAGCTCTTAA AATGCAAGCT GCCAAGACCC 1860
    TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920
    ACCTGCCCGT AGCCAAAGGA TGAGGACCTA ACTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
    GTATGCTCTC GTGGCCACA CCCAGCCTGT CTGCTCAT CTGCAAGCT CAACACTGGC 2040
45 CTCCAAAGTT CCCTTAACAC TTGCAAAATC CTTTATACCT GTGCATTGG ACTTGAGGAC 2100
    ACTGGTTTCT ATCAGAGGT AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
    CTGCACGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
    GGTGAGGGT AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
    AGACAATTG GAGTCAAGAT TTTCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
50 TGAAACAGTG TGTGTGTTT TTCCCTCTA GTTAAGGGAC TATTTATATG TGTATAGGAA 2400
    AGCTGTCTCT TTTTGTGTT TTCTTTAAC AAGGTCCAAA GAAAGATGCA AAGGAGATC 2460
    ACACCCCTGC CCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
    ACATTTGTGC ATTGTTGAC TTGAGGTTA TTATTTATCA AGTCTTGAA GGAAGCAGAA 2580
    AGAGGGACTC CTCTCTCCCT CCGGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
55 TTCTCTGTGT CAGTCAAGCC ACAGGGCCCG CTTCCCTGCA GGAATAAGGG GTAAAAACGTT 2700
    AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAAAATGAA CCAGGTAGAG 2760
    CCACCTCGGG CAGCTGTGAC CATTTCAGAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820
    AACCTGTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTGAG 2880
    TGATCCTGTT CTGTAGACTT TTCTTTCTT TTTTAACCAA ATCCAAAGGA TGTACAGAA 2940
60 AAGCTAGCCA CTGGTATTTT GTTTGTTTAA AAAAAAATAA GAAAGAAAGA AAGAAAGAAA 3000
    AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
    CTGAGTAATC CAATAAGAA CTTTGTATGA CAGCCAGAA GTGTTAGAAC TCTGGCTGAA 3120
    CATTTCATCT CCGTGTGAGT AGAAGGGCTT TATTTCTCCC TTTGATGGG CCCCTTCTTC 3180
    TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
65 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTAGT 3300
    AGATAAGGGA TGCTACTATA TGCTTTTAA AAACAAACAG GGACATTTT ATTATAGATT 3360
    TGATTTTCTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420
    TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
    TTTTAACTC ATTTCAACCA GGAAGCTTTT TTATACATTG CTTAAATCTA CGCAACCCAG 3540
70 AAAATAGTCT CATCTCTTTT TTCTCAAT GAGATCOGTG TTTTATTTTA GCATTAAATT 3600
    AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
    TTTTAAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGAG CTCAAAGTTA ATGTAAACTG 3720
    GAAAGGTTGT GTGTGTTGTC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
    TATACATTT TAATAAATT GCAGTTTCAT TCTTCTGTT TGTGCAAAWG GWMCTAMARM 3840
75 AAMMAAAAC AWYWTGGGG GGGCTGGGC CTGGAAGAAA GTTTTAAACA CCACCTCGGG 3900
    TGGGCGGGG GGGCCAGGT AGGTACGGG ACCACGGGG CCCAAACGGG ACCCCAGAAG 3960
    GAAACCCCTG CCAAGAAAAA GGTGGCGAGA ATCTCCACA CCAGAAAAAA ACGCGCCGGG 4020
    GGAACCCGCA GAGTGTGCG TAAACACAC CCGAAGAGAG AACTCAGAG CACACRAGCG 4080
80 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

```

A6 Protein sequence:

Gene name: ESTs

Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51
 MWLLGFLCLL LSSAAESQLL PGNFTNECN IPGNFMCNSG RCIPGANQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFFPCAS GIHCIIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGQNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 15 VIFVLVVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYSS DTESLNQADL PPRSRSSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTEEV

20 A7 DNA SEQUENCE
 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Nucleic Acid Accession #: NM_002205
 25 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 ATGGGGAGCC GGACGCCAGA GTCCCTCTCT CACGCCGTGC AGCTGGCGTG GGGCCCCCGG 60
 CGCCGACCCC CGCTSSSTGCC GCTGCTGTGT CTGCTSTTGC CGCCGCCACC CAGGGTCGGG 120
 GGCTTCAACT TAGACGGGGA GGGCCACGCA GTACTCTCGG GGGCCCCGGG CTCTTCTTTC 180
 GGATTCTCAG TGGAGTTTAA CCGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCCAAGGCTA ATACCAGCCA GCCAGGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCTT 300
 35 TGGGGTGCCA GCGCCACACA GTGCACCCCC ATTGAATTG ACAGCAAAGG CTCTCGGCTC 360
 CTGGAGTCTT CACTGTCCAG CTCAGAGGGA GAGGAGCCTG TGGAGTACAA GTCCCTGCAG 420
 TGGTTCTGGG CAACAGTTGG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCCACTGTAC 480
 AGCTGGCGCA CAGAGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGCTA CCTCTCCACA 540
 GATAACTTCA CCGGAATTCT GGAGTATGCA CCTGCGCGCT CAGATTTCAG CTGGGCAGCA 600
 40 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGAGATTCA CCAAGACTGG CCGTGTGGTT 660
 TAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCAGATGCC TGCTGTCCAC TCAGGAGCAG 720
 ATTGCAAGAT CTTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGGCA GCTGCAGACT 780
 CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 840
 TTCACTGGTG ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
 45 GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGATCCCC TCTACAACTT CTCAGGGGAA 960
 CAGATGGCCT CCTACTTTGG CTATGACAGT GCGGCCACAG ACGTCAATGG GGACGGGCTG 1020
 GATGACTTGC TGGTGGGGGG ACCCTTGCTC ATGGATCGGA CCGCTGACGG CGGGCCTCAG 1080
 GAGGTGGGCA GGGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CACGCCACCC 1140
 CTTACCTTCA CTGGCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTGAC CCGCTTGGGG 1200
 50 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCCTTTGG TGGGGAGACC 1260
 CAGCAGGGAG TAGTGTGTGT ATTTCTTGGG GGGCCAGGAG GGCCTGGGCTC TAAGCCTTCC 1320
 CAGGTTCTGC TGGAACTTCA GCTGGACTGG CAGAAAGCAGA AGGGAGGGGT ACGGGGGGCA 1380
 CGAGGAGGCC GAGACCTGGA TGGCAATGGA TATCCTGATC TGATTGTGGG GTCCCTTGGT 1440
 55 GTGGACAGGG CTGTGGTATA CAGGGGCCCG CCCATCGTGT CCGCTAGTGC CTCCCTCACC 1500
 ATCTTCCCCG CCATGTTCAA CCGAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
 GCGTGCATCA ACCTTAGCTT CTGCCCTAAT GCCTCTGGAA AACACGTTGC TGACTCCATT 1620
 GGTTCACAG TGGAACTTCA GCTGGACTGG CAGAAAGCAGA AGGGAGGGGT ACGGGGGGCA 1680
 CTGTTCTCTG CCTCCAGGCA GGCAACCTTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT GCAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAAA 1800
 60 CTCTCGCCGA TTCACATGCG TCTCAACTTC TCCTTGGACC CCCAAGCCCC AGTGGACAGC 1860
 CACGGCCTCA GGGCAGCCCT ACATTATCAG AGCAAGAGCC GATAGAGGGA CAAGGCTCAG 1920
 ATCTTGCTGG ACTGTGGAGA AGACAACATC TGTGTGCTCG ACCTGCAGCT GGAAGTGTIT 1980
 GGGGAGCAGA ACCATGTGTA CCTGGGTGAC AAGAAATGCC TGAACCTCAC TTTCCATGCC 2040
 CAGAAATGTG GTGAGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACCGC CCCTCCAGAG 2100
 65 GCTGAGTACT CAGGACTCGT CAGACACCCA GGGAACTTCT CCAGCCTGAG CTGTGACTAC 2160
 TTTGCCGTGA ACCAGAGCCG CTGCTGGTGG TGTGACCTGG GCAACCCCAT GAAGGCAGGA 2220
 GCCAGTCTGT GGGGTGGCCT TCGGTTTACA GTCCCTCATC TCGGGACAC TAAGAAACCC 2280
 ATCCAGTTTG ACTTCCAGAT CCTCAGCAAG AATCTCAACA ACTCGCAAAG CGACGTGGTT 2340
 70 TCCTTTGGGC TCTCCGTGGA GGCTCAGGCC CAGGTCACCC TGAACGGTGT CTCCAAGCCT 2400
 GAGGCACTGC TATTCCCACT AAGCGACTGG CATCCCCGAG ACCAGCCTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCATGTCTAT GAGCTCATCA ACCAAGGCCC CAGCTCCATT 2520
 AGCCAGGGTG TGCTGGAACT CAGCTGTCCC CAGGCTCTGG AAGGTCAGCA GCTCTATAT 2580
 GTGACCAGAG TTACGGGACT CAACCTGACC ACCAATCACC CCATTAAACC AAAGGGCCTG 2640
 75 GAGTTGGATC CGAGGGGTTT CCTGCACCA CAGCAAAAAC GGAAGCTCC AAGCCGACGC 2700
 TCTGCTTCCT CGGGACCTCA GATCTTGAAA TGCCCGGAGG CTGAGTGTIT CAGGCTGCGC 2760
 TGTGAGCTCG GGGCCCTGCA CCAACAAGAG AGCCAAAGTC TGCAATTGCA TTTCCGAGTC 2820
 TGGGCCAAGA CTTTCTTGCA GCGGGAGCAC CAGCCATTTA GCTTCAGTGT TGAGGCTGTG 2880
 TACAAGCCCC TGAAGATGCC CTACCGAATC CTGCTCGGCG AGCTGCCCCA AAAAGAGCGT 2940
 CAGGTGGCCA CAGCTGTGCA ATGGAACCAAG GCAGAAGGCA GCTATGGCGT CCACTGTGG 3000
 80 ATCATCATCT TAGCCATCCT GTTGGGCTTC CTGCTCTAG GTCTACTCAT CTACATCCTC 3060
 TACAAGCTTG GATTCTTCAA ACGCTCCCTC CCATATGGCA CCGCATGGA AAAAGCTCAG 3120
 CTCAAGCCTC CAGCCACCTC TGATGCTTGA

A8 Protein sequence:

5 Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Protein Accession #: NP_002196
 Signal sequence: 1-42
 10 Transmembrane domains: 998-1020
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036
 Cellular Localization: plasma membrane

15 1 11 21 31 41 51
 MGSRTPEPL HAVQLRWGPR RRPPLPLLLL LLLPPPPRVG GFNLDAEAPA VLSGPPGSFF 60
 GFSVEFYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WGASPTQCTP IEFDSKGSRL 120
 LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DFIGTCTYLSL 180
 DNFTRILEYA PCRSDFSWAA GQGYCQGGFS AEFTKTGRVV LGGPGSYFWQ GQILSATQEQ 240
 IAESYYPEYL INLVGQQLQT RQASSIYDDS YLGYSVAVGE FSGDDTDFV AGVPKGNLTY 300
 GYVITILNGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLVVGAPLL MDRTPDGRPQ 360
 EVGRVYVYLG HPAGIEPTPT LTLTGHEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGET 420
 QQGVVVFVPG GPGGLGSKPS QVLQPLWAAS HTPDFFGSAL RGGRLDNGNG YPDLIVGSFG 480
 25 VDKAVVYRGR PIVSASASLT IFPAMFNPEE RSCSLEGNFV ACINLSFCLN ASGKHVADSI 540
 GFTVELQLDW QKQGGVRRRA LFLASRAQLT TQTLILQNGA REDCREMKIY LRNESEFRDK 600
 LSPIHIALNF SLDPQAPVDS HGLRPALHYQ SKSRIEDKAQ ILDCGEDNI CVPDLQLEVF 660
 GEQNHVYLG D KNALNLTFAH QNVGEGGAYE AELRVTAPE AEYSGLVRRH GNFSLSLSCDY 720
 FAVNQSRLLV CDLGNPMKAG ASLWGLRFT VPHLRDTKKT IQDFQILSK NLNNSQSDV 780
 30 SFRLSVEAQA QVTILNGVSKP EAVLFVPSDV HPRDQPKKEE DLGPAVHVY ELINQGPSSI 840
 SQGVLELSCP QALEGQQLLY VTRVTGLNCT TNHFINPKGL ELDPEGLSHH QKREAPSR 900
 SASSGPQILK CPEAECFRLR CELGPHLQGE SQSLQLHFRV WAKTFLQREH QPFSLQCEAV 960
 YKALMPYRI LRQLLPQKER QVATAVQWTK AEGSYGVPLW IILAILFGL LLLGLLIYIL 1020
 35 YKLGPFKRSL PYGTAMERAKQ LKPPATSDA

A9 DNA SEQUENCE

40 Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 ATGAATTTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGCTG TGTGTTTGCT 60
 CAACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120
 GCAGGGCCAA ATTGTGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCCTACT 180
 50 TCTGCAGAT GTGATGATTT AGAAGCCCTA AAAAGAGAGG GTTGCCCTCC AGATGACATA 240
 GAAATCCCA GAGGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CCGTAGCAAA 300
 GGAACAGCA AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCA CAAGTTGGTT 360
 TTGCGATTAA GATCAGGGGA GCCACAGACA TTTACATTAA AATCAAGAG AGCTGAAGAG 420
 TATCCCTAT ACCTCTACTA CCTTATGGAC CTGTCTTACT CAATGAAAGA CGATTGGAG 480
 55 AATGTAATAA GTCTTGGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCGGACTTC 540
 AGAATTGAT TTTGGCTCATT TGTGGAAAAG ACTGTGATGC CTTACATTAG CACAACACAA 600
 GCTAAGCTCA GGAACCCCTG CACAAGTGAA CAGAAGTGCA CCAGCCCAT TAGCTACAAA 660
 AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTGTGTGG AAAACAGCGC 720
 ATATCTGGAA ATTTGGATTC TCCAGAAAGT GGTTCGATG CCATCATGCA AGTTGCAATT 780
 60 TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840
 GGGTTTCAC TTTGCTGGAGA TGGGAAACTT GGTGGCATTT TTTTACCAA TGATGGACAA 900
 TGTCACCTGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
 CACCTTGTC AGAAACTGAG TGAATAAAT ATTACAGCAA TTTTGCAGT TACTGAAGAA 1020
 TTTACGCTG TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
 65 TCTGCAAAAT CTAGCAATGT AATTCAGTTG ATCATTGATG CATACAATTC CCTTTCCTCA 1140
 GAAGTCATT TGGAAAACGG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
 TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCCTAT 1260
 GGAGATGAGG TTCAATTGTA AATTAGCATA ACTTCARAATA AGTGTCCAAA AAAGGATTCT 1320
 GACAGCTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
 70 ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
 AATGGGACAT TTGAGTGTGG CGCGTGACAG TGCAATGAAG GCGGTGTTGG TAGACATTGT 1500
 GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCAG GAAAGAAAAC 1560
 AGTTCAAGAA TCTCGAGTAA CAATGGAGAG TGCGTCTGCG GACAGTGTGT TGTAGGGAAG 1620
 AGGAGATAA CAAATGAAAT TTATTCTGCG AAATTCTGCG AGTGTGATAA TTTCAACTGT 1680
 75 GATAGATCCA ATGCTTAAAT TTGTGGAGGA AATGGTGTGT GCAAGTGTG TGTGTGTGAG 1740
 TGCAACCCA ACTACATGG CAGTGCATGT GACTGTTCTT TGGATACTAG TACTTGTGAA 1800
 GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT 1860
 ACAGATCCGA AGTTTCAAGG GCAAACTGTG GAGATGTGTC AGACCTGCCT TGGTGTCTGT 1920
 GCTGAGCATA AAGAAATGTG TCAGTGCAAG GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
 80 TGCAACAGG AATGTTCTTA TTTTAACTT ACCAAGGTAG AAGTCCGGGA CAAATTACCC 2040
 CAGCGGTCT AACCTGATCC TGTGTCCCAT TGTAAAGGAGA AGGATGTTGA GCACTGTGG 2100
 TTCTATTTTA CGTATTTCAGT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAA 2160
 CCAGAGTGT CCACTGGTCC AGACATCATT CCAATTGTAG CTGGTGTGGT TGCTGGAATT 2220

GTTCTTATTG GCCTTGCACT ACTGCTGATA TGGGAAGCTTT TAATGATAAT TCATGACAGA 2280
 AGGGAGTTTG CTAAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT 2340
 CCTATTATA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA

A10 Protein sequence:

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Protein Accession #: NP_002202.1
 Signal sequence: 1-21
 Transmembrane domains: 732-754
 INB domain: 34-464
 PSI domain: 26-76
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
 SARCDLLEAL KKKGCPDDI ENPRGSKDIK KNKNVTNRSK GTAELKLPED ITQIQPQQLV 120
 LRLRSGEPQT FTLKFKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLN NEMRRITSDP 180
 RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKGE VFNELVGKQR 240
 ISGNLDSPEG GFDAIMQVAV CGSLIGWRNV TRLLVFTDA GFHFGADGKL GGIVLPNDGQ 300
 CHLENNMYTM SHYYDYPRIA HLVOKLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGTI 360
 SANSSNVQL IIDAVNSLSS EVILENGKLS EGVITISYKSY CKNVNGTGE NGRKCSNISI 420
 GDEVFQFEISI TSNKCPKIDS DSPKIRPLGF TEEVEVILQY ICECECQSEB IPESPKEHEG 480
 NGTFEGGACR CNEGRVGRHC ECSTDENVNSB DMDAYCRKEN SSEICSNNGE CVCGQCVCRK 540
 RNDTNEIYSG KFCBCNFMNC DRNGLICGG NGVCKCRVCE CNPNYTGSAK DCSLDTSTCE 600
 ASHGQICNGR GICECGVCKC TDPKFGQOTC EMCQTCLGVC AEHKECVQCR AFNKGEKQDT 660
 CTQECSYFNI TKVESRDKLP QPVQPDVPSH CKEKDVDDCW FYFTYSVNGN NEVMVHVVEN 720
 PECPTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIHDR REFAPKEKEK MNAKWDGTEN 780
 PIYKSAVTTV VNFKYEGK

All DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTIGGTGC TTCTCATTAA AGAGAGTGGG 60
 GCTGTGTCTT ACAACACCTC CAACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAGGT ACACACACCT GGTGCAATT CAAACAAAG AAGAGATTGA GTACCTAAAC 180
 TCCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAAATGT 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
 GAACCCAAAC ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCTGTGA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAACGTG 540
 ACAGCCCTGG AATCCCTCTG GCATGGAAGC CTGGTTTGCA GTACCCCACT GGGAAACTTC 600
 AGCTACAAAT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAAT GTATGTCTCT TGGAGAATGG AGTGCTCTTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTGGG 780
 AGCTTCCCAT GGAACACAAAC CTGTACATTT GACTGTGAAG AAGGATTGTA ACTAATGGGA 840
 GCCCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAG 900
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 OCTGCTGGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
 TTGCAAGGAC CAGCCCAAGT TGAATGCACC ACTCAAGGSC AGTGACACA GCAATCCCA 1080
 GTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAAACCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCCTAGTG CTTCTGCGAG TTTCOGTTAT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
 GGTGTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGTTTGT 1320
 GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTTGT TGCTTTCAGC 1380
 TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAAG AGGTTCCTTC CTGCCAAGTG GTAAAAATGT CRAAGCTGGC AGTTCGGGA 1500
 AAGATCAACA TGAGCTCGAG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCGCTGT 1560
 CCTGAAGGAT GGAGCTCAA TGGCTCTGCA GCTGGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGSCCTGC TACCTACTCT TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 CTTCCTGCTG CTGACTCTC CCTCTGACA TTAGACCATT TTCTCTCTGT GCTTCGGAAA 1740
 TCTTTACGGA AAGCAAGAA ATTTGTTCTT GCCAGCAGT GCCAAGCCT TGAATCAGAC 1800
 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A12 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 Transmembrane domains: 555-573
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRTHLVAI QNKKEIEVLN 60
 SILSYSPSY WIGIRKVVNV WVVVGTXKPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
 DVGMMNDERC SKKKLALCYT AACTNTSCSG HGEVETINN YTCKDPGFS GLKCEQIVNC 180
 10 TALESPHEGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIPACNVV 240
 ECDAVTNPAN GFVECFQNPQ SFPWNTTCTF DCEEGFBLMG AQSLOQTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVRCSSS PAGEFTFKSS CNFTCEEFGM LQGPQAVECT TQGGWTTQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEFSCEQ GFLVKGSKRL QCGPTGEWDN 420
 EKPTCEAVRC DAVHQPPKGL VRCASHPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
 15 WTEVPSCQV VKCSSLAVPG KINMSCSGEP VFGTVCKFAC PEGMTLNGSA ARTCGATGHW 540
 SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPPLMLLRK CLRKAKKVPV ASSCQSLESD 600
 GSYQKPSYLL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCCTTA TTCTGGTGA CCTGATCATC 120
 TCTGTGATGG GCCTTCTGGG GAACAGCGCC ACCATTGGG TCACCCAGGT GCTGCAGAAG 180
 30 AAAGGATACT TGCAGAAAGA GGTGACAGAC CACATGTGA GTTTGGCTTG CTGGACATC 240
 TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTTGACC 300
 AGCTCCAGCT ACACCGCTGC CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCAGCTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCAACCC 420
 TTCAGSTACA AGCCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
 35 GTCACTCTCG CCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCG CCACACGAG 600
 CAGCCCGAGA CTCCCAATAT GTCCATCTGT ACCAACCTCT CCAGCCGCTG GACCGTGTTC 660
 CAGTCCAGCA TCTTCGGGCG CTTCGTGGT TACCTGTGG TCTCTCTCTC GTAGCCCTTC 720
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGCTCGCT GGCCTGGGGC 780
 ACGCGGCTCT CCGAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
 ACCATCATCT TCTGAGGCT GATTGTGTG ACATTGGCGG TATGCTGGAT GCCCAACGAG 900
 ATTCCGAGGA TCATGGCTGC GGCCAAACCC AAGCAAGACT GGACGAGGTC CTACTTCCGG 960
 GGTACATGCA TCTCTCTCCC CTTCGAGAG ACGTTTTTCT ACCTCAGCTC GGTATCAAC 1020
 45 CCGCTCCTGT ACACGGTGTG CTGSCAGCAG TTTGCGGGG TGTTCGTGCA GGTGCTGTG 1080
 TGCGGCTGT CGCTGCAGCA CGCCCAACCAC GAGAAGCGCC TGCGGTGACA TGCGCACTCC 1140
 ACCACGACA GCGCCCGCTT TGTGACGCG CCGTGTCTCT TCGGTCTCCG GCGCCAGTCC 1200
 TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGACGAGGC CGAGCCCCAG 1260
 TCTAAGTCCC AGTCAATTGAG TCTGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCCAGC 1320
 50 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 60 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 Cellular Localization: plasma membrane

65 1 11 21 31 41 51
 MASPSLPQSD CSQIIDSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK 60
 KGYLQKEVTD HNVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHLVLTLS FERYIAICHP FRYKAVSGPC QVLLIGFVW VTSALVALPL LFAMGTEYPL 180
 VNVPSHRGLT CNRSSTRHHE QPETSNSMIC TNLSSRWTVF QSSIFGAFV YLVVLLSVAF 240
 70 MCMNMVQVLM KSQKSGSLAG TRPPQLRKS SEESRTARRQ TIIFLRLIV TLAVCMMENQ 300
 IRRIMAAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSSQ FRRVFVQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTKIFL STFPQSEAEPO 420
 SKSQSLSLBS LEPNSGAKPA NSAAENGQFE REV

A1 ProstateA15 DNA sequence

80 Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

	GGGCTCCGCG	CACACCTCCC	CGCGCCGCGG	CGGCCACCGC	CCGCACTCCG	CGGCTCTGCG	60
	CCGCAACCGC	TGAGCCATCC	ATGGGGGTCTG	CGGGCCGCAA	CCGTCCCGGG	GCGGCTCTGG	120
5	CGGTGCTGCT	GCTGCTGCTG	CTGCTGCCCG	CACTGCTGCT	GCTGGCGGGG	GCCGTCCCGC	180
	CGGGTCGGGG	CGGTGCCCGG	GGGCGCGAGG	AGGATGTAGA	TGAGTGTGCC	CAAGGGCTAG	240
	ATGACTGCCA	TGCGACGCCC	CTGTGTCAGA	ACACACCCAC	CTCCTACAAG	TGCTCCTGCA	300
	AGCCTGGCTA	CCAAGGGGAA	GGCAGGCAGT	GTGAGGACAT	CGATGAATGT	GGAAATGAGC	360
	TCAATGGAGG	CTGTGTCCAT	GACTGTTTGA	ATATTCACAG	CAATTATCGT	TGCACCTGTT	420
10	TTGATGGCTT	CATGTTGGCT	CATGACGGTC	ATAATTGTCT	TGATGTGGAC	GAGTGCTCTG	480
	AGAACAAATG	CGGTCGCCAG	CATACCTGTG	TCAACGTCAT	GGGGAGCTAT	GAGTGCTGCT	540
	GCAAGGAGGG	GTTTTTCCTG	AGTGACAATC	AGCACACCTG	CATTCAACCG	TCCGGAAGAGG	600
	GCCTGAGCTG	CATGAATAAG	GATCACGGCT	GTAGTCACAT	CTGCAAGGAG	GCCCCAAGGG	660
	GCAGCGTCGC	CTGTGAGTGC	AGGCCTGGTT	TTGAGCTGGC	CAAGAACCAG	AGAGACTGCA	720
15	TCTTGACCTG	TAACCATGGG	AACGGTGGGT	GCCAGCACTC	CTGTGACGAT	ACAGCCGATG	780
	GCCAGAGTGG	CAGCTGCCAT	CCACAGTACA	AGATGCACAC	AGATGGGAGG	AGCTGCCTTG	840
	AGCGAGAGGA	CACCTGCTCG	GAGGTGACAG	AGAGCAACAC	CACATCAGTG	GTGGATGGGG	900
	ATAAACGGGT	GAACGSCGCG	CTGCTCATGG	AAACGCTGTC	TGTCACAAT	GGAGGCTGTG	960
	ACCGCACCTG	TAGGATATCT	TGACACGGTG	TCCACTGCAG	TTGTCTCTGT	GGATTCACTC	1020
20	TCCAGTTGGA	TGGGAAGACA	TGTAAAGATA	TTGATGAGTG	CCAGACCCGC	AATGGAGGTT	1080
	GTGATCAATT	CTGCAAAAAA	ATCGTGGGCA	GTTTTGACTG	CGGCTGCAAG	AAAGGATTTA	1140
	AATTATTAAAC	AGATGAGAAG	TCTTGCCAAG	ATGTGGATGA	GTGCTCTTTG	GATAGGACCT	1200
	GTGACCACAG	CTGCATCAAC	CACCTTGGCA	CATTTGCTTG	TGCTTGCAC	CGAGGGTACA	1260
25	CCCTGTATGG	CTTCACCCAC	TGTGGAGACA	CCAATGAGTG	CAGCATCAAC	AACGGAGGCT	1320
	GTGAGCAGGT	CTGTGTGAAC	ACAGTGGGCA	GCTATGAATG	CCAGTGCAC	CCTGGGTACA	1380
	AGCTCCAGTG	GAATAAAAAA	GACTGTGTGG	AAGTGAAGGG	GCTCCTGCCC	ACAAGTGTGT	1440
	CACCCCGTGT	GTCCCTGAC	TGCGTAAGA	GTGGTGGAGG	AGACGGGTGC	TTCTCTCAGT	1500
	GTCACTCTGG	CATTCACTTC	TCTTCAGATG	TCACCACCAT	CAGGACAAGT	GTAACCTTTA	1560
	AGCTAAATGA	AGGCAAGTGT	AGTTTGAAAA	ATGCTGAGCT	GTTCCTCGAG	GGTCTGGGAC	1620
30	CAGCACTACC	AGGAAAGCAC	AGCTCAGTAA	AAGAGAGCTT	CCGCTACGTA	AACCTTACAT	1680
	GCAGCTCTGG	CAACCAAGTC	CCAGGAGCCC	CTGGCCGACC	AAGCAACCCCT	AAGGAAATGT	1740
	TTATCACTGT	TGAGTTTGAG	CTTGAAACTA	ACCAAAAGGA	GGTGACAGCT	TCTTGTGACC	1800
	TGAGCTGCAT	CGTAAAGCGA	ACCGAGAAGC	GGCTCCGTAA	AGCCATCCGC	ACGCTCAGAA	1860
	AGGCGGTCCA	CGAGGAGCAG	TTTCACCTCC	AGCTCTCAGG	CATGAACCTC	GACGTGGCTA	1920
35	AAAGAGCTCC	CAGAACATCT	GAAAGCCAGG	CAGAGTCTCT	TGGAGTGGGC	CAGGGTCATG	1980
	CAGAAAAACA	ATGTGTCACT	TGCAGGGCTG	GGACCTATTA	TGATGGAGCA	CAGGAAACGT	2040
	GCATTTTATG	TCCAATATGA	ACCTTCCAAA	ATGAGGAAGG	ACAAATGACT	TGTGAACCAT	2100
	GCCCAAGACC	AGGAAATTC	GGGCCCCGTA	AGACCCGAGA	AGCTTGGAA	ATGTCTGAAT	2160
	GTGGAGGTCT	GTGTCAACCT	GGTGAATATT	CTGCAGATGG	CTTTGCACCT	TGCCAGCTCT	2220
40	GTGCCCTGGG	CAGTTCACAG	CCTGAAGCTG	GTGGAATCTC	CTGCTTCCCC	TGTGGAGGAG	2280
	GCCTTGCCAC	CAAACTATCAG	GGAGCTACTT	CCTTTTCAGGA	CTGTGAAACC	AGAGTTCAAT	2340
	GTTCACCTGG	ACATTTCTAC	AACACCACTA	CTCACCGATG	TATTGCTTGC	CCAGTGGGAA	2400
	CATACCAAGC	TGAATTGTGA	AAAAATAATT	GTGTTTCTTG	CCCAGGAAAT	ACTACGACTG	2460
	ACTTTGATGG	CTCCACAATC	ATAACCCAGT	GTAAAAACAG	AAGATGTGGA	GGGGAGCTGG	2520
45	GAGATTTTAC	TGGGTACATT	GAATCCCCAA	ACTACCCAGG	CAATTACCCA	GCCAAACCCG	2580
	AGTGTAGCTG	GACCATCAAC	CCACCCCCCA	AGCGCCGCTC	CCTGATCGTG	GTCCCTGAGA	2640
	TCTTCCTGCC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
	CCAATTCCTG	GACAACATAT	GAAACCTGCC	AGACCTACGA	ACGCCCCATC	GCCTTCACCT	2760
	CCAGGTCAAA	GAAGCTGTGG	ATTCAAGTTCA	AGTCCAATGA	AGGGAACAGC	GCTAGAGGGT	2820
50	TCCAGTCCCT	ATACGTGACA	TATGATGAGG	ACTACCAAGG	ACTCATTGAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAAAC	ATCAGGAAAT	ACTTAAGGAT	AAGAACTTAA	2940
	TCAAGGCTCT	GTGTTGATGTC	CTGGCCCATC	CCCAAGACTA	TTTCAAGTAC	ACAGCCCAAG	3000
	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TOCGATTGCT	AOGTTCCAAA	GTGTCCAGGT	3060
	TTTGTAGACC	TTACAAATGA	CTCAGCCCAT	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
55	GGTTGGTGGG	ACAGAGCTGT	CTTCCTTCTG	CATGTACGCA	CAGTCCGGTA	TTGCTGCCTC	3180
	CCGATTCATG	CACCATTAG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGCTAAATT	3240
	GAACTTGGTT	TTTCTTTCCC	AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGGCTGGCT	GAGCTGGACT	3360
	TTGGTCAGCG	TAGGTGAGAC	TCACCTGTCC	TTCTGGGGTC	TTACTCTTCC	TCAAGGAGTC	3420
60	TGTAGTGGAA	AGGAGGCCAC	AGAATAAGCT	GCTTATTCTG	AAACTTCAGC	TTCTCTTAGC	3480
	CCGGCCCTCT	CTAAGGGGAG	CCTCTGCACT	CGTGTGACGG	CTCTGACCAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAAGGAGA	CCCTTGCAAG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGATCC	CAGGAACTTG	3660
	AGTTCTAAGC	AGTGTCTGTG	AAAAAAAATA	GCAGAAAGAA	TTAGAAATAA	ATAAAAACCTA	3720
65	AGCACTTCTG	GAGACAT					

A16 Protein sequence

Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 PFAM domains: EGF-like domains [49-84,132-167,177-213,286-321,407-442]
 CUB_domain [809-918]
 Cellular Localization: may be secreted

	1	11	21	31	41	51	
80	MGVAGRNRP	AAAVLLLLL	LLPPLLLLAG	AVPPGRGAA	GPQEDVDECA	QGLDDCHADA	60
	LQNTFTSYK	CSCKPGYQGE	GRQCEDIDEC	GNELNGGCVH	DCLNIPGNYR	CTCFDGFMLA	120
	HDGHNCLD	ECLERNNGCQ	HTCVNVMGSY	ECCKEGFPFL	SDNQHTCIHR	SEBGLSCMNK	180
	DHGCSHIDC	APRGSVACEC	RPGFELARNQ	RDCILTCHNG	NGGCQHSDD	TADGPECSCH	240
	PQYKMTDGR	SCLEREDTVL	EVTESNTTSV	VDGDKRVKRR	LIMETCAVNN	GGCDRTCKDT	300

5 STGVHCSCPV GPTLQLDGKT CKDIDECQTR NGGCDHFCRN IVGSFDCGCK KQFKLLTDEK 360
 SQQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGPTH CGDTNECSIN NGGQQQVCVN 420
 TVGSYECQCE PGYKLMHNNK DCVEVKGLLP TSVSFPRVSLH CGKSGGGDGC FLRCHSGIHL 480
 SSDVTITRTS VTFKLNKGKC SLKNAELFPE GLRPALEPKH SSVKESFRVY NLTCSGKQV 540
 PGAPGRPSTP KEMFITVEFE LETNQKEVTA SCDLSCIVKR TEKRLRKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQAESCQVG QGHAENQCVS CRAGTYDGA RERCILCPNG 660
 TFQNEEGMT CEPKPRPGNS GALKTPAWN MSECGGLQCP GEYSADGFAP QQLCALGTFQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSPGHPY NTTTHRCIRC PVGTYPPEFG 780
 KNNVCSCPGN TTTDFDGSN ITQCNRRCG GELGDFGTGY ESPNYPGNYP ANTECTWTIN 840
 10 PPPKRRILIV VPEIFLPIED DCGDYLVMRK TSSNSVTY ETCQTYERPI APTSRSKLW 900
 IQPKSNEGNS ARGQVFPVVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFQDV 960
 LAHPQNYFKY TAQESREMF RSFIRLLRSK VSRFLRPYK

A17 DNA sequence

15 Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Nucleic Acid Accession #: none found
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

20 1 11 21 31 41 51
 | | | | | |
 CAAAAGAAA TAGATAAAAT AAATGGAAAA TTAGAAGAGT CTCCTGATAA TGATGGTTTT 60
 CTGAAGGCTC CTGCAGAAAT GAAAGTTTCT ATTCCAATAA AAGCCTTAGA ATTGATGGAC 120
 25 ATGCAAACTT TCAAAAGCAGA GCCTCCCGAG AAGCCATCTG CCTTCGAGCC TGCCATTGAA 180
 ATGCAAAAGT CTGTTCCAAA TAAAGCCCTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240
 GATCAGATGT TCCTTTCAGA ATCAAAACAA AAGAAGTTG AAGAAAATTC TTGGGATTCT 300
 GAGAGTCTCC GTGAGACTGT TTCACAGAAG GATGTGTGTG TACCCAAGGC TACACATCAA 360
 30 AAAGAAATGG ATAAATAAG TGGAAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420
 GATACAGTTC ATTCTTGTGA AAGAACAAGG GAACCTCAAA AAGACCCCTG TGACCCACGT 480
 TCAGGAAAA

A18 Protein sequence

35 Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Protein Accession #: none found
 Signal sequence: none
 Transmembrane domains: none
 40 Cellular Localization: nuclear

45 1 11 21 31 41 51
 | | | | | |
 QKEIDKINGK LEESPNDNGF LKAPCRMKVS IPTKALELMD MQTFKAEPPE KPSAFEPAlE 60
 MQKSVFNKAL ELNQEQLRA DQMFPSKQ KXVEENSWDS ESLRETVSQK DVCVFKATHQ 120
 KEMDKISGKL EDGTSLSKIL DTVHSCERTR ELQKDPDPR SGK

BreastA19 DNA SEQUENCE

55 Gene name: TMPS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | | |
 ACCGGGCACC GGACGGCTCG GGTACTTTTC TTCTTAATTA GGTATGCCC GTGTGAGCCA 60
 GGAAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCCGTGGTG 120
 65 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCCTG AATAGTTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCGCCCTC 240
 TCATTCCGAT CGCTTTTGGG CCTGTGATGAT TTGAAAATAA GTCTGTGTGC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTCCT AATCATGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 70 TCAGGGAAGT ACAGATGTG CTATCTCTTT AAGTGTATCG AGCTGATAGC TOGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCGGTGC TCAGGTTGT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATGT TGCTGTGCC CACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720
 75 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTCG GCCACGTGT TACCTTGCA TGCAAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTCAGTTCC AGGCTACCA CCTGTGCGGG GCTCTGTCA TCACGCCCTT GTGAGTCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTTTGAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 CTAGTTTCCC TGTGAGCAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080
 80 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCGGGCCA 1140
 CTCACCTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGAAAGG TGTGCTGGAC GTCCAGGATG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTGTGCC TGAACCAAGC GGCCTGCCCT TTGATTTCCA ACAAGATCTG CAACACAGG 1320
 GAGGTGTACG GTGGCATCAT CTCCTCTCC ATGCTCTGCG CGGCTACCT GACGGGTGGC 1380

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GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACACG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCTG AGGTGATGAA GACAGCCCGA 1620
TCCTCCCTGT GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCCTTCCA TCTGATTCCA GCACAACCTT 1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CACTCTGTTG CCCAGGCTGG 1800
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
TTGCCCTCAG TTTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACTAATTT 1920
TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
CCTCAATAGA TGTGCTGCT TCAGCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
AGGCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCTCT 2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAGAA 2280
CCAAACCCAC CCTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTCGTT TAAGGCCTAT TTTTCATGAT TCTTTGTAGC ATTTGGTGTG TGAOGTATTA 2400
TTGTCTTTTG ATTCCAATA ATATGTTTCC TTCCTCACA AAAAAAAAAA AAAAAAAAAA 2460
AAAAAAAA

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A20 Protein sequence:

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30

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Gene name: TMPRSS3a
Unigene number: Hs.298241
Probeset Accession #: A1538613
Protein Accession #: BAB20077
Signal sequence: none found
Transmembrane domains: 43-65, 239-261
Tryp_SPC domain: 216-444
Cellular Localization: not determined

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35
40

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1 11 21 31 41 51
MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFPF IIVIGIIALI 60
LALAIGLGIH FDCSGKYRCR SSFKCIBLIA RCDGVSDCKD GEDEYRCVRV GQGNVILQVF 120
TAASWTKMCS DDWKGHYANV ACAQLGPFSY VSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
VTALHHSYVV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
LCGGSVITFL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
LGNIDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCMT SGWGATEDGA GDASPVLNHA 360
AVPLIENKIC NHRDVYGGII SPSMLCAGYL TGVVDSQCGD SGGPLVCQER RLWKLVGATS 420
FGIGCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

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A21 DNA SEQUENCE

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Gene name: ESTs; opposite strand to TRPS1
Unigene number: none
Probeset Accession #: AA428090
Nucleic Acid Accession #: AA428090
Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

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60
65
70
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80

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1 11 21 31 41 51
ATGAAGCCCA GTTTGAAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAAT AGACCAAAGG 60
CAAGTTGTTG GAGAAGAAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAAC 120
TTTTACAGCA CAGATGATCT TATGTCCATA GTGGAGGAAT CAGACAGCTG CTACAAACCGT 180
GATTCTGTTG GGCTTCTCTG TAGAGCTGSA GACAGACTGC AACCCAAGAC AAAACCCAGA 240
GGAAAAACAA CTAACCTCAG CCATTGCCCC AATTTCACCC TTGCTAGTTA TCAGAGTTCA 300
CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGAATTT TATTCTGAGC 360
AAGTGTTTTG TTCAGCTTGC AGTATTAAAA CAAAAAAAC ATTGCCTCCA GCTGCAAAAGC 420
AAGGGCATTG CCATTATGAA AGCCCTCAA AGACTCTCTG CTATTTTCAA AACATGGAAA 480
GAAAAAGGGA AAAAAAGAAA AAAAAATAATA ATTAGAAGGA TTGTTCTCTT AATTGGGGCT 540
CCCAAAATAG AGAAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACTCTCT 600
CAAGCAAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTATT 660
TTTCTTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCTTCTCT ATCTGGATCT 720
GTTCTGCTTC ATTCTCTTT CAAAGTCATC TTTAGGGGAA CTGCGCTGTA TTAATTTGAT 780
TTTAAACCAA CAAATAAGAT ATTGTATATA TTAATTTAAA CTTTTTGAGA TGATTGATTA 840
GGAATTGCAT CATGTTTACA TGAGTATACC GAATTCAAAG TTAACTTCA TAAGCAGGAG 900
TTTTTACACA TCGTAACATA ATCATTACCC AATACTCGAC ACTCAATATT TGATACTCAA 960
CTGAATGTTT TTGAATAAAA CACATTTTTA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020
CTTTTACAC AAAATATATC AGTGAGAGAG TGTGTTTGA AGAAAAAAA TCAAAGCACA 1080
ACAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTTAGA ATGGTGATT 1140
GATTTCACCA TTTCAATTCA GCAGAGCCTG TATATATATA TATATATATA TATATATATA 1200
TATATATATA TATATATATA TATATACAA TGATCTGTAT TTCTATTGTC TAGAAGGATG 1260
AAAGTGAATC CATATAAACC ATACCAACGC CGTTATGTGT AACTGGTGGT AAAAATTAT 1320
TATTCAAGTT TAGATGAAC AGACATCTTT GCTGCTGAA GATTGTTGC ATAAGAAATA 1380
CACCAAGAAC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAACAACAA ATAAATAAAA 1440
ACGAAAAAAT TFCATGTGTT GTAAGAACAG AACTATTATA GCCAACATTC TAGTATTCAA 1500
ATCAGGACTA CAAATTGAAT TCTTTTCTT AGCAACATGA AATCATTCCA TATGAAAGAC 1560
ATTTTCTGCT GGTGAATATT GCTGTAAGTT AAATTTTACA TTGGCATTT GAGATGTTCC 1620
CCCTCATGCT CTCCTCCCAA GTTTTCCATG TGTGTTGCAA ATAGTCCGC

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A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 113-129
 Cellular Localization: not determined

10 1 11 21 31 41 51
 MKPSLKHWD IKMFSEIDQR QVVGEIHLQ VVSVSYLVEN FSDTDDLMSI VEESDSCYNR 60
 DSVGLPGRAG DRLQPKTKPR GKTTNLSHLP NFHLASYQSS LLFQLQGSYY GNLLVEFELS 120
 15 KCFVQLAVLK QKKGCLQLQS KGIAIMKAPQ RLSAIFKTKW EKGKKEKKII IRRICSLIWA 180
 PKNEK

A23 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 ATGAGCGGTG CGGGGGTGGC GGCTGGGAGC CGGCCCCCA GCTCGCCGAC CCGGGGCTCT 60
 CGGCGCGGGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCGCGA GAGCCCGCAG 120
 30 CTCAGGCAGA GCGAGCCGCA GAAACGGAAC CTGGACCTGG AGAAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAA GCTCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCGGCCC TGCCCTCCCA GGCACACTCA 300
 ACACTGCCGC TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CCGGGGCTCA 360
 GGGGGAACAC AGGACGGGGA GCGCCCTCCAG ACTGTCTCTG CCCACCTGGC TGCACTGGCC 420
 35 CCGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGACAGATGC CGCTACCTCT 480
 AGCCGTGGCT GGACGATGTT ATGACGCCAA GCACAGCAGC TGCTGTCTCT GGGAGGCCCA 540
 GGGCCTGAGG TCATTGACGG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CTTCCCTCCT 600
 CCAAGTAGAG CTGAATAGGG AAGGAACCCC TGGGACAGCC CCGGCCCTGC TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
 40 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGT TCCCTTGCCA CTGTGCAAG 840
 GCACTTCCCC ATCTTGACAG CGGCCCCAC CCAGCCGAGC ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTTCC CATTATCTTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGTGGA 960
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCCTA GGGCTCTCCC TTCCAGGGA 1020
 45 GACATGAGAG AGGGGTTGA GGGAGGGCCC TTCCCTAGCC GCTGTGGCAA CTCAGTGG 1080
 CTGTCTCGGG CAAAGTGTGG CCCAAGTCGG CAGCCCGAGC CCGTCACTGC TGGGAGCGCT 1140
 GACAGGACAC GGAAGAGGCG CATGCTTTCC CTGCGGACCT GCTGTTCAT GTGTCCCAAG 1200
 CCTCTCTGCT TTCCAGATGG CCTCTCAGGA AACCACTTT CCAGGCGCTC TGCTCCCTTG 1260
 GCGCTCGCT GGGTCTGCAT CAACGAGTGG TGGGTAGAGC CGGAGGACC CAGCCCTGCC 1320
 50 AGGCTGAGGG AGGCTCTCTC ACAGGACACAC AGGCCAGGAG GCAAGCGTGG CGCTCTTGG 1380
 GCGGTGAGCG CCGCACTGT GCGCTCTCT CTGACAGGCC TCTCCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGCC 1500
 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCAGGA AGGCCGACCT GGAAGAGGAG 1560
 CCCCTACTTC ACAACAGCAA GCTGGACAAA GTTCTGGGG TACAAGGGCA GGCCAGAAAG 1620
 55 GAGAAAGCAG AGGCTCTTAA TGCAAGAGCT GCCTGTATGG GGAACAGCCA GCACCGGGC 1680
 AGCGAGATGG GGGCGGGGGC ACACCCCCCA ATGATCTGTC CCTTCCCTC GCGAAGGCC 1740
 ACCCACTTA GGCAGTGCGA AGTCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCAG 1800
 ACCCAAGAGC TGCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
 CCGGAGGAAG CTAGCTTTCC CAGGACCAA GAAGCCACGC ATTTCGCCAA GGTCCTCCAC 1920
 60 AAGAGCCTCT CCAAGAAATG CCGAGGCCCA CCGTGGCGG AGCGTGCCAT CCGCCCGCA 1980
 CTGAAGCAGC CCCCGAAGAA CAACCTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
 AACCGCGGCC TGCATCGCTC AGTCTTTGA

A24 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

75 1 11 21 31 41 51
 MSGAGVAAGT RPFSSPTPGS RRRRQRPSPV VQSLRPQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQQHSMLAK LHEEIEHLKR ENKGEFARGP RPALPQAHLS TLPLPQHRNT AINSSTRLGS 120
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLLSGSP 180
 GPEVIAGRQV ATGCSPLDLP PSRAEMGRNP WDSPPCARSL PQIAAVARPR ISSPMALSPH 240
 80 MLGAQGIWTH SIQSLPAIW AATMGTKGGS RVLFPCHLSK ALPHPDSPGH PAQDPGLWSQ 300
 AHFPLSLGLG LTSGGHLTGG WSQPGNIAAG AVPRALPSQG DMEKGVDEGP FFSRCGNSSE 360
 LFWKCGPSR QPQPCBAGDA DRTREBAMLS LGTCCSMCPK PSCFPDGPSP NHLSRASAPL 420
 GARWVCINGV WVEPGGPPSA RLKEGSSRTH RPPGKRGRLA GGSADTVRSP ADSLSMSSFP 480
 SVKSISNSAN SQGKARPQPG SFNKQDSKAD VSQKADLEEB PLLHNSKLDK VPGVQGQARK 540

EKAASNAGA ACMGNSQHQG RQMGAGAHPP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
 TQELRHLKSL LEGSQRPQAA PEEASFPRDQ EATHFFPKVST KSLSKKCLSP FVAERAILPA 660
 LKQTFKNNFA ERQKRLQAMQ KRRLHRSVL

5

A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Nucleic Acid Accession #: NM_000949
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 15 GGAGGCTGAA ATCCCCAGAC GCCGGTTTTC TGGGCTGGGC TTTCTGCTTA CTCACCTCTT 60
 CTCCCTCTTT CTGGATTTTA CCGACCGTTC GCGAAACAGC TTTCCACACA ATGGAGCTTC 120
 ATGTCTCTGT GCAGGAAGTA CTATCGACTG GATGTGGCAG ACTTTGCTCC CTGACAAAAC 180
 TAAAGAACTC TCCTATTCTA GGAGGCGAAC ACTGAGGATG CTTTCCACAT GAACCCCTGAA 240
 GTGAACCTCT GATACATTTC CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAAATGTGG 300
 20 CATCTGCAAC CGTTTTCAC TGTCTACTTT TTCTCAACAC CTGCCCTTCTG AATGGACAGT 360
 TACCTCCCTGG AAAACCTGAG ATCTTTAAAT GTCGTTCTCC CAATAAGGAA ACATTCACTT 420
 GCTGTGTGAG GCCTGGGACA GATGGAGGAC TTCTTACCAA TTATTCAGTG ACTTACACCA 480
 GGGAAAGGAG GACATCTCAT CATGAATGTC CAGACTACAT AACCGGTGGC CCAACTCTCT 540
 25 GCCACTTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
 CTAACCCAGT GGAAGCAGT TTCTCGATG AACCTTATGT GSACGTGACT TACATAGTTC 660
 AGCCAGACCC TCCTTTGGAG CTGGCTGTGG AAGTAAAAACA GCCAGAAGAC AGAAAACCTT 720
 ACCTGTGGAT TAAATGGTCT CCACCTACCC TGATTGACTT AAAAATCGGT TGGTTCACGC 780
 TCCTGTATGA TACTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGCTG 840
 30 GGCAGCAAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTTGTCCAGG 900
 TTGCTGCAAC ACCAGACCAT GGATACTGGA GTGCATGGAG TCCAGCGACC TTCATTCCAG 960
 TACCTAGTGA CTTACCATG AATGATACAA CCGTGTGGAT CTCGTGTGCT GTCTTTCTG 1020
 CTGTCTCTG TTTGATTATT GTCTGGGACG TGGCTTTGAA GGGCTATAGC ATGGTGACCT 1080
 GCATCTTTCC GCCAGTTTCT GGGCCAAAAA TAAAGGATT TGATGCTCAT CTGTGGGAGA 1140
 35 AGGGCAAGTC TGAAGAACTA CTGAGTGCCT TGGGATGCCA AGACTTTCTT CCCACTTCTG 1200
 ACTATGAGA CTTGCTGGTG GAGTATTAG AAGTAGATGA TAGTGAGGAC CAGCATCTAA 1260
 TGTCACTCCA TTCAAAGAA CACCCAAGTC AAGGTATGAA ACCACATAC CTGGATCCTG 1320
 ACACGTGCTC AGGCCGGGGG AGCTGTGACA GCCCTTCCCT TTTGTCTGAA AAGTGTGAGG 1380
 AACCCAGGC CAATCCCTCC ACATTCTATG ATCCTGAGGT CATTGAGAAC CCAGAGAATC 1440
 40 CTGAACAAC CCACCTCTG GACCCCACT GCATAAGCAT GGAAGGCAAA ATCCCTTATT 1500
 TTCACTGCTG TGGATCCAAA TGTTCAACAT GGCCCTTACC ACAGCCGAGC CAGCACAAAC 1560
 CCAGATCCTC TTACCACAA ATTACTGATG TGTGTGAGCT GGCTGTGGGC CCTGCAGGTG 1620
 CACCCGACAC TCTGTGTAAT GAAGCAGGTA AAGATGCTTT AAAATCCTCT CAAACCAATTA 1680
 AGTCTAGAGA AGAGGGAAAG GCAACCCAGC AGAGGGAGGT AGAAAGCTTC CATTCTGAGA 1740
 45 CTGACCCAGA TACGCCCTGG CTGCTGCCCC AGGAGAAAAC CCCCTTTGGC TCCGCTAAAC 1800
 CCTTGGATTA TGTGGAGATT CACAAGGTCA ACAAGATGG TGCATTATCA TTGTACCAA 1860
 AACAGAGAGA GAACAGCGGC AAGCCCAAGA AGCCCGGGAC TCCTGAGAAC AATAAGGAGT 1920
 ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCCTGTT GTTGGTGCCA GATCCACATG 1980
 50 CTAATAACGT GCCTTGCTTT GAAGAATCAG CCAAGAGAGC CCCACCATCA CTTGAACAGA 2040
 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGC AGGCTCCAGC 2100
 TGGGTGTTT GATTTACCTG GATCCCGCAT GTTTTACACA CTCCTTTCAC TGATAGCTTG 2160
 ACTAATGGAA TGATTGGTTA AAATGTGATT TTTCTTCAGG TAACACTACA GAGTACGTGA 2220
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAAGCTC CCAGCTCCTT TCATGTCTCA 2280
 TTTTAAACCA CTGCTCTCTT TCTCCAGCAG CTGATTCCAG AACAAATCAT TATGTTTCTT 2340
 55 AACTGTGATT TGTAGATTTA CTTTTGCTG TTAGTTATAA AACTATGTGT TCAATGAAT 2400
 AAAAGCACAC TGCTTAGTAT TCTTGAAGGA CAATGCCAAT AGGTATATCC TCTGAAAAG 2460
 GCTTTCATGA TTTGGCATGG GACAGACGGA AATGAATTTG TCAAAATTTG TTACCATAGA 2520
 AGATGACAA AAGAAATATT TCCACATAGG AAAATGCCAT GAAAATTTCT TTTGAAAAC 2580
 AACTGCATAA CCTTTACACT CCTCGTCCAT TTTATTAGGA TTACCCAAAT ATAACCATTT 2640
 60 AAAGAAAGAA TGCAATCCAG AACAAATTGT TTACATAAGT TCCTATACCT TACTGACACA 2700
 TTGCTGATAT GCAAGTAAGA AAT

A26 Protein sequence:

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Protein Accession #: NP_000940
 Signal sequence: 1-23
 Transmembrane domains: 237-253
 FN3 domains: 28-112, 127-215
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51
 MKENVASATV FTLLPLNTC LLNGQLPPGK PEIFKCRSPN KETFTCWWRP GTDGLPTNY 60
 SLTYHREGT LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVNATNMQG SSPSDELYVD 120
 80 VTYIVQPDPP LELAVEVKQP EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAABW 180
 EIHFAQQOTE FKLLSLHPGQ KYLVQVRCKP DHGYSWAWSP ATFQIPSDP TNDTITVWIS 240
 VAVLSAVICL LIWVAVALKG YSMVTCIFPP VPGPKIKGFD AHLLEKXKSE ELLSALGCQD 300
 FPPTS DYEDL LVEYLEVDDS EDQHLMSVHS KEHPSQGMKP TYLDFDTSRG RGSCDPSLL 360
 SERCEEPQAN PSTFYDFEVI EKPENPETTH TWDPOCISME GKIPYFHAGG SKCSTWPLPQ 420

PSQHNPRSSY HNITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQQREVE 480
 SFHSETDQDT PWLLPQEKTP FGSAPFLDYV EIHKVNKDGAA LSLLPKQREN SGKPKKPGTP 540
 ENNKKEYAKVS GVMDNNILVL VPDPAKQVVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600
 KCRLQLGLLD YLDPACFTHS FH

A27 DNA SEQUENCE

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)

Unigene number: Hs.169266

Probeset Accession #: L07615

Nucleic Acid Accession #: NM_000909.1

Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 | | | | | |
 CATTCCCACC CTTCCTTCTT TAATAAGCAG GAGCGAAAAA GACAAATTCC AAAGAGGATT 60
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATTG CAATATCGGG 120
 AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTATAA 180
 ATAATCTATA ACAACCAAAAC CAATCAAAAT GAATTCAAAC TTATTTTCCC AGGTTGAAAA 240
 TCATTGAGTC CACTCTAATT TCTCAGAGAA GAATGCCAGC CTTCCTGGCTT TTGAAAATGA 300
 TGATTGTGAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTGCTTATG GAGCTGTGAT 360
 CATTCTTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAAC AAAAGGAGAT 420
 GAGAAATGTT ACCAACATCC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTGTCAT 480
 CATGTGTCTC CCTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGTGAGGCG 540
 GATGTGTAAAG TTGAATCCCT TTGTGCAATG TGTTTCAATC ACTGTGTCCA TTTTCTCTCT 600
 GGTTCCTATT GCTGTGGAAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660
 TAATAGACAT GCTTATGTAG GTATTGCTGT GATTGGGTC CTGCTGTGG CTCTCTCTTT 720
 GCCTTTCCCTG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGATGC 780
 GTACAAAGAC AAATAGCTGT GCCTTGATCA ATTTCCATCG GACTCTCAT GGTGTCTTAT 840
 TACCCTCTC CTCTTGGTGC TGCAATATT TTGGTCCACT TGTATTATAT TTATTGTCTA 900
 CTTCAGATA TATATACGCC TAAAAGGAG AAACAACATG ATGACACAAG TGAGAGACAA 960
 TAAGTACAGG TCCAGTGAAA CAAAAGAAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
 ATTTGCACTG TGCTGGCTCC CTCTTACCAT CTTTAACACT GTGTTTGATT GGAATCATCA 1080
 GATCATTTGT ACCTGCAACC ACAATCTGTT ATTCCTGCTC TGCCACCTCA CAGCAATGAT 1140
 ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGGAAC AAAAATCTCC AGAGAGACTT 1200
 GCAGTTCTTC TTCAACTTTT GTGATTTCGG GTCTCGGGAT GATGATTATG AAACAATAGC 1260
 CATGTCCAGG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320
 ATTTAAAAAA ATCAACAACA ATGATGATAA TGAAAAAATC TGAAGTACTT TATAGCCTAT 1380
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
 TCTCCCAAGG AATGGGGTTC AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500
 TTAAGTCTTT TGTGTAGTAT GTCATAATTA CATTTGGAAC AAAAGGTGTG GGCCTTGGGG 1560
 TCTCTGGAAT ATAGTTTGA CCAGACATCT TTGAAGTGTCT TTTGTGAAT TTATGCATAT 1620
 AATATAAAGA CTTTTTAACT GTACTTATG GAATGAAAT TCTTTAAAGT ATTACGATGC 1680
 GCTGACTTCA GAAGTACCTG CCATCCAATA CGGTCAATAG ATTGGGTCTT CTGATTAGA 1740
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
 TAGTGTGTTA CAATAGTAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
 GAAGTCATTC AGAAGTGGTT TGAGGTTTCT GTTTTGTGTT TGTTTTTTTT 1920
 TTTTTTCAAC TTAAGGGAGG CTTTCATTTT CTCCCGACTG ATTGTCACTT AAATCAAAAT 1980
 TAAAAAATGA AAAAAAGAC ATACTTCTCA GCTGCAAAAT TTATGGAGAA TTGGGCACCC 2040
 ACAGGAATGA AGAGAGAAAG CAGCTCCCCA ACITCAAAAC CATTTTGGTA CCTGACAACA 2100
 AGAGCAATTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
 TATATTTATT TGAATTGATG GTCAAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAGTGT 2220
 TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAAT TTGTAGAAAC 2280
 ACRAAATATG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTCAATGTC 2340
 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTTCAC TTACCTAGC 2400
 AGGGAAAAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAACT 2460
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTAAGTAATA GTTGTGTCAT 2520
 GTTAATGTGC CTAATTTTCAT GTATCTTGTA ATCATGATTG AGCCTCAGAA TCATTGAGG 2580
 AACTATATT TTAAGAAACA AGACATACCT CAATGTATTA TACAGATAAA GTATTACATG 2640
 TGTGTGATTT TAAAAGGGCG GACATTTTAT TAAAATCAAT ATTGTTTTTG CTTTTCTGTA 2700
 GGAGTCTCTT TCAAGTTTCAT TTTTCTCAT CCCATGACTT CCCTCCGATG GT

A28 Protein sequence:

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds

Unigene number: Hs.169266

Probeset Accession #: L07615

Protein Accession #: NP_000900.1

Signal sequence: none found

Pfam domains: 7tm_1 [57-91]

Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286,

300-322

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | | |
 MNSTLFSQVE NHSVHNSFSE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60
 LIIILKQKE MRNVNLIIV NLSFSDLLVA IMCLPPTFVY TLMDRWVFE AMCKLNPPVQ 120
 CVSTITVSIPS LVLIAPERHQ LIINERGWPR NNRHAYVGIA VIWVLAVASS LPFLIYQVMT 180
 DEFPQNVITLD AYKDKYVCFD QPPSDSHRLS YTTLLVLQY FGPLCFIFIC YFKIYIRLKR 240
 RNNMDQMDK NKYRSSETKR INIMLLSIVV AFAVCWLELT IFNTVFDWNH QIATCNHNL 300
 LFLCHLTAM ISTCVNPIFY GPLNKNPQRD LQFFNFNCFD RSRDDDYETI AMSTMHTDVS 360

KTSLKQASPV AFKKINNDD NEKI

5 A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (H077T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

10 Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCAGC CAACGCCCTCC 60
GGCTGCCCGG GCTGTGGCGC CAACGCCCTG GACGGCCAG TCCCTTCGCT GCGGGCCGTG 120
GAGCCTCGGC TCGTGGCGCT CTTCTTCGCG GCGCTGATGC TGCTGGGCCT GGTGGGGAAC 180
TCGCTGGTCA TCAGCATCAT CTGCCGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
ATGCCCAACC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTACCGGCC 300
CTGCTGTACC CGTGGCCCGG CTGGGTGCTG GCGCACTTCA TGTGCAAGTT CGTCAACTAC 360
ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
TGGTACGTGA CGTGTGTCCC GTTGGCGGCC CTGCACGCCG GCACGCCCGG CCTGGCGCTG 480
GCTGTGAGCC TCAGCATCTG GGTAGGCTCT GCGGCGGTGT CTGCGCCGGT GCTGGCCCTG 540
CACCGCCTGT CACCGGGGCC GCGCGCTTAC TGCACTGAGG CCTTCCCCAG CCGGCCCTTG 600
GAGCGCGCCT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTGCCCACC 660
TGCGCTGCTG ATCGGCCCAT CTGGGCCCGG TCGCCGTGCG CCCCGGCCCG 720
GCGATAGCGG CCGTGCAGGG GCAGGTGCTG GCAGAGCGCG CAGGCGCCGT GCGGCCCAAG 780
GTCTCGCGGC TCGTGGCGCG CGTGGTCTCT CTCTTCGCGG CTGCTGGGGG CCCCATCCAG 840
CTGTTCTGCT TGCTGCAGGC GCTGGGCCCG GCGGCTCCTT GGCACCCACG CAGCTACGCC 900
GCCTACGCGC TTAAGACCTG GGCTCACTGC ATGTCCTACA GCAACTCCGC GCTGAACCCG 960
CTGCTCTACG CCTTCTCTGG CTGCACTTTC CGACAGGCGT TCCGCGCGGT CTGCCCTTGC 1020
GCGCGCGGCC GCGCCGCGCG CCCCOCGCGG CCGGGAACCT CGGACCCCGC AGCCCCACAC 1080
GCGGAGCTCG ACCGCTGGGG GTCCCAACCG GCCCCGCGCA GCGCGCAGAA GCCAGGGAGC 1140
AGTGGGCTGG CCGCGCGCGG GCTGTGCTGC CTGGGGAGG ACAACGCCCC TCTCTGA

```

35 A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (H077T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

40 Pfam domains: 7tm_1 [59-323]

Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization: plasma membrane

```

45      1      11      21      31      41      51
|      |      |      |      |      |
MHTVATSGEN ASWGAPANAS GCPGCGANAS DGFVPSRAV DAWLVPLEFA ALMLLGLVGN 60
SLVIYVICHK KPMRTVTNPF IANLAATDVT FLCCVPFPTA LLYPLPGWVL GDFMCKFVNY 120
IQQVSVQATC ATLTAMSVDR WYVTVPFLRA LHRRTPRLAL AVSLSIWVGS AAVSAPVLAL 180
HRLSPGPRAY CSEAPPSRAL ERAPALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
ADSALQGQVL AERAGAVRAK VSRVAAVVL LFAACWGPFIQ LFLVLQALGP AGSMHPRSYA 300
AYALKTWAKC MSYSNSALNP LLYAFLGSHF RQAFRRVPCP APRRRPRPRR PGPSDPAAPH 360
AELHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

```

55 A31 DNA SEQUENCE

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM_014246

60 Nucleic Acid Accession #: NM_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

```

65      1      11      21      31      41      51
|      |      |      |      |      |
ATGGGCGCGG CGCGCGCGCC CGTGTGCTGC GTGCTGCTGC TCCTGGCCGC CGCGCGCGCC 60
CTGCGCGCGA TGGGGCTGCG AGCGGCGCGC TGGGAGCGCG GCGTACCCGG CGGGACCGCG 120
GCTTTCGCCC TCCGGCCCGG CTGTACCTAC GCGGTGGGCG CCGCTTCGAC GCCCGGGCG 180
CCGCGGGAGC TGCTGGAAGT GGGCGCGGAT GGGCGGCTGG CAGGACGTGG GCGGCTCTGG 240
GGCGCGGGGC GCGCGCTGCC GCTGCAAGTC CGCTTGGTGG CCGCAAGTGC CCGGACGGCG 300
CTGAGCGCGC CCGTGGCGGC GCGCAAGCAC CTTCGCGGCT GCGGAGCCCG TGCCCGGCTC 360
TGCGGAACCG GTGCCCGGCT CTGCGGGGCG CTCTGCTTCC CGTTCGCCCG CGGCTGCGCG 420
GCGCGCAGC ATTGCGGCT CGCAGCTCCG ACCACCTTAC CCGCTGCGCG CTGCGCGCGG 480
GCGCCAGGCG CCGCTGTGCC CGGCGGTCCC ATCTGCTTGC CGCGGGCGCG CTCGGTCCGC 540
CTGCGTCTGC TGTGCGCCCT GCGCGCGCGG GCTGGCGCGG TCCGGGTGGG ACTGGCGCTG 600
GAGCGCGCCA CCGCGGGGAC GCGCTCCGCG TCGCCATCCC CATCGCGCGC CCGCGCGCG 660
AACTTGCCTG AAGCCCGGGC GGGCGCGGCG CGACGGGCCC GCGGGGCGAC GAGCGGCAGA 720
GGGAGCTGTA AGTTTCGAT GCCCACTTAC CAGGTGGGCT TGTTTGAGAA CGAACCGCG 780
GGCACCCTCA TCCTCCAGCT GCACGCGCAC TACACCATG AGGGCGAGGA GGAGCGCGTG 840
AGCTATTACA TGGAGGGGCT GTTCGACGAG CGCTCCCGGG GCTACTTCCG AATCGACTCT 900
GCCACGGGCG CCGTGAGCAC GGACAGCGTA CTGGACCGCG AGACCAAGGA GAGCGACGTC 960
CTCAGGGTGA AAGCGGTGGA CTACAGTACG CCGCGCGGCT CGGCCACCACT ATACATCACT 1020
GTCTTGCTCA AAGACACCAA CGACCAAGC CCGGTCTTGG AGCAGTCGGA GTACCGCGAG 1080
CGCGTGGCGG AGAACCTGGA GGTGGGCTAC GAGGTGCTGA CCATCCGCGC CAGCGACCGC 1140

```

	GACTCGCCCA	TCAACGCCAA	CTTGGCTTAC	CGCGTGTGG	GGGGCGCGTG	GGACGTCTTC	1200
	CAGCTCAACG	AGAGCTCTGG	CGTGGTGAGC	ACACGGGCGG	TGCTGGACCG	GGAGGAGGCG	1260
	GCCGAGTACC	AGCTCTCTGGT	GGAGGCCAAC	GACCAGGGGC	GCAATCCGGG	CCCGCTCAGT	1320
5	GCCACGGCCA	CCGTGTACAT	CGAGGTGGAG	GACGAGAACG	ACAACTACCC	CCAGTTGAGC	1380
	GAGCAGAACT	ACGTGGTCCA	GGTGCCCGAG	GACGTGGGGC	TCAACACGGC	TGTGCTGCGA	1440
	GTGCAGGCCA	CGGACCGGGA	CCAGGGCCAG	AACGCGGCCA	TTCACTACAG	CATCCTCAGC	1500
	GGGAACGTGG	CCGCCCAATT	CTACCTGCAC	TCGCTGAGCG	GGATCCTGGA	TGTGATCAAC	1560
	CCCTTGGAIT	TCGAGGATGT	CCAGAAATAC	TCGCTGAGCA	TTAAGGCCCA	GGATGGGGGC	1620
10	CGGCCCCGCG	TCATCAATTC	TTTCAAGGGTG	GTGTCTGTGC	AGGTGCTGGA	TGTCAACGAC	1680
	AACGAGCCTA	TCTTTGTGAG	CAGCCCCCTC	CAGGCCACGG	TGCTGGAGAA	TGTGCCCTTG	1740
	GGCTACCCCG	TGGTGACAT	TCAGGCGGTG	GACGCGGACT	CTGGAGAGAA	CGCCCGGCTG	1800
	CACATATCGCC	TGGTGACAC	GGCCTCCACC	TTTCTGGGGG	GCGCAGCGCG	TGGGCTTAAG	1860
	AATCCTGCCC	CCACCCCTGA	CTTCCCCCTT	CAGATCCACA	ACAGCTCCGG	TTGGATCACA	1920
15	GTGTGTGCGG	AGCTGGACCG	CGAGGAGGTG	GAGCACTACA	GCTTCGGGGT	GGAGCGGCTG	1980
	GACCACGGCT	CGCCCCCAT	GAGCTCTCTC	ACCAGCGTGT	CCATCACGGT	GCTGAGCGTG	2040
	AATGACAACG	ACCGCGTGT	CACGACGCC	ACCTACGAGC	TTCTGTGAA	TGAGGATGCG	2100
	CGCGTGGGGA	GCAGCGTGT	GACCTGCAG	GCCCGCGACC	GTGACGCCAA	CAGTGTGATT	2160
	ACCTACCAGC	TCACAGGCGG	CAACACCCCG	AACCGCTTTG	CACCTCAGCAG	CCAGAGAGGG	2220
20	GGCGGCTCTA	TCACCTCTGG	GCTACCTCTG	GACTACAAGC	AGGAGCAGCA	GTACGTGCTG	2280
	CGCGTGACAG	CATCCGACCG	CACACGCTCG	CACACTCGCG	ATGTCTTAAT	CAACGCTCACT	2340
	GATGCCAACCA	CCGACAGGCG	TGTCTTTTCT	AGCTCCCAAT	ACACAGTGAG	TGTGATGAG	2400
	GACAGGCTCT	TGGGCACCTC	CATTGCTACC	CTCAGTGCCA	ACGATGAGGA	CACAGGAGAG	2460
	AATGCCCGCA	TCACCTACGT	GATTGAGGAC	CCCGTGCCCG	AGTTCCCGAT	TGACCCCGAC	2520
25	AGTGGCAGCA	TGTACACCAT	GATGGAGCTG	GACTATGAGA	ACCAGGTGCG	CTACAGCTG	2580
	ACCATCATGG	CCGACGACAA	CGGCATCCCG	CAGAAATCAG	ACACCAACAC	CCTAGAGATC	2640
	CTCATCTCTG	ATGCCAATGA	CAATGACCC	CAGTTCTGT	GGGATTTCTA	CAGGCGTTCC	2700
	ATCTTTGAGG	ATGCTCCACC	CTCGACGAGC	ATCCTCCAGG	TCTCTGCCAC	GGACCGGGAC	2760
	TCAGGTCCCA	ATGGCGCTCT	GCTGTACACC	TTCCAGGGTG	GGGACGACCG	CGATGGGGAC	2820
30	TTCTACATCG	AGCCCCAGTC	CGGTGTGATT	CGCACCCAGC	CGCCGCTGGA	CGCGGAGAA	2880
	GTGGCGGTGT	ACAACTTTTG	GGCTCTGGCT	GTGGATCGGG	GCAGTCCAC	TCCCCTTAGC	2940
	GCCTCGGTAG	AAATGTCAGT	GACCATCTTG	GACATTAAT	ACAAATGCC	CATGTTTGAG	3000
	AAGGACGAAC	TGGAGCTGTT	TGTTGAGGAG	AACAACCCAG	TGGGTCGGT	GGTGGCAAAG	3060
	ATTCTGTCTA	ACGACCTGGA	TGAAGGCCCT	AATGCCCAGA	TCATGTATCA	GATTGTGAA	3120
35	GGGACATGCG	GGCATTTCCT	CCAGCTGGAC	CTGCTCAACG	GGGACCTGCG	TGCCATGGTG	3180
	GAGCTGGACT	TTGAGGTCCG	GCGGGAGTAT	GTGCTGGTGG	TGACGGCCAC	GTGGGCTCCG	3240
	CTGGTGAGCC	GAGCCACGGT	GCACATCCTT	CTCGTGGAAC	AGAATGACAA	CGCGCTGTG	3300
	CTGCCCGACT	TCCAGATCCT	CTTCAACAAC	TATGTCACCA	ACAAGTCCAA	CAGTTTCCCC	3360
	ACCGGCGTGA	TCGGCTGCAT	CCCGGCCCAT	GACCCCGACG	TGTGAGACAG	CCTCAACTAC	3420
40	ACCTTCGTGC	AGGGCAACGA	GCTGCGCCTG	TTGCTGTCTG	ACCCCGCCAC	GGGCGAATCG	3480
	CAGCTCAGCG	GCGACCTTGA	CAACAACCGG	CGCTGAGGAG	CGCTCATGGA	GGTGTCTGTG	3540
	TCTGATGGCA	TCCACAGGCT	CACGGCCTTC	TGCACCTGCT	GTGTCAACAT	CATCACGGAC	3600
	GACATGCTGA	CCACAGCAT	CACGTCCCGC	CTGGAGAACA	TGTCCAGGA	GAAGTTCCTG	3660
	TCGCCGTGCG	TGGCCCTCTT	CGTGGAGGGG	GTGGCCCGCG	TGCTGTCCAC	CACCAAGGAC	3720
45	GAGGTCTTGG	TCTTCAAGCT	CCAGAACGAC	ACCGACGTCA	GCTCCAACAT	CCTGAACGTG	3780
	ACCTTCTCGG	CGCTGTCTGC	TGGCGGGGTC	CGCGGCCAGT	TCTTCCCGTC	GGAGGACCTG	3840
	CAGGAGCAGA	TCTACCTGAA	TCGGAACGCT	CTGACCAACA	TCTCCACGCA	GCGGCTGCTG	3900
	CCCTTCGAGC	ACAACTCTG	CCTGCGCGAG	CCCTGCGAGA	ACTACATGAA	GTGCGTGTCC	3960
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50	ATCCACCCCA	TCAAAGGCTC	GCGCTGCGCG	TGCGCGCCCG	GCTTCAACCG	CGACTACTGC	4080
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	CGCGAGGGCG	GCTACACCTG	CGAGTGCTTC	GAGGACTTCA	CTGGAGAGCA	CTGTGAGGTG	4200
	GATGCCCGCT	CAGGCGGCTG	TGCCAACGGG	GTGTGCAAGA	ACGCGGGCAC	CTGCGTGAAC	4260
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	CGCTTCCACT	TACCACTCTC	CCTCAAGTTT	GGCACTCAGG	AAAGGAACGG	CTTGCTTCTC	4440
	TACAAAGGGC	GCTTCAATGA	GAAGCACGAC	TTTCACTGCC	TGGAGATCGT	GGACGAGCAG	4500
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	GGTGAGAGTG	ACGGGCGGTG	GCACTCTGTG	CAGGTGCAGT	ACTACAACAA	GCCCAATATT	4620
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	GCCCAGGGCA	CTCAGACCGG	TCCTTGGATC	TGACCGGCCC	TCTACTCCTG		4800
	GGGGTGTGCC	CCAACCTGCC	AGAAGACTTC	CCAGTGCACA	ACCGGCAATT	CGTGCGCTGC	4860
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	GGAGGCACCT	GTGTCAACAG	GTGGAATATG	TATCTGTGTG	AGTGTCCACT	CGATTCGCGC	5040
	GGGAAGAACT	GTGAGCAAGC	CATGCCTCAC	CCCCAGCTCT	TCAGCGGTGA	GAGCGTGTG	5100
	TCCTGGAGTG	ACCTGAACAT	CATCATCTCT	GTGCGCTGGT	ACCTGGGGCT	CATGTTCCGG	5160
	ACCGGGAAGG	AGGACAGCGT	TCTGATGGAG	GCCACCATGG	GTGGGCCCAC	CAGCTTTCGC	5220
70	CTCCAGATCC	TGAACAACCTA	CCTCCAGTTT	GAGGTGTCCC	ACGGCCCCCTC	CGATGTGGAG	5280
	TCGGTGATGC	TGTCCGGGTT	GCGGGTGACC	GACGGGGAGT	GGCACCACCT	GCTGATCGAG	5340
	CTGAAGAATG	TTAAGGAGGA	CAGTGAGATG	AAGCACCTGG	TCACCATGAC	CTTGGACTAT	5400
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	GTGGTGGTGC	GAGGCGCCTC	TGAAGACAAG	GTCTCCGTGC	GCCGTGGATT	CGAGGGCTGC	5520
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	CCCGTCTGTG	GACCTCGCCA	CTGTGCCGTC	AGCAAAAGCT	TTGATCCCGA	CTGTAAATAAG	5940
	ACCAAGGGCC	AGTGGCCAA	CAAGGAGAA	TACTACAAGC	TCCTAGCCCC	GGACACCTGT	6000
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	GCTACACAGC	ACACGGGCAC	GCTCTTTGGC	AATGACGTGC	GCACGGCCTA	CCAGCTGCTG	6480
	GGCCACGTC	TTGAGCACGA	GAGCTGGCAG	CAGGGCTTCG	ACCTGGCAGC	CACGAGGAC	6540
	GCCGACTTTC	ACGAGGACGT	CATCCACTCG	GGCAGCGCCC	TCCTGGCCCC	AGCCACCAGG	6600
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	GCCAGCGTCC	CGGTCTCCGA	CACCATCCAT	GAAGAGTTCC	CCAGGGAGCT	GGAGTCTCTC	6840
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	GCCCCGATCA	GCAGGCGGAG	GGGACACCTC	GATGACGCTG	GCCAGTTGCG	CGTCTCTCTG	7020
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	AACACCACTT	TCGGTGACCG	GCCTGACATG	CTGCGCACAG	ACTTGGGCGA	GTCCACCGCC	8280
	TCGCTGGTCA	GCATCTGTCA	GGATGAAGGG	ATCCAGAAGC	TCCGCGTCTC	CTCTGGGCTG	8340
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45	CCCCCAGAGG	AGAGGAAAGG	CATCTTGAAA	AATAAGTCA	CTTACCGGCC	GCGGCTGACG	8820
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70	CAAGGTTTAC	CAAACTGTTT	TTGGAAATTC	ACACCAAGGT	CGGGCCCACT	CGAGGCGAGT	10320
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75	AAAGCTGATC	TGAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCAG	AGTCTCTACA	10620
	CCTGAATGAA	TTATACATGT	GCCTTACCAG	GTGAGTGGTC	TTTCGAAGAT	AAAAAATCT	10680
	AGTCCCTTTA	AACGTTTGGC	CCTGGCGTTT	CCTAAGTACG	AAAAGGTTTT	TAAGTCTTCG	10740
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	CAGGGTGGCC	GTGGAAGGGA	CGGTTTACGG	ACGTGCACTG	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGGAACTG	GCCGGAACCT	TTTGTCCATT	CCCTAGTAGG	CCTGCCACAG	11220

CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTTGAGGAC TTTTITTTTT TGCCATTATT 11280
 TCTTCAGTTT TCTTTTCTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340
 AGACGTTAGA CTTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTC

5 A32 Protein Sequence

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo
 (Drosophila) homolog (CELSR1),
 Hs.252387
 Unigene number: NP_055061
 Protein Accession #: NP_055061
 Signal sequence: 1-20
 Cadherin domains: 250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,
 1110-1199
 Pfam domains: Laminin_EGF [2003-2048], 7tm_2 [2465-2708]
 Latrophilin/GPS domains: 2407-2460
 Transmembrane domains: 1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51
 MAPPPPPVLP VLLLLAAAA LPAMGLRAAA WEPRVPGGTR AFALRPGCTY AVGAACTPRA 60
 PRELLDVGRD GRLAGRRRVS GAGRPLPLQV RLVARSAPTA LSRRRLRARTH LFGCGARARL 120
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 35 DANTRPVFPV SSHYTVSVSE DRFVGTSIAT LSANDEDTGE NARITYVIQD PVPQFRIDPD 840
 SGTMYTMREL DYENQVAYTL TIMAQDNGIP QKSDTTTLEI LILDANDNAP QPLWDFYQGS 900
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 LTEQLKGR L REKLADCEQS PTSSTSSSLG SGGPDCAITV KSPGREPGRD HANGVAMNVR 3000
 TGAQADGSD SEKP

75 A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 ProbeSet Accession #: X95876
 Nucleic Acid Accession #: X95876
 Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 CCAACCAAA GCACCAAAAGC AGAGGGGCGAG GCAGCACACC ACCCAGCAGC CAGAGCACCA 60
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 TCAACGCCAC CCACTGCCAA TACAACCTCC CACAGGTGGG CCGCAGGGCT CTGCGGGTGC 720
 TGCACTGTGT GGGCTGCTTT CTGCTGCCCC TGCTGGTCAT GGCTACTGCT TATGCCACCA 780
 TCTTGGCGCT GCTGCTGGTT TCCAGGGGCG AGCGGCGCCT GCGGGCCATG CGGCTGGTGG 840
 TGGTGGTCTG GGTGGCCTTT GCCCTCTGCT GGACCCCTTA TCACCTGGTG GTGCTGGTGG 900
 ACATCTCATG GACCTGGGCG GCTTTGGCCC GCAACTGTGG CCGAGAAAGC AGGGTAGACG 960
 15 TGGCCAAAGT GGTCACTCA GGCCTGGGCT ACATGCACTG CTGCTCAAC CCGCTGTCTCT 1020
 ATGCTTTTGT AGGGCTCAAG TTCCGGGAGC GGATGTGGAT GCTGCTCTTG CGCTGGGCT 1080
 GCCCAACCA GAGAGGGCTC CAGAGGCAGC CATGCTCTTC CCGCGGGGAT TCATCTGGT 1140
 CTGAGACCTC AGAGGCTCC TACTGGGCT TGAGAGGCG GAATCCGGGC TCCCTTTTCG 1200
 20 CCCACAGTCT GACTTCCCGG CATTCAGGCG TCCTCCCTCC CTCTGCGGCG TCTGGCTCTC 1260
 CCCAATATCC TCGCTCCCGG GACTCACTGG CAGCCCCAGC ACCACAGGT CTCCCGGAA 1320
 GCCACCTCTC CAGCTCTGAG GACTGCACCA TTGCTGCTCC TTAGCTGCCA AGCCCATCC 1380
 TGCCGCCGCA GGTGGCTGCG TGGAGCCCA CTGCCCTTCT CATTTGGAAA CTAACACTTC 1440
 ATCTTCCCA AGTGGCGGA GTACAAGGCA TGGCGTAGAG GGTGCTGCC CATGAAGCCA 1500
 25 CAGCCAGGCG CTCAGCTCA GCACTGACTG TGGCCATGGT CCCCAGAGC TCTATATTG 1560
 CTCTTTTATT TTTATGTCTA AAATCTGCT TAAACTTTT CAATAACAA GATCGTCAGG 1620
 ACCAAAAAAA AAAAAA AAAA AAAA AAAA AAAA AAAA AAAA BHLITERAT 1680
 UREBHCBLAS TPBHCORTHO LOGUESMOUS ECKCRMYLEV SERQVLDAED PAFLENSTIS 1740
 PYDYGENESD FSDSPCPQD FSLNFDRTFL PALYSLFLFL GLLGNVAVAA VLLSQRTALS 1800
 30 STDTPFLHLA VADVLLVLT PLWAVDAVQ WVFGPGLCKV AGALFNINFY AGAFLLACIS 1860
 FDRYLSIVHA TQIYRRDPV RVALTCIVVW GLCLLFLALPD FIYLSANYDQ RLNATHCQYN 1920
 FPQVGRATLR VLQVLVAGFL PLVVMAYCYA HILAVLLVSR GQRRFRAMRL VVVVVAFAV 1980
 CWTPTYHLVYL VDILMDVGV ARNCGRESHV DVAKSVTSGM GYMHCCLNPL LYAFVGVKFR 2040
 EQMWMLEFTRL GRSDQRPQR QSSSRRESS WSETTEASYL GL

35 **A34 Protein sequence**
 Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3
 Unigene number: Hs.198252
 Protein Accession #: P49682
 40 Signal sequence: none found
 Pfam domains: 7tm_1 [70-318]
 Transmembrane domains: 57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323
 DRY box: 148-149
 45 Cellular Localization: plasma membrane

50 1 11 21 31 41 51
 MVLEVS DHQV LND AEVAALL ENFSSSYDYG ENESDSCCTS PPCQDFSLN FDRFLPALY 60
 SLLFLGLL NGAVAVLLS RRTALSSDT FLLHLAVDT LLVLTPLWA VDAVQWVFG 120
 SGLCKVAGAL FNINFYAGAL LLACISFDYR LNIHVATQLY RRGPPARVTL TCLAVWGLCL 180
 LFLALPDFIFL SAHDERLNA THCQYNFPQV GRTALRVQL VAGFLPLLV MAYCYAHILA 240
 VLLVSRGQRR LRANRLVVVV VVAFALCWTY YHLVVLDIL MDLGLALRNC GRESRVDAV 300
 55 SVTSGLYGMY CCLNPLLYAF VGVRFRERMM MLLRLGLCPN QRGLQRQPSS SRRDSSWSET 360
 SEASYSGL

60 **A35 DNA SEQUENCE**
 Gene name: Differentially expressed CO16 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Nucleic Acid Accession #: BC001291
 Coding sequence: 44-541 (start and stop codons are underlined)

65 1 11 21 31 41 51
 GGGGGCGCG CGCGCTGACC CTCCTGGGCG ACCGCTGGGG ACGATGGCGC TGCTGCGCTT 60
 GCTGCTGGTC GTGGCCCTAC CGCGGTGTG GACAGACGCC AACCTGACTG CGAGACAACG 120
 70 AGATCCAGAG GACTCCAGC GAACGGACGA GGTGACAAT AGAGTGTGGT GTCATGTTTG 180
 TGAGAGAGAA AACACTTTC AGTGCCAGAA CCCAAGGAGG TGCAATGGA CAGAGCCATA 240
 CTGCGTTATA CGCGCCGTGA AAATATTTCC ACGTTTTTTC ATGGTTGCGA AGCAGTGCTC 300
 CGCTGGTTGT GCAGCGATGG AGAGACCCAA GCCAGAGGAG AAGCGTTTC TCTGGAAGA 360
 GCCATGCCCT TCTTTTACC TCAAGTGTG TAAATTCGC TACTGCAATT TAGAGGGGCC 420
 75 ACCTATCAAC TCATCAGTGT TCAAGAATA TGCTGGGAGC ATGGGTGAGA GCTGTGGTGG 480
 GCTGTGGCTG GCCATCTCC TGCTGCTGGC CTCCATTGCA GCCGCGCTCA GCCTGCTCTG 540
 AGCCACGGGA CCGCCACAGA CTGAGCCTTC CGGAGCATGG ACTCGCTCCA GACCGTGTGC 600
 ACCTGTGCA TTAACCTGT TTTCTGTGA TTACCTCTG GTTTGACTTC CCAGGGTCTT 660
 GGGATGGGAG AGTGGGATC AGGTGCACTT GGCTCTTAAC CCTCAAGGGT TCTTTAACTC 720
 80 ACATTCAAG GAGTCCAGA TCTCTGAGT AGTGATTTTG GTGACAAGTT TTTCTTTTG 780
 AAATCAAACC TTGTAACCTA TTTATTGCTG ATGGCCACTC TTTTCTTGA CTCCCTCTG 840
 CCTCTGAGGG CTCTAGTATT GATGGGAGG GAGGCCAAG TACCACTCAT GGAGAGTATG 900
 TGCTGAGATG CTCCGACCT TTCAAGTGAC GCAGGAACAC TGGGGAGTGG TGAATGATTG 960
 GGGTGAAGAC ATCCCTGGAG TGAAGGACTC CTCAGCATGG GGGGAGTGG GGCACAGTT 1020
 AGGGCTGCCC CCATTCCAGT GGTGGAGCG CTGTGGATGG CTGCTTTTTC TCAACCTTTC 1080

5 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTG AAGAACTTA GACTTCACCC 1140
 ACCAGCTGGC ACAGGTGCAC AGATTCATAA ATTCCACAC GTGTGTGTTT AACATCTGAA 1200
 ACTTAGGCCA AGTAGAGAGC ATCAGGGTAA ATGGCGTTCA TTTCTCTGTT AAGATGCAGC 1260
 CATCCATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAACAAT ACAAGGGGAC 1320
 TTCAAAGTT CACGAAAAAA AAAAAAATA AAAAAAATA AAAAAAATA AAA

A36 Protein sequence:

10 Gene name: Differentially expressed C016 gene (clone MGC:5257)
 Unigene number: Hs.69517
 Probeset Accession #: AA447522
 Protein Accession #: AAH01291
 Signal sequence: 1-17 (first underlined sequence)
 Transmembrane domain: 146 - 162
 15 Cellular localization: plasma membrane

20 1 11 21 31 41 51
 | | | | | |
 MALLALLLVV ALPRVWTDAN LTAQRDPED SQRTDEGDNR VNVHVCEREN TFEQNPFRRC 60
 KWTEPYCVIA AVKIFPRFFM VAKQCSAGCA AMERPKPEEK RFLLEEFMPF FYLKCKKIRY 120
 CNLEGGPPINS SVFKEYAGSM GESCGGLWLA ILLLLASIAA GLSLSL

A37 DNA SEQUENCE

25 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

30 1 11 21 31 41 51
 | | | | | |
 35 AGCAACGACG CCGGGCAGCG GAGCGGCGCG CCGCGCCATG TGGCTGCTGG GGCCTGCTGG 60
 CCTGCTGCTG AGCAGGCGCG CGGAGAGCCA GCTGCTCCCC GGGAACTACT TCACCAATGA 120
 GTGCAACATA CCAGGCAACT TCATGTGACG CAATGGACGG TGCAATCCCG GCGCCTGGCA 180
 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTCGAAATGT GGCCCAACCT TCTTCCCTCG TGCCAGCGCG ATCCATTGCA TCATTGGTGG 300
 40 CTTCGGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCG CTTTGCTCCA CCGCCCGCTA CCCTGCAAG AACGGCTCT GTATTGACAA 420
 GAGCTTCATC TGCGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 AAGTTCTCAA GAACCCGGCA GTGGCGAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
 TTACCCGAGC ATCACTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
 45 CCTGCTGGCA CTGGTCTTGC ACCACGAGCG GAGCGGAAC AACCTCATGA CGCTGCCCGT 660
 GCACCGGCTG CAGCACCGTG TGCTGCTGTC CCGCTGGTG GTCTGGGACC ACCCCACCA 720
 CTGCAACGTC ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 GAATGCGTGG GAAGTAGGCT CCCACCCCTC CTACTCCGAG GCTTGTCTGG ACCAGAGGCC 840
 TGCGTGGTAT GACCTTCTCT CACCGCCCTA CTCTTCTGAC ACGGAATCTC TGAACCAAGC 900
 50 CGACCTGCCC CCCTACCGGT CCGGGTCCGG GAGTGCCCAAC AGTGCCAGCT CCCAGGCAGC 960
 CAGCAGGCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
 GGGCACTGCT GAGCCCAAGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
 AGTTATCTCA AAGTGCATAT GGGTTAATCT GCTCTGACTT GTTCCATTC TAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCACTGTGA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 55 AACTATCTCT GCATTCCCTT CCTCCCCAGC ACTTCAGAGA TGTTTTCTTG GCGTCTCAGT 1260
 TGACATGATC TGTGTGCGGT CTTTCTGTC AGGTCACTCT TCCCTGGGGA CCGAGATCA 1320
 CACCCCTATT TTTCACATTA TTCTGTTTCT GTTGAGAGAG CAGCATATAA AACAGTATTG 1380
 AAATAGGCTG GAGAGAGACA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 CGCTGGACCC AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTGTGGGA TTTGGGTTAG 1500
 60 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCAACCCCG CAAAAAATTT CCATTGTAGC 1560
 ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAAACCT TGAAGCTGAG TAACACCCCT CAGCAGTCGG AACGTTATTT TGGTTTGTG 1680
 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTTG CCCAAGAATG 1740
 CTCACTCTGA GAGCTTTCTT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
 65 GAGCCCTCTC CATGAGTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCCAAGACCC 1860
 TACACTGTCC CTGGCTCTAC AGCCACTTAC CTGTTTCTG GACTGTCAAC CTCACAGCTG 1920
 ACCTGCCCCG AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGACCTGGCT 1980
 GTATGTCCCT GTGGCCCACA CCCAGCCTGT CTGCTCATT CATGCAGCCT CAACACTGGC 2040
 CTCCAAAGTT CCCTTAACAC TTGCAAAGTC CTTTTACCT GTGCATTGG ACTTGAGGAC 2100
 70 ACTGGTTTCT ATCAGAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CAGCTCTCTC TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 GGTGAGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 AGACAATTGG GAGTCAAGAT TTTCATTGTT GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 75 TGAAACAGTG TGTTTGTGTT TTCCCTTCTA GTTAAGGAGC TATTTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAAGGAGATC 2460
 ACACCTGTGC CCGCTGAGC CCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 ACATTGTGTC ATTTGTGAC CTTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580
 AGAGGGACTC CTCTCTCCCT CCGTGATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
 80 TTCTCTGTGT CCACTCAGCC ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAAAAGTT 2700
 AGGTGTGTTT TGSCAAGAAA CCACACTGAC TGATGAGGGG TAAAAAGGAA CCAGGTAGAG 2760
 CCACCTCGGG CAGCTGTAC CCATTAGAAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820
 AACCTGTTTG ACCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTTCAG 2880
 TGATCTGTTT CTGTAGACTT TTCTTCTTT TTTTAAACCA ATCCAAAGGA TGTTACAGAA 2940
 AAGCTAGCCA CTGTATTTT GTTTTGTGTT AAAAAAATA GAAAGAAAGA AAGAAAGAAA 3000

AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTTGATGGGG CCCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAACTC CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTGTAGT 3300
 AGATAAGGGA TGCTTACTAA TGCTTTTAA AACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTAT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GSAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCCAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAAT GAGATCCGTG TTTTATTTTA GCATTAAAT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGTTGT GTGTGCTTGC TTTTGTGTT TTGGTTAGGC TTGGTTTGT TTTTAAATTT 3780
 TTATACTTTC TAATAAATTT GCAGTTTTCAT TCITTTCTGTT TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC ANYWTTGGGG GGGCTTGGGC CTCGGAAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGCGCGG GGGCCACAGT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960
 GAAACCCCTGG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCCCCGGG 4020
 GGAAACCGCA GAGTGTTCGG TAAACACAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A38 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MWLLGPLCLL LSSAAESQLL PGNFNECN IPGNFMSNG RCIPGAWQCD GLPDCFDKSD 60
 KEKCPKAKSK CGPTFPFCAS GIHCIIIGRFR CNGFEDCPDG SDEENTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGNNQD NSDEESCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDHPHNC VTYNVNNGIQ 240
 YVASQAQNA SEVGSPPSYS EALLDQRPW YDLPPFPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

A39 DNA sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGCTGCTG GCTTCTTGAT GAGTCCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCGAGG GCGAGGCGAG 120
 GACCGGGAGA GGGAGAGCG GCGGAGGCT GCGGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGAGGCGG AGAAGGGGA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
 CCGCGGCGC CGCCAGCTGG GCAGGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCT 300
 CGCTTGGCT CTGAGCTTTC CCGGGGAGG GTCCGGTTGC CAGTGAACCC TCCAGAGGCT 360
 TCGGACGAC AGCCCCGGGG GCCTTCTGAC TGCAATCCGA GATTTCATC AGCGAGTGCA 420
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGA TGGCTTAGGA 480
 GCTCCTGGAC CTAGGGCGCG GCGTCTGCG CTCTGGGGG TCGCGGCGA GGGGAGTGGC 540
 CCGCGCGGA AGCGCGCGG GACAGTCAGT GACGAGGCC GGGGGTCCG GGGGCCACGA 600
 CTTCTCGGAG ACCGTCTTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
 TGTGGGGCGC TCGCGCTCG TCCGTCTCCT CATCCTGGAA CGCGCTTCG CTCCTGCAGC 720
 TGCTGCTGGC TCGCTGCTG GCGGGCGGG CGAGGGCCCA GCGCGAGTA CTGCCACGCG 780
 TGGCTGGAAG CGCAGGGCGT CTGGCGCATC GGCCTCCAGT GTCCCGAGCG CTTGACGGCG 840
 GCGACGCCA CCATCTGCTG CGGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCTCG ACCAGGGCGG CTGCGACAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGSC 960
 CGGGCGGACA AAGACGGGCT CCGACGGCTC GGCAGGGCTT CATGCTTAG GGGTACCCAA 1020
 GGAGACGGG AGGGTGGGCC CCCACCGCTG AGGGCTGGC AGCGGTGCTC CCTGAAGGC 1080
 TCCCGAAAG GAAGGCGACT CTTAGGGCT TTCCGGGGG TGCTGCCCGG TGCCAGAGCG 1140
 CGCGGATTCC CATCTTCTCC ACBGGCGGCG CCTCTTCCC TGCAGCGGCC CGCTTGGCC 1200
 ATCTACGTG CGTTCCTCAT TGTGTGCTCC GTGTTGTGCG CCTTATCAT CTGCGGCTCC 1260
 CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320
 GCGCCAGGG GTAACCGCTT GATGAGGACC ATCCCATGA TCCCACTGCG CAGCACTCC 1380
 CGGGGTCTGT CTCAAGCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCAG CGCCAACTCC 1440
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 CAGATTGTG CACATCAAGG GCAGTATCTG CATCCCCAT ACSTGGGGA CAGGTGAGC 1620
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACBGGCTGCA GCCTGGCTAC 1680
 AGGCAGATT AGTCCCTT CCTCACACC AACAGTGAA AGAAGATGA CCAGCGGTG 1740
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTG GTGGTATTTA TGGCAGGATT CCTTGGATG 1860
 GCTTCATTG CCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGGT ATCATTGATT TATGATGAA AACCGGCTC AGCTGAGAT GACTGTGATG 1980
 TTGCTGATG GTGTATAACA AATGCTTGA TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTCTTTT 2100

5 TGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATCTCC CTTTACTGG GACTTTTTTT 2160
 TTTTITTTTT TTTTITTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGGGATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCAACA CTCTGGCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TGTATTTTT 2340
 TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCTGA CCTCAAGCAA 2400
 TCTGCCCTGC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTT TTTTCTTA ATGCATCCAA GGTTAAGGGG AAGACGCAAA TAACAGGACT 2520
 ATTCTAAAAG GAAACCTGTT TGAACCTGTT GAGATCAGTC ATCAGTCTCA GTATCCACA 2580
 10 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTT GTCTATTTT GTGCTTTGG 2640
 GGGCCTATT TGTGCTTTT TACCTTATGT AGAGATCTTA TTCAAAGTG ATTTCTACA 2700
 TTAAGAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
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 TTGATTGTAT CTTAATTTTC TGGCTTAAAG GTGACATCTG AGAGGTAATG CATCTTTTT 2880
 15 TATATTGAAA TCATAAACTA TCACCCGCTG CTTCTCTGAG TTACTTTTAA TTTGCTTTG 2940
 TGGTTATGTT TTGGCGTTTC CTCTCTGTTG GTTTTCAGAG CCCCATGTCT ATATAGTCT 3000
 GAGTGCAGTG AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCCA GATCTGATA 3060
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 TAGCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACAGATAC GATTACTTT 3180
 20 GCAGATCTA AGGCTTTTTA TACTCTTGT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
 GATTGTAAAG AGAAAGCTT TTCAAAGAG GATTGCCTT CTCTCCAC ACTGTTCTG 3300
 AITTCCTCTC TCTTTCAGG CTCAAAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
 CAAATCAAG TGAATTTAT TGTGTGTTCT TTACTTATAT AAAAAAGAT AACTTTAAG 3420
 ATGTGCACT ACATTTCCAA CTGCTAGCAC AACCAAGTAT TTGTAATTAA ACAAATCGCT 3480
 25 GTATGTTATG GTCTTCTACA CATTATGTC TATAGATATC TATCGATCAT CTTTCTATT 3540
 TGTTCATGA CTGAATAATG TAAACCAAGT GTTGCCAATT GGTATCATCA ATGATATCA 3600
 TTTTATAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAATA TTTTATGAT 3660
 TGAATAAAAA AAAAAAATA AAAAAAATA

30 A40 Protein sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 35 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular localization: not determined

40 1 11 21 31 41 51
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 MLSGFLMSPS TQHQAYQTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
 GEAEKNRGE PPWIRAQQO PRPPFAGQAP GTAAGGAQDP RLPRGRSRGR VRLVPKPEA 120
 SGRQPRGPD CIPFPSSASA TEKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180
 45 PRGKRRTVS DEARSPGPR LLGDRPALSG DALSAAPRVV CGALAARFSP HPGTPLRSCS 240
 CCLWRCWRG RGPGEYCHG WLDAGQVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGCND DRQGGAGEPG RADKDGPRRL GRASCLRGTO GDGEGAPFPV RAWQRCSPFG 360
 SPKGRQLLRA FPGLLPRARR RGFSSSPRGG PSFLQRPALP IYVPFLIVGS VEVAFIILGS 420
 LVAACCCRL RPKQDPQQR APGGNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480
 50 GARAPPTRSQ TNCCLPEGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGYL HPPYVGYTVQ 540
 HDSVPMTAVP FFMGLQPGY RQIQSPFPHT NSEQMYPVAV TV

A41 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 (H.sapiens)
 55 Unigene number: Hs.100686
 ProbeSet Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
 | | | | |
 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
 CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGTCACAG TTTCTTCCAA CCTTGCCATT 120
 65 GCAATAAAAA AGGAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
 ACTTGGGTAC AAACCTTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
 ATGTTTATT ATCACCTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGCCC 300
 CAAATGAAG AAATACAAGA AATGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
 GAAACCACTG ATAAGAAATT ATCACCTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420
 70 GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
 TATGAGCCTC GGGATTATAC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAGT CAAATTCAT 600
 GAAGAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
 75 TTACTATTTA GTTTTITTA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
 TCTGAAAAA AAAAAAATA AAAAAAATA

A42 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 (H.sapiens)
 80 Unigene number: Hs.100686
 ProbeSet Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted


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1      11      21      31      41      51
5  |  |  |  |  |  |
  MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
  PLMVIHHLED CQYSQALKKV FAQNEEIQEM AQNKFIMLNL MHETTDKNLS PDGQYVPRIM 120
  FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

```

10 A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
20 |  |  |  |  |  |
  ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
  ATTCTCCAAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
  TTTCTAGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
  TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTGCGCTT CTGCAGTCAT CAGTGTTTTA 240
  ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTCAGTT 300
  GCCTTTGTTC AGGAATATCG TTCAAGAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
  CCAGAATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
  CCAGGTGATA CAGTTTGCTT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTTGTTF 480
  GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTC 540
  AAGGTGACAG TCCTTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
  GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAAG GTGTTGTCAT TGAACAGGA 660
  GAAAAATCTG AATTGGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
  CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGGTATA 780
  ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840
  ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTCAAGTGC 900
  ACGCTAGCTC TTGGTGTATT GAGAAATGGT AAGAAAAGGG CCATTGTGAA AAGCTGCTC 960
  ATGTTTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGGA AACACTGAGC 1020
  AAGAAATGAA TGACTGTATC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
  GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTTGTTGAT GTGATGTTGT TCATGGATTG 1140
  TATAACCCAG GTTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
  AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTC TAATTGCTCT TGCAATGAAG 1260
  ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAA CTGAATACCC TTTTAGCTCT 1320
  GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
  TGGTTTATGA AAGGTGCTTA CGAACCAAGT ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
  GGCAGACCTT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGGA GAAGGCACGC 1500
  ATGGGCTCAG CGGGACTCAG AGTTCCTGCT TTGGCTCTCT GTCTCGAACT GGGACAGCTG 1560
  ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
  ACAACACTCA TTGCTTCAGG AGTATCAATA AAAATGATTA CTGGAGATTC ACAGGAGACT 1680
  GCAAGTGCAG TCGCCAGCTG TCTGGGATTG TATTCCAAAA CTTCAGCAGT AGTCTCAGGA 1740
  GAAGAAATAG AAAAAATGGA TGTTCAGCAG CTTCACAAAA TAGTACCAAA GGTTCAGTA 1800
  TTTTACAGAG CTAGCCCAAG GCACAAGATG AAAATTAATA AGTCGCTACA GAAGAACGGT 1860
  TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCGA TTGCTCTGAA GGCTGCAGAC 1920
  ATGGAGATTG CGATGGGCCA GACTGTGTAC GATGTTTGCA AAGAGGCAGC AGACATGATC 1980
  CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
  AATAACATTA AAAATTTTCT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACCTTA 2100
  ATCTCATTTG CTACATTAAT GAACCTTCTC AATCCTCTCA ATGCCATGCA GATTTGTGG 2160
  ATCAATATTA TTATGATGGG ACCCCAGCTC CAGAGCCTTG GAGTAGAACC AGTGATATAA 2220
  GATGTCTTTC GTAACCTTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTTGATA 2280
  CTTAAATAC TTGTTTCATC AATAATCAAT GTTTGTGGGA CTTTGTGTTG CTTCCTGGCGT 2340
  GAGCTACGAG ACAATGTGAT TACACCTCGA GACACACAAA TGACCTTCAC ATGCTTTGTG 2400
  TTTTGTGACA TGTTCATGTC ACTAAGTTCC AGATCCCGA CCAAGTCTGT GTTTGAGATT 2460
  GGAAGTGTGA GTAATAGAAT GTTTGTCTAT GCAGTTCTTG GATCCATCAT GGGACAATTA 2520
  CTAGTTATTT ACTTTCCTCC GCTTCAGAA GTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
  GATCTGTGTG TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
  AAGGTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
  CTGAGATAT GA

```

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Protein Accession #: AAF27813
 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

```

1      11      21      31      41      51
80 |  |  |  |  |  |
  MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKKYI 60
  SQFKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQEYRSEK SLEELSKLVP 120
  PECHCVREK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSIDES SLTGETTPCS 180
  KVTAPQPAAT NGDLASRSNI APMGTLVRCG KAKGVVIGTG ENSBPGEVFK MQQAEAPKT 240
  PLQKSMDDLK QQLSFYSFPI IGIIMLVGWL LGKDILEMFT ISVSLAVAAL PEGLPIVVTV 300

```

5 TLALGVMMV KGRAIVKCLP IVETLGCCNV ICSDKTGTLT KNEMTVTHIF TSDGLHAEVT 360
 GVGYNQFGEV IVDGDVVHGF YNPAVSRIE AGCVCNDAVI RNNTLMGKPT EGALIALAMK 420
 MGLDGLQDDY IRKAEYPFSS EQKNMAVKCV HRTQODRPEI CFMKGAYEQV IKYCTTYQSK 480
 10 GQTLTLTQQQ RDVYQDEKAR MGSAGLRVLA LASGPGLGQL TFLGLVGIIID PPRTGVKEAV 540
 TLLIASGVSI KMITGDSQET AVAIA SRLGL YSKTSQSVSG BEIDAMDVOQ LSQIVPKVAV 600
 FYRASPRHMK KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADMI 660
 LVDDDFQTIM SAIEEGKGIY NNIKNFVRFO LSTSI AALTL ISLATLMNFP NPLNAMQILW 720
 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
 ELRDNVITPR DTTMTFTCFV FDFMFNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMQQL 840
 15 LVYFPPIQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSREIKQ KHVSTSTSSSF 900
 LEV

A45 DNA sequence

15 Gene name: ESTs
 Unigene number: Hs.157601
 Probeset Accession #: W07459
 Nucleic Acid Accession #: AC005383
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCGTAGAAG TGAAGTACTT 60
 25 TTTTATTATG AGACCTGGGC CGATGCCGCT TTAACAAACG CGAGGGGCTC TATGCACCTC 120
 CTTGGGCGTA GTTCTCCGA CCTCAGCCGG GTCCGGTCTG GCCGCCCTCT CCCAGGAGAG 180
 ACAACACAGT GTCCACAGTG GCAGCCGCGC CCCGGGCGCC CCTCTGTGA TCCCGTAGCG 240
 CCCCCGCGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGCGAC CGAGCGCTGG 300
 TCGCCGCTCT CCTTCCGTTA TATCAACATG CCCCCTTCC TGTGTCTGGA GGCCGTCTGT 360
 30 GTTTTCTCTG TTTCCAGAGT GCCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAACAAA 420
 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCACTGGAC 480
 ATCATGTTTC TTTTAGATGG GTCTAACAGC GTCCGGAAGG GGAGCTTTGA AAGGTCCAGT 540
 CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGGATTCTT TTAACCCCAA 660
 CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
 35 CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCTTGGAG GCAGAAATGC TTCTGTGCCC 780
 CAGATCTCTA TCATGCTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAGT 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGGTGGGAG 900
 GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGCAGCAAG TGCTGTGTGC TGAGCAGGTG 960
 40 GAGGATGCCA CCAAGCGGCT CTTCAGCACC CTCAGCAGCT CGGCCATCTG CTCCAGCGCC 1020
 ACGCCAGACT GCAGGGTCGA GGCTCACCCC TGTGAGCACA GGAACCTGGA GATGGTCCGG 1080
 GAGTTCCGCT GCAATGCCCA ATGCTGGAGA GGATCGCGGC GGACCTTTGC GGTGTGCTGT 1140
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTCTA CCAACCTTGC CACCTGCTAC 1200
 AGGACCACTT GCCCAGGCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
 45 CCAGAAGGAG TGAACGCTA CCAAGTGCCTC TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCCAGCTCC TCTTCTGCTT GGACAGCTCT 1380
 GCGGGCAACA CTCTGGACCG CTCTCTGCGG GCCAAAGTCT TGTGTGAAGG GTTTGTGCGG 1440
 GCGGTGCTGA GCGAGGACTC TCGGGCCGGA GTGGGTGTGG CCAATACAG CAGGGAGCTG 1500
 CTGGTGGCGG TGCTGTGGGG GGAGTACCAG GATGTGCTCG ACCTGTGCTG GAGCCTCGAT 1560
 50 GGCATTCCCT TCGGTGTGGG CCCCACCTTG ACGGGCAGTG CCTTGGGCA GGCGCAGAG 1620
 CTGGCTTGTG GAGCGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGGTTTGT 1680
 CTCACTGAGT CACTCTCCGA CGATGAGGTT GCGGGCCAG CGCGTACGC AAGGGCGGGA 1740
 GAGCTGTCTC TGCTGGGTGT AGGCAGTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCTT 1860
 55 GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1920
 CTGCTCTTCA TGTGGACAC CTCTGCCTCA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
 AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGG 2040
 CTGGTGTGTG ATGGCAGCCA GGTGCAGACT GCCTTCCGCG TGAACACCAA ACCCACCCGG 2100
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTTACCTAG GTGGGTGGGG CTCAGCCGGC 2160
 60 ACCGCCCTGC TGACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTTGGT 2220
 GTCCCAAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGGC CAGAGGATGC AGCCGTTCTT 2280
 GCCCAGAAGC TGAGGAACRA TGGCATCTCT GTCTTGTGCG TGGGCGTGGG GCCTGTCTTA 2340
 AGTGAGGGTC TGCGAGGGCT TGCAAGTCCC CGGATTCCC TGATCCACGT GGCAGCTTAC 2400
 GCGGACCTGC GGTACCAACA GACGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460
 65 CCAGTCAACC TCTGCAAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CCTGCAGAA 2520
 GGGAGCTAAC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCACTGCGA GAACCGTGAG 2580
 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGTGAGATTG TTGAGACGCC CCTGAGGCAC 2640
 ATGGCTCCCG TGCAAGAGGG CAGCAGCCGT ACCCTCCCA GCAACTACAG AGAAGGCCCTG 2700
 70 GGCACTGAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCCC CAGGTCTCTA GAATGTCTGC 2760
 TTCCCGCTGT GGCAGGACC ACTATTCTCA CTGAGGGAGG AGGATGTCCC AACTGCAGCC 2820
 ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACCCACA AACGATGTTG TTGAAAAGTT 2880
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTCAT 2940
 CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTGGAAG ACTTAAATTT AGCGGCCTGA 3000
 CGTTCCTTTG CACACAATCA ATGCTCGCCA GAATGTTGTT GACACAGTAA TGCCACAGCAG 3060
 75 AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAAGCA 3120
 CCAGCTTTTC CACTTCCCCA GAGACATTCT GGATGCATTG GCATTGAGTC TGAAGGGGGG 3180
 CTTGAGGGAC GTTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAAGA GACTTGGAAA 3240
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGATGGGGGA GGGGCTGAGT 3300
 80 TGTGCATGGG CCGAGTCTG GAGGGCCACG TAAATCGTT CTGAGTCTG AGCAGTGTCC 3360
 ACCTTGAAGG TCTTC

A46 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

```

10      1      11      21      31      41      51
      |      |      |      |      |      |
      MPFFLLLEAV CVFLFSRVFP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMPLLDGSN 60
      SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFFLDSFST QQEVKARIKR 120
      MVFKGGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTG KSQGDVALPS KQLKERGVTV 180
      FAVGVRFFRW EELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
      PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCGPGCD 300
      SQPCQNGTGC VP EGLDGYQC LCPLAFGGBA NCALKLSLEK RVDLLFLDLS SAGTTLDGFL 360
      RAKVVFVRV RAVLSEDSRA RVGVATYSRE LLVAVPVGBY QDVPDLVWSL DGIPFRGGPT 420
      LTGSALRQAA ERGFGSATRT GQDRPRRVVV LLETSHSEDE VAGPARHARA RELLLLVGS 480
      EAVRAELEEE TGSPKHMVYV SDPQDLFNQI PELQGLKCSR QRPQCRQAL DLVFMLDISA 540
      SVGPENFAQM QSFVRSCALQ FEVNPDTVQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
      APYLGGVGA GTALLHIYDK VMTVQRGARF GVPKAVVVLV GGRGAEDAAV PAQKLNNNGI 660
      SVLVVGVGPV LSEGLRRLAG PRDSLIVHAA YADLRVHQDV LIEWLCEAK QFVNLCQSPS 720
      CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSSCVCVS QGMILETPLR HMAFVQEGSS 780
      RTPPSNYREG LGTEMVPTFW NVCAQGP
  
```

COLON

30 **A47 DNA SEQUENCE:**
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 35 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```

40      1      11      21      31      41      51
      |      |      |      |      |      |
      CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
      CTACACTCAG CTTTGGGCTC CTGCTCTCTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120
      GCAATAAAAA AGGAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
      ACTTGGGTAC AAACCTTATG AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
      ATGGTTATTC ATCACTTGGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
      CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
      GAAACCACTG ATAAGAATT ATCACCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
      GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
      TATGAGCCTC GGGATTATCC CCTATGATA GAAACATGA AGAAGCAAT AAGACTTATT 540
      CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCCT TCAAAGAGT CAAATTTCT 600
      GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
      TTACTATTTA GTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTAAATA 720
      TCTGAAAAAA AAAAAAAA AAAAAAAA
  
```

55 **A48 Protein sequence:**
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 60 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

```

65      1      11      21      31      41      51
      |      |      |      |      |      |
      MMLHSALGLC LLLVTVSSNL AIAIKKEKRP POTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
      PLMVIHLED CQYSQALKKV FAQNEBIQEM AQNKFIMLNL MHEITDKNLS PDGQYVFRIM 120
      FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL
  
```

75 **A49 DNA SEQUENCE**
 Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 Probeset Accession #: AA478599
 Nucleic Acid Accession #: NM_005682
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

```

80      1      11      21      31      41      51
      |      |      |      |      |      |
      CGGCAGCAGG GTCTCGCTCT GTCACACAGG CTGGAGTGCA GTGGTGATGAT CTGGGCTCAT 60
      CGTAACCTCC ACCTCCGGG TTCAAGTGAT TCTCATGCCT CAGCCTCCCG AGTAGCTGGG 120
      ATTACAGGTG GTGACTTCCA AGAGTGACTC CGTCGGAGGA AAATGACTCC CAGTCGCTG 180
  
```

5 CTGCAGACGA CACTGTTCTT GCTGAGTCTG CTCTTCCTGG TCCAAGGTGC CCAOCCGAGG 240
 GGCCACAGGG AAGACTTTTCG CTCTCTGAGC CAGCGGAACC AGACACACAG GAGCAGCTCTC 300
 CACTACAAAC CCACACACAGA CCTGCGCATC TCCATCGAGA ACTCCGAAGA GGCCTCTCAC 360
 GTCCATGTCCC CTTTCCCTGC AGCCCACTCT GCTTCCCGAT CCTTCCCTGA CCCACAGGGC 420
 CTCTACCACT TCTGCTCTTA CTGGAACCGA CATGCTGGGA GATTACATCT TCTCTATGGC 480
 AAGCGTGACT TCTTGCTGAG TGACAAAGCC TCTAGCTCC TCTGCTTCCA GCACAGGAG 540
 GAGAGCCTGG CTCAGGGCCC CCGCTGTGTA GCCACTTCTG TCACCTCTCTG GTGGAGCCCT 600
 CAGAACATCA GCCTGCCAG TGCCGCCAGC TTCACCTTCT CCTTCCACAG TCTTCCCCAC 660
 10 ACGGCCGCTC ACAATGCCCTC GGTGGACATG TGCAGACTCA AAAGGGACCT CCAGCTGCTC 720
 AGCCAGTTCC TGAAGCATCC CCAGAAAGGC TCAAGGAGGC CCTCGGCTGC CCCCGCCAGC 780
 CAGCAGTTGC AGAGCTTGA GTCGAACTG ACCTCTGTGA GATTTCATGG GGACATGGTG 840
 TCCTTCGAGG AGGACCGGAT CAACGCCACG GTATGGAAGC TCCAGCCAC AGCCCGCCTC 900
 CAGGACCTGC ACATCCACTC CCGGCAGGAG GAGGAGCAGA GCGAGATCAT GGAGTACTCG 960
 GTGCTGCTGC TCGAACACT CTTCAGAGG ACGAAAGGCC GGAGCGGGGA GGCTGAGAAG 1020
 15 AGACTCTCC TGGTGGACTT CAGCAGCCAA GCCCTGTTCC AGGACAAGAA TTCCAGCCAA 1080
 GTCTGCTGCT GCGAGCTGGA GGGGATTGTG GTACAGAAAC CCAAGTAGC CAACCTCAG 1140
 GAGCCCGTGG TGCTCACTTT CCAGCACCGA CTACAGCCGA AGAATGTGAC TCTGCAATGT 1200
 GTGTTCTGGG TTGAAGACCC CACATTGAGC AGCCCGGGG ATTGGAGCAG TGCTGGGTGT 1260
 20 GAGACCGTGC GCTCTGAGAC CCAACATCC TGCTTCTGCA ACCACTTGAC CTACTTTGCA 1320
 GTGCTGATGG TCTCTCTGGT GAGGTTGAGC CCGCTGCACA AGCACTACCT GAGCTCTCTC 1380
 TCCTACGTGG GCTGTGTGCT CTCTGCCCTG GCCTGCCCTT TCACCATTGC GCCTACCTC 1440
 TGCTCCAGGG TGCCCTGCC GTGCAGGAGG AAACCTCGGG ACTACACCAT CAAGGTGCAC 1500
 ATGAACCTGC TGCTGGCGGT CTCTCTGCTG GACACGAGCT TCCTGCTCAG CGAGCCGGTG 1560
 25 GCCTGCGTGC GCTCTGAGGC TGGCTGCCGA GCCAGTGCCA TCTTCTGCA CTCTCCCTG 1620
 CTCACCTGCC TTCTCTGATG GGGCTCGAG GGGTCAACCC TCTACCGACT CGTGGTGGAG 1680
 GTCTTTGGCA TGTATGTCTT TGGCTACCTA CTCAGCTGA GCGCCATGGG CTGGGGCTTC 1740
 CCCATCTTTT TGGTGACGCT GGTGGCCCTG GTGGATGTGG ACACTATGG CCCATCATC 1800
 TTGGCTGTGC ATAGGACTCC AGAGGGCGTC ATCTACCTTT CCATGTGCTG GATCCGGGAC 1860
 30 TCCTTGGTCA GCTCTGATCA CAACCTGGGC CTCTTCAGCC TGGTGTCTCT GTTCAACATG 1920
 GCCATGTGAG CCACCATGGT GGTGCAGATC CTGCGGCTGC GCCCCACAC CCAAAAGTGG 1980
 TCACATGTGC TGACATGCTT GGGCTCAGC CTGGTCTTGG GCGCTGCCCT GGCTTGATC 2040
 TTCTCTCTCT TTGCTTCTGG CACCTTCCAG CTGTGCTCTC TCTACCTTTT CAGCATCATC 2100
 ACCTCTCTCC AAGGCTTCTT CATCTTCATC TGGTACTGGT CCATGCGGCT CGAGCCCGG 2160
 35 GGTGGCCCTT CCCTCTGAA GAGCAACTCA GACTGCGCCA GGCTCCCAT CAGCTCGGGC 2220
 AGCACCCTGT CCAGCCGATG CTAGGCTCTC AGCCCACTG CCCATGTGAT GAAGCAGAGA 2280
 TCGCGCTCTG TCGACACTGT CCGTGGCCCG CCGAGCCAGG CCGAGCCCA GGCCAGTCAG 2340
 CCGCAGACTT TGGAAAGCCC AACGACCATG GAGAGATGG CCGTTGCCAT GGTGGACGGA 2400
 CTCCCGGGG TGGGGCTTTT GAATTGGCCT TGGGGACTAC TGGGCTCTCA CTCAGCTCCC 2460
 40 ACGGACTCA GAAGTGGCCG GCCATGCTGC CTAGGGTACT GTCCCCACAT CTGTCCCAAC 2520
 CCAGCTGTGAG GCCTGTCTCT TCCTTACMAC CCCTGGGCCC AGCCTCATG CTGGGGGCCA 2580
 GGCTCTGAG CTGAGGGTCT TGGCACATCC TTAATCTGT GCCCTGCTCT GGGACAGAAA 2640
 TGTGGTCCA GTTGTCTCTG CTCTCTGTGT CACCTGAGG GCACTCTGCA TCCTCTGTCA 2700
 TTTTAACTCT AGGTGGCACC CAGGGCGAAT GGGGCCAGG GCAGACCTTC AGGGCCAGAG 2760
 45 CCCTGGCGGA GGAGAGGCC TTTGCCAGGA GCACAGCAGC AGCTCGCTTA CCTCTGAGCC 2820
 G

A50 Protein sequence

50 Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 Protein Accession #: NM_005682.1
 Signal sequence: 1-26
 GPS domain: 342-394
 55 Pfam domain: 7tm_2 [400-665]
 Transmembrane domains: 410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
 Cellular Localization: plasma membrane

60 1 11 21 31 41 51
 | | | | |
 MTPQSLLQTT LFLLSLLFLV QGAHGRGHRE DFRFCSQRNQ THRSSLYHKP TPDLRISIEN 60
 SEEALTIVHAP FPAAHPSRS FPDPRGLYHF CLYWNRHAGR LHLLYGKRD LLSDKASSLL 120
 CFQHQEESLA QGPPLLATSV TSWHSPQNIS LPSAASFTFS FHSPPTHAAH NASVDMCELK 180
 65 RDLQLLSQFL KHPQKASRRP SAAPASQQLQ SLESKLTSVR PMGDMVSFEE DRINATVVKL 240
 QPTAGLQDLH IHSRQSEEQS RIMEYSVLLP RTLPORTKGR SGEAEKRLLL VDFSSQALPQ 300
 DKNSSQVLGE KVLGIVVQNT KVANLTFEIV LTFQHQQLPK NVTLCQVFWV EDPTLSSPGH 360
 WSSAGCETVR RETQTSFCFN HLTIFYAVLMV SSVEDDAVHK HYLGLLSYVG CVVSALACLIV 420
 70 TIAAYLCRSR PLPCRRKPRD YTIKVHMLL LAVFLDTSF LLSEPVALTG SEAGCRASAI 480
 FLHFSLLTCL SWMGLLEGYNL YRLVVEVFGT YVPGYLLKLS AMGNGPPIPL VTLVALVDVD 540
 NYGPIILAVH RTEPGVIYPS MCWIRDSLVS YITNLGLPSL VPLENMAMLA TMVQILRLR 600
 PHTQKNSHVL TLLGLSLVLG LFWALIFFSF ASGTFLVLVL YLFSIITSFQ GLFIFIWYS 660
 MRLQARGGPS PLKNSNSDCAR LPISSGSTSS SRI

A51 DNA SEQUENCE

75 Gene name: Hypothetical protein FLJ20063
 Unigene number: Hs.5940
 Probeset Accession #: AA053660
 Nucleic Acid Accession #: AA053660
 80 Coding sequence: 218-1360 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CCCCCATGAC TTTGTACAGC TACTTCACTG CTTCCTCCCA ATTAGTACAC ATAGTTCCTC 60

5
10
15
20
25
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35
40
45

CACAATTCCT ACACCTGCTC CCCCCATAAT CAGTACACAT AGTTCCTCCA CAATTCCTAT 120
ACCTACTGCT GCAGACAGTG AGTCAACCAC AAATGTAAAT TCATTAGCTA CCTCTGACAT 180
AATCACCGCT TCATCTCCAA ATGATGGATT AATCACAATG GTTCCTTCTG AAACACAAAG 240
TAACAATGAA ATGTCCCCCA CCACAGAAGA CAATCAATCA TCAGGGCCTC CCATCTGGCAC 300
CGCTTTATTG GAGACACAGC CCCTAAACAG CACAGGTCCC AGCAATCCTT GCCAAGATGA 360
TCCCTGTGCA GATAATTCGT TATGTGTTAA GCTGCATAAT ACAAGTITTT GCCTGTGTTT 420
AGAAGGGTAT TACTACAACT CTCTACATG TAAGAAAGGA AAGGTATTCC CTGGGAAGAT 480
TTCAGTGACA GTATCAGAAA CATTGACCC AGAAGAGAAA CATTCCATGG CCTATCAAGA 540
CTTGCAATAGT GAAATTAATA GCTTGTTTAA AGATGTATTT GGCACATCTG TTTATGGACA 600
GACTGTAAAT CTTACTGTAA GCACATCTCT GTCACCAAGA TCTGAAATGC GTGCTGATGA 660
CAAGTTTGTG GATGTAAACAA TAGTAACAAT TTTGGCAGAA ACCACAAGTG ACAATGAGAA 720
GACTGTGACT GAGAAAAATTA ATAAAGCAAT TAGAAGTAGC TCAAGCAACT TTCTAAACTA 780
TGATTTGACC CTTGCGTGTG ATTATTATGG CTGTAACCAG ACTGCGGATG ACTGCCCTCA 840
TGGTTTAGCA TGCAGATTGA AATCTGACCT GCAAAGGCCT AACCCACAGA GCCCTTTCTG 900
CGTTGCTTCC AGTCTCAAGT GTCCTGATGC CTGCAACGCA CAGCACAAAG AATGCTTAAT 960
AAAGAGAGT GTTGGGGGCC CTGAGTGTGC GTGCGTGCCC GGCTACCAGG AAGATGCTAA 1020
TGGGAACGTC CAAAAGTGTG CATTGGCTA CAGTGGACTC GACTGTAAGG ACAAAATTTCA 1080
GCTGATGCTC ACTATTGTGG GCACCATCGC TGGCATTTGC ATTCTCAGCA TGATAATTGC 1140
ATTGATGTGC ACAGCAAGAT CAAATAACAA AACCAAGCAT ATTGAAGAAG AGAACTTGAT 1200
TGACGAAGAC TTTCAAAATC TAAAACTGCG GTGCACAGGC TTCACCAATC TTGGAGCAGA 1260
AGGGAGCGTC TTTCCTAAGG TCAGGATAAC GGCTCCAGG GACAGCCAGA TGCAAAATCC 1320
CTATTCAAGA CACAGCAGCA TGCCCCGCC TGACTATTAG AATCATAAGA ATGTGGAACC 1380
CGCCATGGCC CCAACCAAT GTACAAGCTA TTATTAGAG TGTTAGAAA GACTGATGGA 1440
GAAGTAGACA CAGTAAAGA TCTGGCCTCC GGGTTTITTC TTCCATCTGA CATCTGCCAG 1500
CCTCTCTGAA TGGAAGTTGT GAATGTTTGC AACGAATCCA GCTCACTTGC TAAATAAGAA 1560
TCTATGACAT TAAATGTAGT AGATGCTATT AGCGCTTGT AGAGAGGTGG TTTTCTTCAA 1620
TCAGTACAAA GTACTGAGAC AATGGTTAGG GTTGTITTTT TAATTCTTTT CCTGGTAGGG 1680
CAACAAGAAC CAITTTCAAT CTAGAGGAAA GCTCCCCAGC ATTGCTGTCT CCTGGGCAAA 1740
CATTGCTCTT GAGTTAAGTG ACCTAATTCC CCTGGGAGAC ATACGCATCA ACTGTGGAGG 1800
TCCGAGGGGA TGAGAAGGGA TACCCACCAT CTTTCAAGGG TCACAAGCTC ACTCTCTGAC 1860
AAGTCAGAA AGGGACACTG CTTCTATCCC TCCAATGGAG AGATTCTGGC AACCTTTGAA 1920
CAGCCCAGAG CTTGCAACCT AGCCTCACCC AAGAAGACTG GAAAGAGACA TATCTCTCAG 1980
CTTTTTCAGG AGGCGTGCCT GGAATCCAG GAACITTTTG ATGCTAATTA GAAGGCTTGG 2040
ACTAAAAGT TCCATATGAG GGTGCACTCT ACAGTTTTTG AAATGCTAGG AGGCAGAAAG 2100
GGCAGAGAGT AAAAAACATG ACCTGGTAGA AGGAAGAGAG GCAAGGAAA CTGGGTGGGG 2160
AGGATCAATT AGAGAGGAG CACCTGGAT CCACCTTCTT CCTTAGTCC CCTCTCCAT 2220
CAGCAAGGA GCACCTCTCT AATCATGCC TCCCGAAGC TGGCTGGGAG AAGGTTTAAA 2280
AACAAAAAT CCAGAGTAA GAGCCTTAGG TCAGTTTGA ATTGAGAGCA AACTGTCTGG 2340
CAAAGGGTGC GAGAGGGAGC TTGTGCTCAG GAGTCCAGCC GTCCAGCCTC GGGGTGTAGG 2400
TTTCTGAGT GTGCCATTGG GGCCTCAGCC TTCTCTGGTG ACAGAGGCTC AGCTGTGGCC 2460
ACCAACACAC AACCAACAC ACACAACCAC ACACACAAAT GGGGGCAACC ACATCCAGTA 2520
CAAGCTTTTA CAAATGTTAT TAGTGTCTCT TTTTATTCT AATGCCTGT CCTCTTAAA 2580
GTTATTATAT TTGTTATAT TATTGTCTCT TGACTGTAA TTGTGAATGG TAATGCAATA 2640
AAGTGCCITT GTTAGATGGT GAAAAAATA AAAAAAATA AAAAAAATA A

A52 Protein sequence:

Gene name: Hypothetical protein FLJ20063
Unigene number: Hs.5940
Probeset Accession #: AA053660
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 289-311
EGF domain: 45-74
SEA domain: 80-196
Cellular Localization: plasma membrane

60
65
70
75

1 11 21 31 41 51
MVPSETQSNV EMSPTTEDNQ SSGPPTGTAL LETSLNSTG PSNPQDDPC ADNSLCVKLH 60
NTSPFLCLEG YYNSSTCKK GKVPFGKISV TVSETFDPEE KHSMAVQDLH SEITSLFKDV 120
FGTSVYGVTV ILTVSTSLSP RSEMRAADKF VDVITVILA ETTSDNEKTV TEKINKAIRS 180
SSSNFLNYDL TLRCDYVGCN QTADDCLNGL ACDCKSDLQR PNPQSPFCVA SSLEKCPDACN 240
AQHKQCLIKK SGAPEACVY PGYQEDANGN CQKCAFYSG LDCKDKFQLI LTIIVGTIAGI 300
VILSMIALI VTARSNNKTK HIEEENLIDE DFQNLKLRST GFTNLGAEGS VFPKVRITAS 360
RDSQMGNPYS RHSSMRPRDY

A53 DNA SEQUENCE

Gene name: TMPRSS3a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Nucleic Acid Accession #: AB038157
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80

1 11 21 31 41 51
ACCGGSCACC GGAACGGCTCG GGTACTTTG TTTCTTAATTA GGTGATGCCC GTGTGAGCCA 60
GGAAGGGCTG GTGTTTATGG GAAGCCAGTA ACCTGTGGC CTACTATCTC TTCCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
AGAGGTCCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTTGA AGCCCCCTTC 240

5 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCCT AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAAGT ACAGATGTGCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCAATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
 10 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGAGGGGA 780
 TGTGCTCTG GCCACGTGGT TACCTTGAG TGCACAGCCT GTGTCATAG AAGGGGCTAC 840
 AGCTCAGCA TCGTGGGTGG AAACATGTCC TTGCTCTGC AGTGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGCA TCAACGCCCT GTGGATCCTC 960
 ACTGCTGCAC ACTGTGTTTA TGAATTGTAC CTCCCAAGT CATGGACCAT CCAGTGGGT 1020
 15 CTAGTTTCCC TGTGGACAA TCCAGCCCA TCCCACTGG TGGAGAAGT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGCAAT GACATCGCCC TTATGAAGCT GGCAGGGCCA 1140
 CTCAGTTCA ATGAATGAT CCAGCCTGTG TGCCTGCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 TCCCTCTGCC TGAACACGCG GCGCGTCCCT TTGATTTC ACAAAGTCTG CAACACAGG 1320
 20 GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGAATGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAAGAG GAGTGGGACA AGTAGCCACC TGAGTTCTG AGGTGATGAA GACAGCCCGA 1620
 25 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
 TTCCGGCAAC AGTAGCAGCG CCGAAAGAGG CACCCCTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTCCTT TTGTTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCTCTAGC TCCCTCAGC GCTGGGACCA CAGGTGCCCG CCACCAACC CAACTAATT 1920
 30 TTGATTTTTT AGTAGAGACA GGGTTTCAAC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCTGTCT TCAGCCTCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
 AGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGCTCTGC AAAATTCCTG 2160
 ACGAGATAAG CAGTTATGTG ACCTCAGTGG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 35 GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGGTT TTCTCTCTA GGGACCAGAA 2280
 CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGCCCTAT TTTCAATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
 TTGTCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAAAA

40 A54 Protein sequence:
 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 45 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPc domain: 216-444
 Cellular Localization: plasma membrane

50
 1 11 21 31 41 51
 | | | | |
 MGENDPFAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFPF IIVIGIILI 60
 55 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GQONAVLQVF 120
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREBPV SIDHLLPDDK 180
 VIALHHSVIV REGCASHVIV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFQGYH 240
 LCGGSVITPL WITTAARCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGA GDASPVLNHA 360
 60 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWHEQMER DLKT

A55 DNA SEQUENCE
 Gene name: Putative G protein-coupled receptor GPCR150
 65 Unigene number: Hs.97101
 Probeset Accession #: AA215333
 Nucleic Acid Accession #: NM_014373
 Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 | | | | |
 GTGGCCTCGA GGTGGTGGCA GGGCCGCCCC CTGCAGTCCG GAGACGAACG CACGGACCGG 60
 GCTCCGGGAG GCAGGTTCCG CTGGAAGGAA CCGCTCTCCG TTGCTCTAC ACTTGCGCAA 120
 75 ATGTCTCCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
 AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAAATAG GAAGATCATC AGTCAAGGAA 240
 GACCACTCGG AGAGGACAGA AAATGAAGCA GTGTTTATC ATGTGTATT TTTTCAAGTCT 300
 TCTTGAAATT TAACTAAAAA TATGACTGCT CTCTCTCAG AGAAGTCTC TTTTCAAGTCT 360
 CAGTACGTC AAACAAACCA GCCCCTAGAC GTTAACTATC TGCTATTTCT GATCATACT 420
 80 GGGAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAAT 480
 TTTATGGAAT ATTTTGTGAT TTCATAGCA TTCGTTGATC TTTTACTTTT GGTAAACATT 540
 TCCATTATAT TGTATTTCAG GGATTTTGTG CTTTAAGCA TTAGGTTTCA TAAATACCA 600
 ATCTGCCTAT TTAATCAAT TATTTCTTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC 660
 CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCTAAAA CAACCAAGCT TTTATTTAAG 720
 TGTCAAAAT TATTATTATT CTTTACAGTA ATTTTAATT GGAATTCAGT CCTTGCTTAT 780

	GTTTTGGGAG	ACCCAGCCAT	CTACCAAAGC	CTGAAGGCAC	AGAATGCTTA	TTCTCGTCAC	840
	TGTCCTTTCT	ATGTCAGCAT	TCAGAGTTAC	TGGCTGTCAT	TTTTCATGGT	GATGATTTTA	900
	TTGTAGCTT	TCATAACCTG	TTGGGAAGAA	GTTACTACTT	TGGTACAGGC	TATCAGGATA	960
5	ACTTCTCTATA	TGAATGAAAC	TATCTTATAT	TTTCTTTTTT	CATCCCACTC	CAGTTATACT	1020
	GTGAGATCTA	AAAAAATATT	CTTATCCAAG	CTCATTTGCT	GTTTTCTCAG	TACCTGGTTA	1080
	CCATTGTGAC	TACTTCAGGT	AATCATGTGT	TTACTTAAAG	TTCAGATTCC	AGCATATATT	1140
	GAGATGAATA	TTCCCTGGIT	ATACTTTGTC	AATAGTTTTT	TCATTGCTAC	AGTGTATTGG	1200
	TTTAATTGTC	ACAAAGCTAA	TTTAAAAGAC	ATTGGATTAC	CTTTGGATCC	ATTTGTCAAC	1260
10	TGGAAGTGCT	GCTTCATTCC	ACTTACAATT	CCTAATCTTG	AGCAAATTGA	AAAGCCTATA	1320
	TCAATAATGA	TTGTTTAATA	TTATTAATTA	AAAGTTACAG	CTGTCAATAAG	ATCATAATTT	1380
	TATGAACAGA	AAGAACTCAG	GACATATTAA	AAAATAAACT	GAACATAAAC	AACTTTGGCC	1440
	CCCTGACTGA	TAGCATTCCA	GAATGTGTCT	TTTGAAGGGC	TATACCAATT	ATTAAATAGT	1500
	GTITTTATTT	AAAAACAAA	TAATTCCAAG	AAGTTTTTAT	AGTTATTTCAG	GGACACTATA	1560
15	TTACAAATAT	TACTTTGTGA	TTAACACAAA	AAGTGATAAG	AGTTAACATT	TGGCTATACT	1620
	GATGTTTGTG	TTACTCAAAA	AACTACTG	ATGCAAACTG	TTATGTAAAT	CTGAGATTTC	1680
	ACTGACAACT	TTAAGATATC	AACCTAAACA	TTTTTATTAA	ATGTTCAAAT	GTAAGCAAGA	1740
	AAAAAAA						
20	<u>A56 Protein sequence</u>						
	Gene name:	Putative G protein-coupled receptor GPCR150					
	Unigene number:	Hs.97101					
	Protein Accession #:	NP_055188					
	Signal sequence:	none found					
25	Transmembrane domains:	23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297					
	Cellular Localization:	plasma membrane					

	1	11	21	31	41	51	
30	MTALSSSENC	FQYQLRQTNQ	PLDVNYLLFL	IILGKILLNI	LTLGMRRKNT	CQNFMEYFCI	60
	SLAFVLLDLL	VNISIIILYFR	DFVLLSIRFT	KYHICLFTQI	ISFTYGLPHY	PVFLTACIDY	120
	CLNFSKTKL	SFKCQKLFYF	FTVILIWISV	LAYVLGDPFI	YQSLKAGNAY	SRHCFPFVSI	180
	QSYWLSFFMV	MILFVAFITC	WEEVITLVQA	IRITSYMNST	ILYPPFSSHS	SYTVRSKKIF	240
35	LSKLIVCFLS	TWLPFVLQV	IIVLLKVQIP	AYIEMNIPWL	YFVNSPLIAT	VYWFNCHKLN	300
	LKDIGLPLDP	FVNWKCCFIP	LTIPNLEQIE	KPISIMIC			

	<u>A57 DNA SEQUENCE</u>						
40	Gene name:	ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]					
	Unigene number:	Hs.19322					
	Probeset Accession #:	AA088458					
	Nucleic Acid Accession #:	AA088458					
45	Coding sequence:	862-1995 (underlined sequences correspond to start and stop codons)					

	1	11	21	31	41	51	
	GCCCTTGAGC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAR	AGGAGCTGGA	GCAGGAGAAG	GAGGTGCTGC	TGCAGGGTTT	GGAGATGATG	120
50	GCGCGGGGCC	GCGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCCCG	180
	CTGGGCCAGA	GCAAGGCGAG	GCGCGACTTT	GCGGCTGCAG	GGAGCCCCCG	CCCACTGGGG	240
	GCGTACTGCG	CCAAGGTACA	AGAGGTGGCC	GCGTGCCTGG	GCGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GCGCCCTGCC	CCCGTCTCTC	TCCGGGCCCC	CCTGCCCTGC	CCTGACGTCC	360
	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
55	CTCACCCAGG	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAACTCG	480
	GCGCTCATTA	AGCAGCTGTT	TGAGGCCCGC	GCCCTGAGCC	AGCAGGACGG	GGGACCTCTG	540
	GATTCACACT	TCACTCTATC	CTTGTGGGCC	GCGTGGGCCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTCGA	GCGTGGGCGC	CCCATCGCAC	CCACCTCTCT	TGGCTGGAGA	CCCCCGGCAG	660
60	GCCCAGGCGC	AGTCCCGGAG	TGGGCGCCTT	CCTGCGCGCC	TGCGCAGATG	GGCTCCCCAG	720
	GCTTGGCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTTTGGGCTC	CTGGTTGYTG	780
	ACATGGGCTG	GGGGCTCTCT	TGAGTCCGCA	TAGTCCGCGC	CTACTACTGG	CGCTGTTCAG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCGCCG	TTTCCAGCGG	TGCCGCGCTG	900
	GGTCCCATCT	TCAGGGAAAG	GCACTGCCCA	CGCCAGGCTG	CACITCCAAC	AACGGGCGAG	960
65	AGAGGGCGCG	GGGCGGCTCC	GACCGCGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGAGGAGG	TGGCTGTAGC	TCGGACGGAC	GGAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAGCGGGG	GGTGCTTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTCCG	ACTTCAGGTT	1140
	CTGGCCCAAG	CTGAGGGACC	CTGGCTGCAG	CGGATCGGCA	CGCGGGGTGG	GCGAGAGCTT	1200
	GGCTGTCATG	TGCCTCCAC	AGACCTGGGG	GTGATGGCCT	TCCCCCTCTT	GGCCGGGACG	1260
70	TTGCCCCCAG	TTGAGTCCCA	CACAACTCC	TGTAGGCTTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCACGTCA	TAGGCAAGGC	CTGTTTCCCC	CGACTCAGGA	TTTCCAAGGC	1380
	CTGGGGTCTC	GCTCAACCCC	CTTTGCTCTC	ACGCCAGGCC	TGTCCCCAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAAC	GAGAAACCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCCTGCCCC	GGCCCACTCC	CGCTGGTGCT	1560
75	GGAGTAGCGA	CTGTGGGGTG	GGCCCTGCTC	AGCCCAACCT	GGAGGGTCCC	AGTGTACCCA	1620
	GAACACGGGG	CACGGCAACA	GCACTGATGG	GTTCTGCAGC	CCAGGGCCCC	CGATGCGGGG	1680
	TCAGTGTGTG	TGGGGCGCAG	GGCCTCCGAT	GCGGGTCCAG	TGCGTGGGGG	GCGCAGGGCC	1740
	CCGATGCGGG	GGTCAGTGCG	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCACTTTGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGTCTCAGAG	GAGGGGGCCT	GGCAGGCAGC	GTGGCAACTC	1860
80	CCTTCCGGAG	CCCAGCTCCA	TGCTAACCTG	CCCACAGCAA	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCAACT	GGTCTGACGG	GGTGTCCAGG	GACAGGCCCA	AGTCAGGCCA	GCACTGACGT	1980
	GCCCTCTAC	GGAAGAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCCTGG	2040
	ACCTCCTGGG	CAGGAAGGGG	TGCAGGTCCT	GAGGGCCTGT	GCCCCACAGC	CCGACACCCC	2100
	AGGTGGACTG	CAGCGCAGTG	GCTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCCCGACAGA	2160
	GGCTGGGGTC	TGCCCCACAG	GGCCTCCCCA	CGTCTGCCCT	TGAGGGTGCC	TGCCATGCCC	2220

5 TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCCGG 2280
 GGTGACTTCA TCAGGAGACC GCCCACAATAG AGCTGGACCC CGCAGCTGAA GCGGAAATGT 2340
 GAGACAGGCT GGCACCTCCG GAAAAAATGC CTTTCAGCCT TGGTGTTCGG TGCAAGGTGA 2400
 AAAGAAATAG GTCTCCACAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCCTGGAGAC 2460
 CACGAGGGGA GAATTTAAAG GCCCCGCGTG GCAGGGTCTA GGTGGCTGGC AGAGGCACAT 2520
 GCAGACCCTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
 GAGCAGCGCT CCTGGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAGGT ACATACACGT 2640
 GCGTGCACAC TGTGATGACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGGG 2700
 10 CAGAAGTGTC CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACACCA GGCCTCAGGA 2760
 TTTTGTGTGG ATCAAGTTCC AAGGAAAAGG AACATCTCAG CCGGGCGTGG TGGTTCACGC 2820
 CTGGAATCCC AGCATTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATTCTCT ACARAAAAA AAAAAGAAAG AAGAAAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 15 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTITT ATATATCTAA 3060
 AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A58 DNA sequence

Gene name: ESTs
 Unigene number: Hs.157601
 20 Probeset Accession #: W07459
 Nucleic Acid Accession #: AC005383
 Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC CGCTAGAAAG TGAAAGTACTT 60
 TTTTATTTCG AGACCTGGGC CGATGCGCGT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
 CTTGGCGGTA GTTCTCCGGA CCTCAGCCGG GTGCGGTCTG GCGGCCCTCT CCCAGGAGAG 180
 30 ACAAAACAGG GTCCACACGT GCAGCCGCGC CCGGGCGGCC CCTCTGTGA TCCCGTAGCG 240
 CCCCCTGGCC CGAGCCGCGC CCGGCTCTGT GAGTAGAGCC GCGCGGCAC CGAGCGCTGG 300
 TGCGCGCTCT CCTTCCGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GCGCGTCTGT 360
 GTTTTCCTGT TTTCCAGAGT GCGCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAAA 420
 35 GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGGC TGCAGTGGAC 480
 ATCATGTTTC TGTTAGATGG GTCTAACAGC GTCCGGAAGG GGAGCTTTGA AAGTCCAAAG 540
 CACTTTGCCA TCACAGTCTG TGACGCTCTG GACATCAGCC CCGAGAGGGT CAGAGTGGGA 600
 GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGGATTCAIT TTCAACCCAA 660
 CAGGAAGTGA AGGCAAGAAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
 40 CTTGCTCTGA AATACCTTCT GCACAGAGGG TTGCCTGGAG GCAGAAATGC TTTCTGTGCC 780
 CAGATCTCTA TCATCGTCAC TGATGGGAAG TCCCAGGGGG ATGTGGCACT GCCATCCAAG 840
 CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGGG TCAGGTTTCC CAGTGGGAG 900
 GAGCTGCACT CACTGGCCAG CGAGCCTAGA GGGCAGCAGG TGCTGTGGGC TGAGCAGGTG 960
 GAGGATGCCA CCAAGCGCCT CTTACGACCC CTCAGCAGCT CGGCCATCTG CTCACGCGCC 1020
 ACGCCAGACT GCAGGGTCTG GGCTCACCCC TGTGAGCACA GGACGCTGGA GATGGTCCGG 1080
 45 GAGTTGCTCG GCAATGCCCC ATGCTGGAGA GATCGCGGGG GGACCTTTCG GGTGCTGGCT 1140
 GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTTAA CCAACCTTGC CACTGTCTAC 1200
 AGGACCACTT GCCAGGGCCC CTGTGACTCG CAGCCCTGCC AGAATGGAGG CACATGTGTT 1260
 CCAGAAGGAG TGGAGCGCTA CCAGTGCCCT TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC 1320
 TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCGACCTCC TCTTCTGTCT GGACAGCTCT 1380
 50 GCGGGCACCA CTCTGGACGG CTTCCTGCGG GCCAAAGTCT TCGTGAAGCG GTTTGTGCGG 1440
 GCCGTGCTGA GCGAGGACCTC TCGGGGCCGA GTGGGTGTGG CCACATACAG CAGGAGCTG 1500
 CTGGTGGCGG TGCTGTGGGG GGAGTACCAG GATGTGCCTG ACCTGGTCTG GAGCTCTGAT 1560
 GGCACTTCTG GAGGCGCCAC CAGGACAGGC CAGGACCGGC CAGTGAAGT GGTGTGTTTG 1620
 55 CTACCTTAGT CACTCTCGGA GATGAGGTT GCGGGCCAG CGCTCAGCAG AAGGCGCGCA 1740
 GAGCTGTCTC TGCTGGGTGT AGGCACTGAG GCGGTGCGGG CAGAGCTGGA GGAGATCACA 1800
 GGCAGCCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAATCCCTT 1860
 GAGCTGCAGG GGAAGCTGTG CAGCGGCGAG CGGCCAGGGT GCGGACACA AGCCCTGGAC 1920
 CTGCTCTTCA TGTGAGACAC CTCTGCTCTA GTAGGGCCGG AGAATTTTGC TCAGATGCAG 1980
 60 AGCTTTTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGC 2040
 CTGGTGGTGT ATGGCAGCCA GGTGCAAGCT GCCTTGGGGC TGGACACCAA ACCCACCCGG 2100
 GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CCTACCTAG GTGGGGTGGG CTCAGCCGGC 2160
 ACCGCCCTGC TGCAATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTTGGT 2220
 GTCCCAAGAG CTGTGGTGGT GCTCACAGGC GGGAGAGGGC CAGAGGATGC AGCGTTCTT 2280
 65 GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTTGGTGG TGGGCGTGGG GCCTGTCTCA 2340
 AGTGAGGGTC TGCGAGGCTC TGCAAGTCCC CCGGATTCCT TGATCCACGT GGCAGCTTAC 2400
 GCCGACCTGC GGTACCAACA GGACGTGCTC ATTGAGTGGC TGTGTGAGA AGCCAAGCAG 2460
 CCAGTCAACC TCTGCAAAAC CAGCCCGTGC ATGAATGAGG GCAGCTGCTG CCTGCAGAA 2520
 GGGAGCTACC GCTGCAAGTG TCGGGATGGC TGGGAGGGCC CCCACTGCGA GAACCGTGA 2580
 70 TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GATGAGATTC TTGAGACGCC CCTGAGGCAC 2640
 ATGGCTCCCG TGCAGGAGGG CAGCAGCGGT ACCCTTCCCA GCAACTACAG AGAAGGCTGT 2700
 GGCACGTAAA TGGTGCCTAC CTTCTGGAAT GTCTGTGCC CAGGTCTTGA GAATGTCTGC 2760
 TTCCCGCGGT GGCCAGGACC ACTATTCTCA CTGAGGAGG AGGATGTCCC AACTGCAGCC 2820
 75 ATGCTGCTTA GAGACAAAG AGCAGCTGAT GTCAACCCCA AACGATGTTG TTGAAAAAGT 2880
 TTGATGTGTA AGTAAATACC CACTTCTGT ACCTGCTGTG CTTTGTGAG GCTATGTCTAT 2940
 CTGCCACCTT TCCTTTGAGG ATAAACAAGG GGTCTGTAAG ACTTAAATTT AGCGGCTCTA 3000
 CGTCTCTTGG CACACAATCA ATGCTGCCCA GAATGTTGTT GACACAGTAA TGCCAGCAG 3060
 AGGCCTTTAC TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAGACA 3120
 GCAGCTTTTC CACTTCCCCA GAGACATCTT GGATGCATTT GCATTGAGTC TGAAGGGGGG 3180
 80 CTTGAGGGAG GTTTGTGACT TCTTGGCGAC TGCCCTTTGT GTGTGGAAGA GACTTGGAAA 3240
 GGTCTCAGAC TGAATGTGAC CAATTAACCA GCTTGGTTGA TGAATGGGGA GGGGCTGAGT 3300
 TGTGATGGG CCCAGGTCTG GAGGGCCAGG TAAATCTGTT CTGAGTCTGT AGCAGTGTCC 3360
 ACCTTGAAGG TCTTC

A59 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLEAV  CVFLFSRVPP  SLPLQEVHVS  KETIGKISAA  SKMMWCSAAV  DIMFLLDGSN  60
    SVGKGSFERS  KHFAITVCDG  LDISPERVRV  GAFQFSSTPH  LEFPLDSFST  QQEVKARIKR  120
    MVFKGGRTET  ELALKYLLHR  GLPGGRNASV  PQILIIIVTDG  KSQGDVALPS  KQLKERVTV  180
    PAVGVRRPFW  EELHALASEP  RGQHVLLAEQ  VEDATNGLPS  TLSSSAICSS  ATPDCRVEAH  240
    PCEHRTLEMV  REFAGNAPCW  RGSRRTLAVL  AAHCPFYSWK  RVFLTHPATC  YRTTCPGPCD  300
    SQPCQNGGTC  VPEGLDGYQC  LCPLAFGGEA  NCALKLSLEC  RVDLLFLDLS  SAGTTLDGFL  360
    RAKVFVVRKF  RAVLSSEDSRA  RVGVATYSRE  LLVAVPVGEY  QDVPLVWNSL  DGIPFRGGPT  420
    LTGSALRQAA  ERFGSARTT  QQDRPRRVVV  LLTESHSEDE  VAGPARHARA  RELLLLGVS  480
    EAVRAELEEI  TGSFKHVMVY  SDPQDLFNQI  PELQGLCSR  QRPGRCTQAL  DLVFMLDTSA  540
    SVGPENFAMV  QSPVRSCALQ  FEVNPDTVQV  GLVVYGSQVQ  TAFGLDTKPT  RAAMLRAISQ  600
    APYLGGVGSA  GTALLHIYDK  VMTVQRGARP  GVPKAVVVL  GGRGAEDAAV  PAQKLNNNGI  660
    SVLVVGVGPV  LSEGLRLLAG  PRDSLHVAA  YADLRVHQDV  LIENLCEGAK  QPVNLCKPSP  720
    QNNEGSCVLQ  NGSYRCKCRD  GWEGPHCENR  EWSSCSVCVS  QGNILETPLR  HMAPVQEGSS  780
    RTPPSNYREG  LGTEMVPTFW  NVCAFGP
  
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTACAGG  ATCCTGACAG  TGATCAACCT  CTGAACAGCC  TCGATGTCAA  ACCCTGCGC  60
    AAACCCGTA  TCCCATGGA  GACCTTCAGA  AAGGTGGGGA  TCCCATCAT  CATAGCACTA  120
    CTGAGCCTGG  CGAGTATCAT  CATTGTGGTT  GTCTCATCA  AGGTGATTCT  GGATAAATAC  180
    TACTTCCTCT  GGGGCGAGCC  TCTCCACTTC  ATCCCGAGGA  AGCAGCTGTG  TGACGGAGAG  240
    CTGGACTGTC  TCTTGGGGGA  GGACGAGGAG  CACTGTGTCA  AGAGCTTCCC  CGAAGGGCCT  300
    GCAGTGGCAG  TCCGCTCTCT  CAAGGACCGA  TCCCACTGTC  AGGTGCTGGA  CTGGGCCACA  360
    GGGAACTGGT  TCTCTGCTGT  TTTGACAAAC  TTCACAGAAG  CTCTGCTGTA  GACAGCCTGT  420
    AGGCAGATGG  GCTACAGCAG  CAAACCCACT  TTCAGAGCTG  TGGAGATTGG  CCCAGACCAG  480
    GATCTGGATG  TTGTTGAAAT  CACAGAAAC  AGCCAGGAGC  TCGCATGCG  GAACTCAAGT  540
    GGGCCCTGTC  TCTCAGGCTC  CCTGGTCTCC  CTGCACTGTC  TTGCTGTGG  GAAGAGCCTG  600
    AAGACCCCCC  GTGTGGTGGG  TGGGGAGGAG  GCCTCTGTGG  ATTCTTGGCC  TTGGCAGGTC  660
    AGCATCCAGT  ACGACAAACA  GCACGTCTGT  GGAGGGAGCA  TCTCGACACC  CCACTGGGTC  720
    CTCACGGCAG  CCCACTGCTT  CAGGAAACAT  ACCGATGTGT  TCAACTGGAA  GGTGCGGGCA  780
    GGCTCAGACA  AACTGGGCGA  CTTCCTCATC  CTGGCTGTGG  CCAAGATCAT  CATCATTGAA  840
    TTCAACCCCA  TGTACCCCAA  AGACAATGAC  ATGCGCCTCA  TGAAGCTGCA  GTTCCCACTC  900
    ACTTCTCTAG  GCACAGTCAG  GCGCATCTGT  CTGCCCTTCT  TTGATGAGGA  GCTCACTCCA  960
    GCCACCCAC  TCTGATCAT  TGGATGGGGC  TTTACGAAGC  AGAATGAGG  GAAGATGTCT  1020
    GACATATGTC  TGCAGGCGTC  AGTCCAGGTC  ATTGACAGCA  CACGGTGCAA  TGCAGACGAT  1080
    GCGTACCAGG  GGGAGTGCAC  CGAGAAGATG  ATGTGTGAC  GCATCCCGGA  AGGGGTGTG  1140
    GACACTGCC  AGGGTGACAG  TGGTGGGCCC  CTGATGTACC  AATCTGACCA  GTGGCATGTG  1200
    GTGGGCATCG  TTAGCTGGGG  CTATGGCTGC  GGGGGCCCGA  GCACCCAGG  AGTATACACC  1260
    AAGGTCTCAG  CCTATCTCAA  CTGGATCTAC  AATGTCTGGA  AGGCTGAGCT  GTAA
  
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

```

1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQDP  LNSLDVKPLR  KPRIPMETPR  KVGIPITIAL  LSLASIIIVV  VLIKVILDKY  60
    YFLCGQPIHF  IPRKQLCDGE  LDCPLGEDEE  HCVKSPFPEG  AVAVRLSKDR  STLQVLDSAT  120
    GNWFSACFDN  FTEALAETAC  RQMGYSKPT  FRAVEIGPDQ  DLDVVEITEN  SQELMRNNS  180
    GPCLSGSLVS  LHCLACGKSL  KTRPVVGGEE  ASVDSWPDQV  SIQYDKQHVC  GGSILDPHVV  240
    LTAHCFRKH  TDVFNWKVRA  GSDKLGSFPS  LAVAKIIIE  FNMYPKOND  IALMKLQFPL  300
    TFSGTVRPI  LPPFDEELTP  ATPLWIIIGW  FTKQNGGKMS  DILLQASQV  IDSTRCNADD  360
    AYQGEVTEKM  MCAGIPGGGV  DTCQGDSSGP  LMYQSDQWRV  VGIVSWGVC  GGPSTPGVYT  420
    KVSAYLNWIY  NVWKAEI
  
```

A62 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

10
 1 11 21 31 41 51
 | | | | |
 CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
 CTGAGATCCT TGCCTAGCT ACATCCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
 15 CGGCTGCTCC TATTGCTGAG CTGCCTGGCC AAAACAGGAG TCCTGGGTGA TATCATCATG 180
 AGACCCAGCT GTGCTCCTGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
 AAGCTGAGGA ACTGCTCTGA TGCCGAGCTC GAGTGTCACT CTTACGGAAA CGGAGCCAC 300
 CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
 CAGAGAAGCC AGCCGATATG GATTGGCCTG CAAGACCCAC AGAAGAGGCA CGAGTGGCAG 420
 20 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
 AAGCACTGTG CTGAGATGAG TCCTCAATAC AACTTTTTAA CTTGGAGCAG CAACGAATGC 540
 AACAAAGGCC AACACTTCCT GTGCAAGTAC CGACCAATGA GCAAGAATCA AGATTCTGCT 600
 AACTCCTGCA CCAGCCCGCT CCTCTTCCTT TCTGTAGCTC TGGCTAAATC TGCTCATTAT 660
 25 TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720
 GGCTTAGAGA CAGAACTTT AGCATTGGGC CCAGTAGTGG CTTCTAGCTC TAAATGTTTG 780
 CCGCCGCACT CTTTCCACA GTATCCTTCT TCCTCTCTCC CTGTCTCTG GCTGTCTCGA 840
 GCAGTCTAGA AGAGTGCATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
 AAGAGTTTGA AGACAGAAGC AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
 30 ACACCTTCTC GCCTCTCTC CATTGCTGAC ACCCCACCCC AGCCACTCAA CTCTGCTTG 1020
 TTTTTCCTTT GGCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGGTTG ATGTGGGCA 1080
 TACATTCCTT TAATAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA

A63 Protein sequence:

35 Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 40 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

45 1 11 21 31 41 51
 | | | | |
 MASRSMLLLL LLSCLAKTGV LGDIIMRPSC APGNFYHKS CYGYFRKLNR WSDAELEQCS 60
 YNGAHLASI LSLKEASTIA EYISGVQRSQ PIWIGLHDPQ KRQWQWIDG AMYLRSWSG 120
 50 KSMGGKHKCA EMSSNNNFLT WSSNECNKRQ HFLCKYRP

A64 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 55 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51
 | | | | |
 GCGGAACACC GGCCCCCGCT CGCGGCAGCT GCTTCAACCC TCTCTCTGCA GCCATGGGGC 60
 TCCCTGTGGG ACCTCTGCGG TCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
 CCTCCGAGCC GTGCCGCGCG GTCTTTCAGG AGGCTGAAGT GACCTTGAGG GCGGGAGGCG 180
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTCAAT GGGCTGCCCT GGGCAAGAGC 240
 65 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
 AAAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAA GGCAAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTGGCT GTAGAGAAGG 540
 70 AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GACCCCATG AACATCTCCA 660
 TCATCGTGAC CGACCAAGAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGA 720
 GTGTCTTAGA GGGAGTCCTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
 75 AGGACCCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGGCT GGCACGGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGCGAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 ACAATGCTCC CATGTTTGAC CCCAGAAAGT ACGAGGCCCA TGTGCCTGAG AATGCAGTGG 1080
 GCCATGAGGT GCAGAGGCTG ACGGTCACTG ATCTGGACGC CCCCAACTCA CCAGCGTGGC 1140
 80 GTGCCACCTA CTTGTTCTAG GCGGCTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGCATC CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
 AGCACACCTT GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCTAACCT 1320
 CCACAGCCAC CATAGTGGTC CACGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACCTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAGA CCCTGACAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500

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CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
ATGGAAGCCC TCCACCACTT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCTCTAG CCCCCTCAGA TCACCATCTG CAACCAAAGC CCTGTGCGCC 1740
ACGTGCTGAA CATCAGCGAC AAGGACCTGT CTCCCCACAC CTCCCCCTTC CAGGCCACGC 1800
TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTTT TCTCTGTCTG 1920
ACCATGGCAA CAAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTGGAAC CTGCCCTGGA CCTTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCTTGGCTCT GCTGTTCCTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
TCAAGGAGCC CTCCTACTC CCAGAAGATG ACACCCGTGA CAACGCTTTC TACTATGGCG 2160
AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
TGTAACGTC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
AGCGCGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG 2400
AGGGCAGCGG CTCCAGCGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCGCTT CAAGAAGCTG GCAGACATGT 2520
ACGGTGGCGG GGAGGACGAC TAGCGCGCCT GCCTGCAGGG CTGGGGACCA AACGTCAGGC 2580
CACAGAGCAT CTCGAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTC 2640
GGAAGTGCCG GTAGCAACTT GCGGAGAGCA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
TCTTAGCCTT TCCAGTAGGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCC AGGGTTGGCT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAATA 2820
TGCTCAACCC TGTGCTCTGG GCCTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
TCGGAATGGA ACCTTCTTAG GCCTCTGGT GCAACTTAAT TTTTATTTT AATGCTATCT 2940
TCAAAACGTT AGAGAAAGTT CTTCAAAGT GCAGCCACGA GCTGCTGGGC CCACCTGGCG 3000
TCTGCACTT CTGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCGTTTTT 3060
ATACTGAGTG TGCTAGGTT GCCCTTATT TTTTATTTT CCTGTGCGT TGCTATAGAT 3120
GAAGGCTGAG GACAATCGTG TATATGTACT AGAATTTTT TATTAAGAA A

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A65 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

40
45
50
55

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1 11 21 31 41 51
MGLPRGPLAS LLLQLQVCWLQ CAAEPCRAV FREAEVTLA GGAQEPGQA LKQVFMGCPG 60
QBPALFSTDN DDPTVRNGET VQERRSLKER NPLKIPPSKR ILRRHKRDWV VAPISVPENG 120
KGPPFPRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLILN KPLDREETAK 180
YELFGHAVSE NGASVEDPMN ISIIIVTDQND HKPKFTQDTF RGSVLEGLVP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSIHSQ EPKDPHDLMF TIHRSTGTIS VISSGLDREK VPEYTLTIOA 300
TMDMGDGSST TAVAVVEILD ANDNAPMFDP QRYEARVPEN AVGHEVQRLT VTDLDAPNSP 360
AWRATYLYNG GDDGDHPTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGITPTGEPVC VYTAEDPDKE NQKISYRILR 480
DPAGWLANDP DSGQVTAVGT LDREDEQFVR NNIEYVMVLA MDNGSPPTTG TGTLLLTLLD 540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPTSPFQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCFGP WKGGFILPVL 660
GAVLALLFLL LVLLLLVRKK RKIKEPLLLP EDDTRDNVFP YGEBGGGEED QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
DYESGSGDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKCLA DMYGGEED

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A66 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

70
75
80

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1 11 21 31 41 51
ATGATTCCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
ATTCTCCAGG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
TTTCATGGCT CGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
TCTCAGTTTA AAAATCCCCT TATTATGCTG CTCTGGCTTT CTGCAGTCAT CAGTGTITTA 240
ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
CCAGATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGGCCG AGACTTGGTT 420
CAGGTGTATA CAGTTTGCCT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACGCTGTGTT 480
GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTICT 540
AAGGTGACAG CTCTCAGCC AGCTGCAACT AATGAGATC TTGCATCGAG AAGTAACATT 600
GCCTTTATGC GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTTCAT TGGAAACAGGA 660
GAAAATTCCT AATTGSGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
CCTCTGCAGA AGAGCATGGA CCTCTAGGA AAACAACCTT CCTTTTACT CTTTGTGATA 780
ATAGGAATCA TCATGTTGGT TGGCTGTGTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840

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5	ATTAGTGTA	GTTTGGCTGT	AGCAGCAATT	CCTGAAGGTC	TCCCCATTGT	GGTCACAGTG	900
	ACGCTAGCTC	TTGGTGTAT	GAGAAATGGT	AAGAAAAGGG	CCATTGTGAA	AAAGCTGCCT	960
	ATTGTTGAA	CTCTGGGCTG	CTGTAATGTG	ATTGTTTCAG	ATAAACTGG	AACACTGACC	1020
	AAGAATGAAA	TGACTGTTAC	TCACATATTT	ACTTCAGATG	GTCTGCATGC	TGAGGTTACT	1080
	GGAGTTGGCT	ATAATCAATT	TGGGGAAGTG	ATTGTTGATG	GTGATGTTGT	TCATGGATTTC	1140
	TATAACCCAG	CTGTTAGCAG	AATTGTTGAG	GCGGGCTGTG	TGTGCAATGA	TGCTGTAATT	1200
	AGAAACAATA	CTCTAATGGG	GAAGCCAACA	GAAGGGGCTT	TAATTGCTCT	TGCAATGAAG	1260
	ATGGGTCTTG	ATGGACTTCA	ACAAGACTAC	ATCAGAAAAG	CTGAATACCC	TTTTAGCTCT	1320
10	GAGCAAAAGT	GGATGGCTGT	TAAGTGTGTA	CACCGAACAC	AGCAGGACAG	ACCAGAGATT	1380
	TGTTTTATGA	AAGGTGCTTA	CGAACAAAGT	ATTAAGTACT	GTACTACATA	CCAGAGCAAA	1440
	GGGAGACCT	TGACACTTAC	TCAGCAGCAG	AGAGATGTGT	ACCAACAAGA	GAAGGCACGC	1500
	ATGGGCTCAG	CGGGACTCAG	AGTTCCTGCT	TTGGCTCTTG	GTCTGAACT	GGGACAGCTG	1560
	ACATTTCTTG	GCTTGGTGGG	AATCATTGAT	CCACCTAGAA	CTGGTGTGAA	AGAAGCTGTT	1620
	ACAACACTCA	TGCGCTCAGG	AGTATCAATA	AAAAATGATTA	CTGGAGATT	ACAGAGACT	1680
15	GCAGTTGCAA	TGCGCAGTCG	TCTGGGATTG	TATTCACAAA	CTTCCAGTTC	AGTCTCAGGA	1740
	GAAGAAATAG	ATGCAATGGA	TGTTCAAGCAG	CTTTCACAAA	TAGTACCAAA	GGTTGCAGTA	1800
	TTTTACAGAG	CTAGCCCAAG	GCACAAGATG	AAAATTATTA	AGTCGCTACA	GAAGAACGGT	1860
	TCAGTTGTAG	CCATGACAGG	AGATGGAGTA	AATGATGCAG	TTGCTCTGAA	GGCTGCAGAC	1920
20	ATTGGAGTTG	CGATGGGCCA	GACTGGTACA	GATGTTTGCA	AAGAGGCAGC	AGACATGATC	1980
	CTAGTGAGAT	ATGATTTTCA	AACCAATATG	TCTGCAATCG	AAGAGGGTAA	AGGGATTAT	2040
	AATAACATTA	AAAATTTCGT	TAGATTCCAG	CTGAGCACGA	GTATAGCAGC	ATTAACTTTA	2100
	ATCTCATTTG	CTACATTAAAT	GAACCTTCCT	AATCCTCTCA	ATGCCATGCA	GATTTTGTGG	2160
	ATCAATATTA	TTATGGATGG	ACCCCCAGCT	CAGAGCCTTG	GAGTAGAACC	AGTGGATAAA	2220
25	GATGTCAATC	GTAAACCTCC	TGCAACTCGG	AAGACAGCA	TTTGAATAA	AAACTTGATA	2280
	CTTAAATATC	TTGTTTATC	AATAATCATT	GTTTGTGGGA	CTTGTGTTGT	CTTCTGGCGT	2340
	GAGCTAGCAG	ACCAATGTGAT	TACACCTCGA	GACACAACAA	TGACCTTCAC	ATGCTTTGTG	2400
	TTTTTTGACA	TGTTCAATGC	ACTAAGTTC	AGATCCAGCA	CCAAGTCTGT	GTTTGAGATT	2460
	GGACTCTGCA	GTAATAGAAAT	GTTTGTCTAT	GCAGTCTCTG	GATCCATCAT	GGGACAATTA	2520
30	CTAGTTATTT	ACTTTCTCTC	GCTTCAGAAAG	GTTTTCAGCA	CTGAGAGCCT	AAGCATACTG	2580
	GATCTGTTGT	TTCTTTTGGG	TCTCACCTCA	TCAGTGTGCA	TAGTGGCAGA	AATTATAAAG	2640
	AAGGTTGAAA	GGAGCAGGGA	AAAGATCCAG	AAGCATGTGA	GTTCGACATC	ATCATCTTTT	2700
	CTTGAAGTAT	GA					
35	A67 Protein sequence:						
	Gene name:	ATPase, Ca++ transporting, type 2C, member 1					
	Unigene number:	Hs.106778					
	Probeset Accession #:	N51919					
	Protein Accession #:	AAF27813					
40	Signal sequence:	none found					
	Transmembrane domains:	60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878					
	Pfam domains:	Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]					
	Cellular Localization:	not determined					
45	1	11	21	31	41	51	
	MIPVLTSKKA	SELPVSEVAS	ILQADLQNGI	NKCEVSHRRA	PHGWNFEDIS	EDEPLWKKYI	60
	SQPKNPLIML	LLASAVISVL	MHQFDDAVSI	TVAILIVVTV	AFVQEYRSEK	SLEELSKLVP	120
50	PECHVREK	LEHTLARDLV	PGDTVCLSVG	DRVPADLRLE	EAVDLSDIES	SLTGETTPCS	180
	KVTAPQPAAT	NGDLASRSNI	AFMGLTVRCG	KAGGVVITG	ENSEFGEVFK	MMQAEAPKT	240
	PLQKSMDLIG	QLSFSYSPGI	IGIIMLVGWL	LGRDILEMPT	ISVSLAVALAI	PEGLPIVVTV	300
	TLALGVMRMV	KKRAIVKCLP	IVETLGCNV	ICSDKTGTLT	KNEMTVTHIF	TSDDLHAEVT	360
	GVGYNQFGEV	IVDGDVVHGF	YNPAVSRIVE	AGVCNDAVI	RNNTLMGKPT	EGALIALAMK	420
55	MGLDGLQDDY	IRKAEYPPSS	BQKMAVKCV	HRTQQDRPEI	CFMKGAYEQV	IKYCTTYQSK	480
	GQTLTLTQQQ	RDVVYQEKAR	MGSAGLRVLA	LASGPGLQGL	TFLGLVGIID	PPRTGVKEAV	540
	TTLIAGSVSI	KMITGDSQET	AVAIASRLGL	YSKTSQSVSG	BEIDAMDVQQ	LSQIVPKVAV	600
	PYRASPRHKM	KIISLQKNG	SVVAMTCDGV	NDAVALKAAD	IGVAMGQGT	DVCKEADMI	660
	LVDDDPQTIM	SAIEEGKGIY	NNIKNFVRPQ	LSTSIALLTL	ISLATLNNFP	NPLNAMQILW	720
60	INTIMDGPPA	QSLGVEPVDK	DVIRKPPRNW	KDSILTKNLI	LKILVSSII	VCGLTFVFWR	780
	ELRDNVITPR	DTTMTFTCPV	FFDMFNALSS	RSQTKSVFEI	GLCSNRMFCY	AVLGSIMQGL	840
	LVITYFPPLQK	VFQTESLSIL	DLLFLGLLTS	SVCIIVASIIK	KVERSRREKIQ	KHVSSTSSSF	900
	LEV						
65	A68 DNA SEQUENCE						
	Gene name:	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)					
	Unigene number:	Hs.170195					
	Probeset Accession #:	BE616633					
	Nucleic Acid Accession #:	NM_001719					
70	Coding sequence:	123-1418 (underlined sequences correspond to start and stop codons)					
	1	11	21	31	41	51	
75	GGGCGCAGCG	GGGCGCGTCT	GCAGCAAGTG	ACCGACGGCC	GGGACGGCCG	CCTGCCCCCT	60
	CTGCCACCTG	GGGCGGTGCG	GGCCCGGAGC	CCGGAGCCCG	GGTAGCGCGT	AGAGCCGGCG	120
	CGATGCACGT	GCGCTCACTG	CGAGCTGCGG	CGCGCACAG	CTTGTGGCG	CTCTGGGCAC	180
	CCCTGTTCCT	GCTGCGCTCC	GCCCTGGCCG	ACTTCAGCCT	GGACAACGAG	GTGCACTCGA	240
	GCTTCATCCA	CGGCGCGCTC	CGCAGCCAGG	AGCGGCGGGA	GATGCAGCGC	GAGATCTCTT	300
80	CCATTTTGGG	CTTGCCCCAC	CGCCCGGCC	CGCACCTCCA	GGGCAAGCAC	AACTCGGCAC	360
	CCATGTTCAT	GCTGGACCTG	TACAACGCCA	TGGCGGTGGA	GGAGGGCGGC	GGGCGCGCG	420
	GCCAGGGCTT	CTCTACCCC	TACAAGCGCG	TCTTCAGTAC	CCAGGGCCCC	CCTCTGGCCA	480
	GCCTGCAGAA	TAGCCATTTC	CTCACCGAGC	CCGACATGGT	CATGAGCTTC	GTCAACCTCG	540
	TGGAACATGA	CAAGGAATTC	TTCCACCCAC	GCTACCCACA	TCGAGAGTTC	CGGTTTGATC	600
	TTCCAGAGAT	CCAGAAAGGG	GAAGCTGTCA	CGGACGCCGA	ATTCCGATTC	TACAAGGACT	660

5	ACATCCGGGA	ACGCTTCGAC	AATGAGACGT	TCGGATCAG	CGTTTATCAG	GTGCTCCAGG	720
	AGCACTTGGG	CAGGGAATCG	GATCTCTTCC	TGCTCGACAG	CCGTACCCTC	TGGGCTCGG	780
	AGGAGGGCTG	GCTGGTGT	GACATCACAG	CCACCAGCAA	CCACTGGGTG	GTCAATCCGC	840
	GGCAACAACCT	GGGCTGCGAG	CTCTCGGTGG	AGACGCTGGA	TGGGCAGAGC	ATCAACCCCA	900
	AGTTGGCGGG	CCTGATTGGG	CGGCACGGGC	CCCAAGAACAA	GCAGCCCTTC	ATGGTGGCTT	960
	TCTTCAAGGC	CACGAGGTC	CACCTCCGCA	GCATCCGGTC	CACGGGGAGC	AAACAGCGCA	1020
	GCCAGAACCG	CTCCAAGACG	CCCAAGAAC	AGGAAGCCCT	GCGGATGGCC	AACTGGCAG	1080
	AGAACAGCAG	CAGCGACCAG	AGGCAGGCCT	GTAAGAAGCA	CGAGCTGTAT	GTGAGCTTCC	1140
10	GAGACCTGGG	CTGGCAGGAC	TGGATCATCG	CGCTGAAGG	CTACGCCGCC	TACTACTGTG	1200
	AGGGGGAGTG	TGCTTCCCT	CTGAACCTCT	ACATGAAGCG	CACCAACCAC	GCCATCGTGC	1260
	AGACCTGGT	ACACTTCATC	AACCCGAA	CGGTGCCAA	GCCCTGCTGT	GCGCCACGC	1320
	AGCTCAATGC	CATCTCCGTC	CTCTACTTCG	ATGACAGCTC	CAACGTCTATC	CTGAAGAAAT	1380
	ACAGAAACAT	GGTGTCCGG	GCCTGTGGCT	GCCACTAGCT	CCTCCGAGAA	TTCAGACCCCT	1440
	TTGGGGCCAA	GTITTTCTGG	ATCCTCCATT	GCTCGCCTTG	GCCAGGAACC	AGCAGACCAA	1500
15	CTGCCCTTTG	TGAGACCTTC	CCCTCCCTAT	CCCCAACTTT	AAAGGTGTGA	GAGTATTAGG	1560
	AAACATGAGC	ACCATATGGC	TTTTGATCAG	TTTTTTCAGT	GCAGCATCCA	ATGAACAAGA	1620
	TCCTACAAGC	TGTGCAGGCA	AAACCTAGCA	GGAAAAAATA	ACAACGCATA	AAGAAAAATG	1680
	GCGGGGCCAG	GTCTATGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
20	TTATGAGCGC	CTACCAGCCA	GGCCACCCAG	CCGTGGGAGG	AAGGGGGCGT	GGCAAGGGGT	1800
	GGGCACATTG	GTGTCTGTGC	GAAAGGAAAA	TTGACCCGGA	AGTTCTCTGA	ATAAATGTCA	1860
	CAATAAACG	AATGAATG					

25	<u>A69 Protein sequence:</u>	
	Gene name:	bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
	Unigene number:	Hs.170195
	Probeset Accession #:	BE616633
	Protein Accession #:	NP_001710.1
	Signal sequence:	1-30
30	Pfam domains:	TGfb_propeptide [37-281]
	Transmembrane domains:	none found
	Cellular Localization:	secreted

35	1	11	21	31	41	51	
	MHVRSLRAAA	PHSFVALWAP	LFLLRSALAD	FSLDNEVHSS	FIHRRRLRSQE	RREMQREILS	60
	ILGLPHRFRP	HLQGHKNSAP	MFMLDLYNAM	AVEEGGGPGG	QGFSYPYKAV	FSTQGPPLAS	120
	LQDSHFLTDA	DMVMSFVNLV	EHDKEFFHPR	YHHRFRFDL	SKIPEGEAVT	AAEFRIYKDY	180
40	IRERFNETF	RISVYQVLQE	HLGRESDLFL	LDSRTLWASE	EGWLVDITDA	TSNHVVNPR	240
	HNLGLQLSVE	TLGDQSQINPK	LAGLIGRHGP	QNKQPFMVAF	FKATEVHFRS	IRSTGSKQRS	300
	QNRSKTPKNQ	EALRMANVAE	NSSSDQRQAC	KKHELYVSFR	DLGNQDWIIA	PEGYAAYYCE	360
	GECAFLPNYS	MNATNHAIVQ	TLVHFINPET	VPKPCCAPTQ	LNAISVLVYP	DSSNVILKKY	420
45	RNMVVRACGC	H					

Cervical

50	<u>A70 DNA sequence</u>	
	Gene name:	bone morphogenetic protein receptor IB (ALK-6)
	Unigene number:	Hs.87223
	Probeset Accession #:	AA250737
	Nucleic Acid Accession #:	NM_001203
	Coding sequence:	274-1782 (underlined sequences correspond to start and stop codons)

55	1	11	21	31	41	51	
	CGCGGGGCGC	GGAGTCGGCG	GGGCTCGCG	GAAGCGGGGC	AGTGCGGAGA	CCGCGGCGCT	60
	GAGGACGCGG	GAGCGGGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
	GTGAAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCCTCTGATT	180
60	CATAACCAT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTTAAA	CTTACAAGCC	240
	TGCCATAAGT	GAGAAGCAAA	CTTCTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAAATTA	300
	AATGTGGCA	CCAAGAAAGA	GSATGGTGAG	AGTACAGCCC	CCACCCCGCG	TCCAAAGGTC	360
	TTGCGTGTGA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TGCGAGCACA	420
	GACGGATATT	GTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCCCTGT	GGTCACITCT	480
65	GGTTGCCCTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTGGGG	ACACTCCCAT	TCCTCATCAA	540
	AGAAGATCAA	TTGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAGACCT	ACACCCTACA	600
	CTGCTCCAT	TGAAAAACAG	AGATTTTGTT	GATGGACCTA	TACACCACAG	GGCTTTACTT	660
	ATATCTGTGA	CTGCTGTAG	TTTGCTCTTG	GTCCTTATCA	TATTATTTTG	TTACTTCCGG	720
	TATAAAGAC	AAGAAACAG	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACTTAC	780
70	ATTCCTCTCG	GAGAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGA	840
	TCAGGCCTCC	CTCTGCTGGT	CCAAGGACT	ATAGCTAAGC	AGATTGAGT	GGTGAACAG	900
	ATTGGAAAG	TCGCTATGG	GGAAGTTTGG	ATGGGAAAGT	GGCGTGGCGA	AAAGTAGCT	960
	GTGAAAGTGT	TCTTCACCAC	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
	ACAGTGTGTA	TGAGGCATGA	AAACATTTTG	GGTTTCATTG	CTGCAGATAT	CAAGGGGACA	1080
75	GGGTCCCTGGA	CCGATTTGTA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
	TATCTGAAGT	CCACCAACCT	AGAAGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
	AGTGGCTTAT	GTCATTTACA	CACAGAAATC	TTTAGTACTC	AAGGCACACC	AGCAATTGCC	1260
	CATCGAGATC	TGAAAAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACCTG	CTGTATTGCT	1320
	GACCTGGGCC	TGGCTGTGTA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
80	ACTCGAGTGT	GCACCAACAG	CTATATGCCCT	CCAGAAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
	AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCCTCAT	CCTTTGGGAG	1500
	GTTGCTAGGA	GATGTGTATC	AGGAGGTATA	GTGGAAGAAT	ACCAGCTTCC	TTATCATGAC	1560
	CTAGTGCCCA	GTGACCCCTC	TTATGAGGAC	ATGAGGGAGA	TTGTGTGCAT	CAAGAAGTTA	1620

5 CGCCCTCAT TCCCAAACCG GTGGAGCAGT GATGAGTGT TAAGGCAGAT GGGAAAACTC 1680
 ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAAA 1740
 ACACCTGCCA AAATGTGAGA GTCCAGGAC ATTAACTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
 TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTTGCTTC CCAGTGGGTT CAGACCTCAC 1920
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTG GCGGAGAGAA CCGTTGGGTA ACTTGTCAA GATATGATGC AT

10 A71 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / U89326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

20 1 11 21 31 41 51
 | | | | | |
 MLLRSAGKLN VGTKKEDGES TAPTTPRPKVL RCKCHHCPPE DSVNNICSTD GYCFTMIEED 60
 DSGLPVVTSG CLGLEGGDFQ CRDTPPIPHQR RSIECCTERN ECNKLHPTL PPLKNRDFVD 120
 GPIHRRALLI SVTVCSLLLV LIILFCYFRI KRQETRPYS IGLEQDETYI PPGESLRDLI 180
 25 EQSQSSGSGS GLPLLVRRTI AKQIQMVKQI GKGRYGEVVM GKWRGEKVAV KVFPTTEAS 240
 WPRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
 MLKLAYSVS GLCHLHTEIF STQKPAIAH RDLKSKNILV KNGTCCAD LGLAVKFISD 360
 TNEVDIPNT RVGTGRYMPF EVLDESINRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
 30 EEYQLPYHDL VSPSPSYEDM REIVCIKKLR PSFPNRWSSD ECLRMQMKLM TECWAHPAS 480
 RLTLALRVKKT LAKMSESQDI KL

Bladder

A72 DNA SEQUENCE

35 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 | | | | | |
 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGGCG 60
 AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
 45 CTGAGCCTGG CGAGTATCAT CATTGTGTTT GTCTTCATCA AGGTGATTCT GGATAAATAC 180
 TACTTCTCTT GGGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACCGAGAG 240
 CTGGACTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
 GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360
 50 GGGAACTGGT TCTCTGCCTG TTTCGACAA TFCACAGAAG CTCTCGCTGA GACAGCCTGT 420
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
 GATCTGGATG TTGTTGAAAT CACAGAAAC AGCCAGGAGC TTGCATGCG GAACCTCAAGT 540
 GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
 55 AGCATCCAGT ACGACAAACA GCACGTCTGT GAGGGGAGCA TCCTGGACCC CCACTGGGTC 720
 CTCACGGCAG CCCACTGTCT CAGGAAACAT ACCGATGTGT TCACTGGAA GGTGCGGGCA 780
 GGTCTAGACA AACTGGGCA CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATATTGAA 840
 TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCCCTCA TGAAGCTGCA GTTCCCCTC 900
 ACTTCTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 60 GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGTTGCAA TGCACAGCAT 1080
 GGTACACAG GGAAGATCAG CGAGAAGATG ATGTGTGTCG GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCC AGGATGACAG TGGTGGGCCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
 65 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

A73 Protein sequence:

70 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 75 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

80 1 11 21 31 41 51
 | | | | | |
 MLQDPDSQDP LNSLDVKPLR KPRIPMETFR KVGIPILIAL LSLASIIIVV VLKRVILDKY 60
 YFLCGQPLHF IPRKQLCDGE LDCPLGEDEE HCVKSPFEGP AVAVRLSKDR STLQVLDSAT 120

5 GNNFSACFDN FTEALAEATAC RQMGYSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEE ASVDSWPMQV SIQYDKQHVC GGSILDPHV 240
 LTAARCFRKH TDVFNWKVRA GSDKLGSFSPS LAVAKIIIE FNPMPKND IALMKLQFPL 300
 TFSGTVRPIC LPFFDEELTP ATPLWILGW FTKQNGKMS DILLQASVQV IDSTRCNADD 360
 AYQGEVTEKM MCAGIPEGGV DTCQDSSGGP LMYQSDQMHV VGIVSNYGC GGPSTPGVYT 420
 KVSAYLNIY NVWKAEL

A74 DNA SEQUENCE

10 Gene name: ESTs, Weakly similar to CGH7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
GCCCTTGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
CTGAAGAAAA AGGAGCTGGA GCAGGAGAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCGCG 180
CTGGGCCAGA GCAGAGCCAG GCGCGACTTT GGGGCTGCAG GGAGCCCCCG CCCACTGGGG 240
CGGTACTGCG CCAAGGTACA AGAGGTGGCC CGGTGCTGCG GGGAGCTGCT GGCTGCAGCC 300
TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCGGGGCCCC CCTGCCCTGC CTGAOGTCC 360
ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGCG TGAAGGAGCA GAACCGACTC 420
CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCACGC AGCTGGAGCA GGAGAAGTCG 480
GCGCTCATTA AGCAGCTGTT TGAGGCCCCG GCGCTGAGCC AGCAGGAGCG GGGACCTCTG 540
GATTCCACTC TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCTGGCACTC 600
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CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGACGGCCT 1080
GTAAGCGGGG GGTGCCCTGC TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
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CTGGGGTCTT GCTCACCCCC CTTTGTCTTC ACGCCAGGCC TGTCCCCAGG TTTCAGCTGG 1440
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ACACTGTCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCAACTC 1860
CCTTCGGAG CCCAGTCCA TGCTAACCTG CCCACAGCAA CCCCACAGAG CCACATTCCC 1920
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TGGGGGATCC TGGCATCTTT ACTGGACTGG AAGCAGGAGA CAGAACAGTG TCTGTCCGG 2280
GGTGACTTCA TCAGGAGACC GCCCAGATAG AGCTGGAACC CGCAGCTGAA GCGGAAATGT 2340
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AAAGAAATAG GTCTCTCCAG TTTACAGCTT GAAATCAGGC TAGTGAGTGG CCTGGAGAC 2460
CACGAGGGGA GAATTTAAAG GCCCGGCTG GCAGGCTCTA GGTGGCTGGC AGAGGCACAT 2520
GCAGACCTTG CCTGGAGCCT GCCCTAGGAC GCTGGGCGGG TCAGTCTCCG TGCAGGATGT 2580
GAGCAGCGTC CCTGGCTCT ATCCGCGAGG TGCCAGTAGC GTGTGCAAGT ACATACAGT 2640
GCGTGACAC TGATGATGACA CCGGAAATG TCTCAGGATG TTGAAATGTG TCCTTGGGG 2700
CAGAAGTGTG CCCAGTTGAG AATCTGCCCC AGAGGAACAC ACCCACCA GGCCTCAGGA 2760
TTTTGTGTG ATCAAGTTCC AAGGAAAGG AACATCTCAG CCGGGCGTGG TGTTTACGCG 2820
CTGGAATCCC AGCATTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
CCCCATCTCT ACAAAAAA AAAAAAGAAG AAAAAAATG AGAGATCCAG GTTTAAAAAT 2940
TCATAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
AGAAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

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A75 DNA SEQUENCE

75 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Nucleic Acid Accession #: AB035089
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
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CAGTTCTAGT AAAAGGGAGA ACATCAATAT AGGATGTTTC TTAGCAATAG AAAAAGGAAG 120
CCAAGAGGAA TTAGGGAGAG AGTTATAAGA GATCAGCAAG GGGACAGGGT TAGATTGGT 180
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10	GGATTCTCTG	AGCCAATGAA	GTTGGTGTAT	GTTTATGAAA	TATCAAGAGA	CATAAGTTGG	780
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25 A76 Protein sequence:
 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Protein Accession #: BAB21525
 Signal sequence: none found
 30 Transmembrane domains: none found
 Serine Proteinase Inhibitor domain: 13-390
 Cellular Localization: secreted

35 1 11 21 31 41 51
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45 A77 DNA SEQUENCE
 Gene name: hypothetical protein FLJ13459
 Unigene number: none found
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 Nucleic Acid Accession #: XM_047266
 50 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

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 GCCTCGGAG CCAATCAGCT ATGAGCTCAG AGTTGTCATC TGGAAACCGG AGGATGTGGT 600
 65 TCTGGATGAC GAGAATCCAC TCAACGGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGACGTT CACTTCAACT CCCTGACTGG 720
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTTGAC TACCTGCCCA CGGAGCGGGA 780
 GGTGAGCGTC TGGCGCAGGT CTGGACCCCT TGCCCTGGAG GAGGCGGAGT TCGGCAGGCC 840
 TGCACTGCTG GTCCCTGAGG TCTGGGACTA TGACCGCATC TCTGCCAATG ACTTCTTGG 900
 70 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCSTGGGGCC CGGGGCCCGG AGCTCTGCTC 960
 TGTGCAGCTG GCCCGCAATG GGGCCGGGCC GAGGTGCAAT CTGTTTCTGCT GCGCGCGCCT 1020
 GAGGGGCTGG TGGCGGTAG TGAAGCTGAA GGAGGCAGAG GACGTGGAGC GGGAGGCGCA 1080
 GGAGGCTCAG GCTGGCAAGA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GCGCAGAAGA 1140
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCTCT ACGGGCAAGG TGGAGGCAGA 1200
 75 GTTTGAGCTG CTGACTGTGG AGGAGGCCGA GAAACGCCCA GTGGGAAGG GCGGAAGCA 1260
 GCCAGAGCCT CTGGAGAAAC CCAGCCGCCC CAAACTTCC TTCAACTGGT TTGTGAACCC 1320
 GCTGAAGACC TTGTCTTCTT TCATCTGGCG CCGTACTTGG CGCACCTTGG TGCTGCTGCT 1380
 ACTGGTCTG CTACCGCTCT TCCTCTCTCT GGTCTTCTAC ACCATCCCTG GCCAGATCAG 1440
 CCAGGTCACT TTCCGTCCCC TCACAAGTG ACTCTGCTGT ACCTTGGACA CTCACCCAGG 1500
 80 GTGCCAACCC TTCAATGCCT GCTCTGGAA GTCTTCTTCA CCATGTGAG CTACCCGAGA 1560
 GTCTAGTGCT TCCTCTGAAT AAACCTATCA CAGCCACTG

A78 Protein sequence:
 Gene name: hypothetical protein FLJ13459

Unigene number: none found
 Probeset Accession #: XM_047266
 Protein Accession #: XP_047266
 Signal sequence: none found
 5 Transmembrane domains: 291-313
 C2 domain: 27-86
 Cellular Localization: plasma membrane / ER

10 1 11 21 31 41 51
 MWIDIFPQDV PAPPVVDIKP RQPISYELRV VIWNTEDVVL DDENPLTGEM SSDIYVKSXV 60
 KGLEHDKQET DVHFNSLTGE GNFNWRPFVR FDYLPTEREV SVWRRSGPFA LEEAEFRQPA 120
 15 VLVLLQVWDYD RISANDFLGS LELQLPDMVR GARGPBLCSV QLARNGAGPR CNLFRCLRLR 180
 GWNFVVKLKE AEDVEREAQE AQAGKKKRRQ RRRKGRPEDL EFTDMGGNVY ILTGKVEAEF 240
 ELLTVBEEAK RPYGKGRKQP EPLEKPSRPK TSFNWFWNPL KTFVFFIWR RYRTLVLVLLL 300
 VLLTVFLLLV FYTIPQISQ VIFRPLHK

A79 DNA SEQUENCE

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Nucleic Acid Accession #: AL137708
 25 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

30 1 11 21 31 41 51
 GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCTTTCTGT CTGTCTCCTT GCTCTGCCCC 120
 AGACTGGGGG GCTGCGAGAG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
 ATGGCTTGGG CTGGGCCCCT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCCAGG 240
 35 CTCTTGTGGG CAAAGCAGGG GAGGCGCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300
 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCGCTG 360
 GGGTCAACCT AGGCCCATG TAGCACCTTG GTTCCCTGTC CTGTAGGTGA CAGGAGCCAG 420
 CCCAGCCAGG TGTGCTCCCT CCCAGGCCCT TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
 CGCCGCCCCC ACCTTCTCTC CCACCCACAT GCCCAAGGGT GGCAGGCAG GCAGGTGGAC 540
 40 GAGTCAGGAG AGCGCGTAGT TCAGTGTGTG TGGAAATGTT TGGCCGCTCC CAGCTGCACC 600
 CTGCCCTTAC CTGCCACAC CTACCTTCA TCCTCAGGCG CTGCGGCCCT GAGCCCTGCTC 660
 CAGGAATGCA CCTTTAGCCC AGGCCTGCTC AGTGAGCTCC GCCGACAGCC AGCCCTGCTC 720
 CTCCCGCAT GACCCTGCAG ACCCTCTGG GCTTCCAAGT TCCTGGGGGG TGCACTGAAC 780
 ATGCTCCACC TGCACTGGCTG GCAAAACATG GTGGGCCCA GCTGTGGTGC GTGCTGGGGT 840
 45 AGAGGCAAGG AAGTGATGGG ACCGCAGAGA TGAGACCCCC AGGGATGAGA TGGGACCCCC 900
 AGGCAGGGCC GAGGTCGCTG GGGCCAGGAG AGAGAAGCAG GAGAGGAGAG AGCTTCTCTG 960
 TGGAGGACGC ATCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGAA GGCAGGGACT 1020
 AGGCTGCCCA GGCCTGCTCT GCTTGGCTGG GCTTGGGGGG TGCTGGGAGG TGGCTGGGAG 1080
 GCTGGGCTTG GGCAGCTAAG CTGAGCTTT GGCAGGGTCC CAGAGCTTCC CTCCCTTCA 1140
 50 CTCTCTGCTG CACAGAACCC TCGCCCTTGG CCACCCCTGG CTGCTCTCTT GCTCTGGCAG 1200
 ACCCAGCACT GCTGCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCGGGA GGGGCCACCC 1260
 TCCAGCTCA CCGAGCTTCC TGGGCGGCTT CTTCACAAAC AGCAGGGTAG AAAGATGGGG 1320
 CACCCACAG TCTCTCCAG TCCCCCGGCC CAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380
 ATTCCAGACC TTGTCGCGG GACCCCTTGT GAGTTGTGGG ATTCCCAAGA GGGGTGTGGG 1440
 55 GATAACCCAG CCAAGTGGGG GCTGCAGCTG TCCACAGATG CACTCAGCCT GGCCTCTACC 1500
 CCAGGGGCCCT GCTGGGCTCT CATTGCGGCG GCCCTTGCGG CGGGCGTCTC CTCTGTCTCC 1560
 TGCTCTCTGT GTGCTGCTTG CTGCTGCTGC CGCCGCCACA GGAAGAAGCC CAGGGACAA 1620
 GAGTCCGCTG TCTTGGGAG TGGCCGCGGC ACCACCAACA CCCACTGGT GAGGAGCGGC 1680
 TCCTTGCTCA CTACGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGGCAGCGA 1740
 60 GGCAGTTCA GCGCCAGGGA TGGTTAAACC CCCACAGAG CAGGGCGTGG AGGACCTTCC 1800
 TGGCAGGGAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCAT 1860
 GGGCCCGAGG GAGCCACAGC GGGTTCTTGA GGAAGGCAGG GGGTACCCCA GATGCCAAGT 1920
 TTTGGGTGGG TTTGGCCGGT CTCACAGAGC GAAGCCGAGC ATTGTGCTCT GTTGGGTGGC 1980
 CTGGCCTGGA GGCAGGGGGT CTGACCCAT GTCATGCAAG GGCTGCCCGG GAGCCAGGG 2040
 65 CTCTGATGAG GCATGATGTC AGCACCACTT GCCCTTGTG CCACTCACT CAGGTGCAA 2100
 CCTGATGTGG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCTGCAG 2160
 CTCTCCCTGG AGTTGCACTT TGAAGCCAG GAGGTGAAGG GCGCCGCTGC GCAGGACCA 2220
 CGGTTCTGCG AGTTTCCGGA AAGGGTGACG GGGGAAGGGC AGACCCCATG CCCTGGGTGG 2280
 TGGGGAGCTG ACAGGGCAGG GGCCTTGGC TGAGCCCAAC CGCTGGCTC CCAGATCAGG 2340
 70 GTGGGCTGGA GGCAGGCAGC CGACCTGAGG CTGGGGGCA CCGTGAACC CTATGCCCG 2400
 GTCAGCGTCT CCACCCAGGC CGGACACAGA CATGAGACAA AAGTGCAACG AGSCACGCTC 2460
 TGCCCGGTGT TTGACGAGAC CTGCTGCTTC CACGTGAGTC AGGGATGGTC GGTGGGTGG 2520
 GCCTGGACCG CTGGATGGGC CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GGCCTGGGCA 2580
 GCTGGGTGGG CTTGAGCTAG GGCAGCAGGG CTTGGCTCAC GCGCTGCTCT CAGATCCCGC 2640
 75 AGGCGGAGCT GCCAGGGGCT ACCCTGCAGG TGCAGCTTTT CAACTTCAAG CGCTCTCGG 2700
 GGCATGAGCC CCTGGGTGAG CTCCGTCTGC CACTGGGCAC CGTGATCTG CAGCATGTTT 2760
 TGGAGCACTG GTACTCTCTG GGCCTGCGCG CTGCCACTCA GGTGAGGTGC TGTTCACAG 2820
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CTTGCCCTAT GGGCCATCGG AAAGACAGGC 2880
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCAACTCGG CCAGATCAC CTCCCGGGC 2940
 80 TGAAGCCCTT CTGTCTGCCC ACAGCCGAG CAGTCCGGG AGCTGTGCTT CTCTCTCGG 3000
 TACGTGCCCA GCTCAGGCGG GCTGACCGTG GTGGTGTCTG AGGCTCGAGG CTTGCGTCCA 3060
 GGACTTGACG AGCCCTACGT GAAGGTCCAG CTCATGCTGA ACCAGAGGAA GTGGAAGAG 3120
 AGAAGACAG CACCAAAAAA GGGCAGGGG GCGCCCTACT TCAATGAGGC CTTCACCTTC 3180
 CTGGTGCCTT TCAGCCAGGT CCAGAAATGT GACCTGTGTC TGGCTGTCTG GACCCGAGC 3240
 CTGCGCTCC GAATGAGCC CGTAGCAAG GTGCACCTGG GTGCCCGGCG CTCGGGCGAG 3300

CCCCCTGCAGC ACTGGGCAGA CATGCTGGCC CACGCCCGGC GGCCCATGTC CCAGCGGCAC 3360
 CCCCCTGGGC CAGCCAGGGA GTTGGACCGC ATGCTGGCCC TGCAGCCCCC CCTTCGCTGT 3420
 CGCCTGCCCT TCCCCACTC CTGAATGCAC CACATGCCTC TGTCTCCCCG CTGAGCCCAG 3480
 GCACCTTGCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCCT GCC

A80 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Protein Accession #: CAB70885
 Signal sequence: none found
 Transmembrane domains: 69-85
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGHPPVSPSA PAPAGTTAIP GLIPDLVAGT PCELDWSQEG CGDNPAKWGL QLSTDALSLA 60
 STPGPRWALI AGALAAGVLL VSCLLCACCC CRRHRKKPR DKESVGLGSA RGTTHLVR 120
 SGLSLTQSRE GLKSLRLSPG QRGEFSPRDO LPTTEAGR

A81 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51
 | | | | |
 GCGGAACACC GGCCCGCGGT CGCGGCAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCTCTGTGG ACCTCTCGCG TCTCTCTCCTC TTCTCCAGGT TTGCTGGCTG CAGTGCGCGG 120
 CCTCOGAGCC GTGCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG CGCGGAGCGG 180
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTAT CATGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGCGGAG ACAGTCCAGG 300
 AAAGAGAGTC ACTGAGAGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAAAT GGCAAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATG AACATCTCCA 660
 TCATCGTAGC CGACCAAGAT GACCAACAGC CCAAGTTTAC CCAGGACACC TTCGAGGGA 720
 GTGCTCTAGA GGGAGTCTTA CAGGTACTTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAT AATGGGTGGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
 AGGACCCACA CGACCTCATG TTCACAATTC ACCGAGACAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGGCT GGACCGGGAA AAGTCCCTCG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
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 GCGATGCTCC CATGAGGCTG ACGTCACTG ATCTGGAACG CCCCACTCA CCAGCGTGGC 1140
 GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCAGGGCATC CTGACAAACA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
 AGCACACCTC GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCTAACCT 1320
 CCACAGCCAC CATAGTGGTC CAGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTTGAGGTC CAGGAGGSCA TCCCCACTGG GGAGCCTGTG TGTGTCTACA 1440
 CTGCAGAAAG CCTGACAAAG GAGAATCAAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500
 CAGGTTGGCT AGCCATGGAG CCAGACAGTG GGCAGGTGAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGATGAC CGAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
 ATGGAAGCCC TCCACCAACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGCCC AGTCCCTGAG CCCCGTCAAG TCACCATCTG CAACCAAAGC CCTGTGGGCC 1740
 ACGTGTGAA CATCACGGAC AAGAACCTGT CTCCCCACAC CTCCCTTTTC CAGGCCACAG 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACACTT TCTCTGTCTG 1920
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGAAAC CTGCCCTGGA CCCTGGAAGG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCC CCTCCTACTC CCAGAAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAAGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GGAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCRA CTTTATAATT GAGAACCTGA 2340
 AGGCGGCTAA CACAGACCCC ACAGCCCCGC CCTACGACAC CCTCTTGGTG TTCGACTATG 2400
 AGGCGAGCGG CTCGAGCGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
 ACCAAGATTA CGATTATCTG AACGAGTGGG GCAAGCGCTT CAAGAACTGT GCAGACATGT 2520
 ACGGTGGCGG GGAGGAGCAG TAGGCGGCCT GCGTGCAGGG CTGGGACCA AACGTGAGGC 2580
 CACAGAGACT CTCCAAGGGG TCTCAGTTCC CCTTCAGCT GAGGACTTGG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GCGGAGACA GGCATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG GCAGTTTGAC TTCAGCACTG AAAACCTCTC 2760
 CACCTGGGCC AGGTTTGCCT CAGAGGCCAA GTTTCCAGAA GCCTCTTACC TGCCGTAATA 2820
 TGCTCAACCC TGTGTCTCTG GCCTGGGCTC GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCACTTAAT TTTTTTTTTT AATGCTATCT 2940
 TCAAAAGGTT AGAGAAAGTT CTTCAAAGT GCAGCCAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGTG TGCCTAGGTT GCCCTTATT TTTTATTTTC CCGTGTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAATCGTG TATATGTACT AGAAGCTTTT TATTAAGGAA A

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)

Cellular localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MGLPRGPLAS LLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPQQA LGKVFMGCPG 60
QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
KGPFPPQRLNQ LKSNKDRDTK IPYSITGPGA DSPPEGVFAV EKETGWLILN KPLDREBIAK 180
YELFGHAVSE NGASVEDPMN ISIIVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
DEDDAIYTYN GVVAYSISHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
TMDGDGSGTT TAVAVVEILD ANDNAPMFDP QKYBAHVPEV AVGHEVQRLT VTDLDAPNSP 360
AWRATYILMG GDDGDHPTIT THPESNQGIL TTRKGLDFEA KNQHTLYVEV TNEAPFVLKL 420
PTSTATIVVH VEDVNEAPVF VPPSKVVEVO EGIPTEGPVC VYTAEDPDKE NQKISYRILR 480
DPAGWLAMDP DSGQVTAVGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLTLLTLID 540
VNDHGPVPEP RQITICNQSP VRHVLNITDK DLSPTSFPQ AQLTDDSDIY WTAEVNEEGD 600
TVVLSLKKFL QDQTYDVHLS LSDHGNKEQL TVIRATVDCD HGHVETCPGP WKGGFILPVL 660
GAVLALLFL LVLALLVRKK RKIKEPLLLL EDDTRDNVFP YGEGGGGEDD QDYDITQLHR 720
GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDITLVF 780
DYEGSGSDAA SLSSTSSAS DQDQDYDYLN EWGSRFKKLA DMYGGEDED

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A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCAGCGTGG CTGTGGCCTC 60
GGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTACACTTC GCCATGAGTT TCCTGATCGA 120
CTCCAGCATC ATGATTACCT CCCAAATACT ATTTTTTGA TTTGGGTGGC TTTTCTTCAT 180
CGCCCAATTG TTAAAGACT ATGAGATACG TCAGTATGTT GTACAGGTGA TCCTCTCCGT 240
GACGTTTGCA TTTCTTGCA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
GAATAGCAGC TCCCGTTATT TTCACTGGAA AATGAACCTG TGCCTAATTC TGCTGATCCT 360
GGTTTTCATG GTGCCCTTTT ACATTGGCTA TTTTATGTG AGCAATATCC GACTACTGCA 420
TAAACAACGA CTGCTTTTTT CCTGTCTCTT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
ACTAGAGATG CCTCTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
CATCAGCCGG GTTGGTGTGA TTGGAGTGAC TCTCATGGCT CTCTTCTCTG GATTTGGTGC 600
TGTCAACTGC CCATACACTT ACATGTCTTA CTCTCTCAGG AATGTGACTG ACACAGATAT 660
TCTAGCCCTG GAACGGCGAC TGCTGCAAAC CATGGATATG ATCATAAGCA AAAAGAAAG 720
GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGAA GTGCATAACA AACCATCAGG 780
TTTCTGGGGA ATGATAAAAA GTGTTACCAC TTCAGCATCA GGAAGTGAAA ATCTTACTCT 840
TATTCAACAG GAAATGGATG CTTTGGGAAG ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
TGATCTATAT GCTACCAAGG AGAGAATAGA ATACTCCAAA ACCTTCAAGG GGAATATTT 960
TAATTTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGGCTACCAT 1020
CAATATTGTT TTTGATCGAG TTGGGAAAAA GGATCCTGTC ACAAGAGGCA TTGAGATCAC 1080
TGTGAATTAT CTGGGAATCC AATTGATGT GAAGTTTGG TCCCAACACA TTTCTTCTAT 1140
TCTTGTGGA ATAATCATCG TCACATCCAT CAGAGGATTG CTGATCACTC TTACCAAGTT 1200
CTTTTATGCC ATCTTAGCA GTAAGTCCCT CAATGTCAAT GTCTGTCTAT TAGCACAGAT 1260
AATGGGCATG TACTTTGTCT CCTCTGTGCT GCTGATCCGA ATGAGTATGC CTTTAGAATA 1320
COGCACCATA ATCACTGAAG TCCTTGAGGA ACTGCAGTTC AACTTCTATC ACCGTTGGTT 1380
TGATGTGATC TTCTGGTCA GCGCTCTCTC TAGCATACTC TTCTCTTATT TGGCTCACAA 1440
ACAGGCACCA GAGAAGCAAA TGSCACCTTG AACTTAAAGC TACTACAGAC TGTTAGAGGC 1500
CAGTGGTTTC AAAATTAGA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
ATAAACAAAC AAAATGCTAT GGTAGCATT TACCTTCA TAGCATACTC CTTCCCTCTC 1620
AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAACCTCAG 1680
ACRAATACTA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
CCAAGAACT AAAGGTGAAA AATACACTGG AACTCTGGGG CAAGACATGT CTATGTAGC 1800
TGAGCCAAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAAGGTTA TAGCTTTGCC 1860
TTGAGATTGA CTCATTAATA TCAGAGACTG T

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A84 Protein sequence

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Protein Accession #: NP_057418.1
 Signal sequence: none found
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446
 Cellular Localization: plasma membrane

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1      11      21      31      41      51

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10
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MSFLIDSSIM	ITSQILFFGF	GWLFFMRQLF	KDYEIRQYV	QVIFSVTFAP	SCTMFELIIF	60
EILGLVNSS	RYFHWKMLC	VILLILVFM	PFYIGYFIVS	NIRLLHKQL	LFSCLLWLT	120
MYFFWKLGDP	PFILSPKHGI	LSIEQLISRV	GVIGVILMAL	LSGFGAVNCP	YTYMSYFLRN	180
VTDTDLALE	RRLLQTMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGFWGM	IKSVTTSASG	240
SENLTLIQBE	VDALIELSRQ	LPLETADLYA	TKERIEYSKT	FKGKYFNFLG	YFFSIYCVWK	300
IFMATINIVP	DRVGKTDVPT	RGIEITVNYL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
ITLTKFPYAI	SSSKSSNVIV	LLLAQIMGY	FVSSVLLIRM	SMPLEYRTII	TEVLGELQFN	420
FYHRWFDVIF	LVSLSSILF	LYLAHKQAPE	KQMAP			

A85 DNA SEQUENCE:
 Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51	
GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACCTC	TTGTTGGCCA	GGCTGGAGTG	60
CAATGGCACA	ATCTCAGCTT	ACTGCAACCT	CCGCCTCCCG	GGTTCAAGCG	ATTCTCCTGC	120
CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACCTAATT	180
CTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCTG	240
ACCTCAGGTG	ATCCACTTGC	CTTGGCCTCC	CAAAGTGCTA	GGATTACAGC	CGTGAAGCTG	300
TGCGTGGCTG	ATTCCTTTTT	TGTTGTTGGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCGCCC	360
AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATAAACC	TCCACCTCCT	GGTTTCAAGT	420
GATCCTCCCA	CTTAGCCTCT	CTGAGTAGCT	GTGATTACAG	GGGTGCACCA	CCACACCCGG	480
CTAATTTATT	TATTTTATT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGTTCTCAAA	540
CTCCTGACT	CAAGGGATCC	GCTGCTCTCC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
AGTCACCATG	CCTGACCTTA	TAATCTTAA	GTCAATTTTT	CTGGTCCATT	TCTTCTCTAG	660
GGTCCTTACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TAACTTCAT	GATTCAACAA	720
AGGAAGATGA	AGTGATTCAT	GATTAGAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
TTTGGTTTAA	ATTAATATAT	TAAATATCTA	AAAACATTTT	TGGATACATT	GTTGATGTGA	900
ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCAATCTTTC	ATTTCCCCAG	960
TGCAGTTTTT	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
CCATAATGAA	CAAAGTGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
AACTAAGCTT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAAC	GTTAAACCAA	1140
TTATGATGAT	GGCAACAAC	CCAGAGGACT	GGTTGAGTTT	GTTGCTCAAA	CTAGAGAAAA	1200
ACAGTGTTC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTCGTTAC	AGTCAAGCAA	1260
TTGAAGCGCT	TCCCCAGAGT	AAATATGGCC	AAAATGAGAG	TTTGTCTAGA	ATTCAAGTGA	1320
GATTGCTGTA	ATTAAAGACT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
CCAGAGCAAA	CTGGAAGAAA	TTTGCTTTTG	TTTATATATC	TTTGTCAAAA	TTTGAAGTGT	1440
CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
TACCACTAGA	AATGCTGGAA	ATTGCCCTGC	GGAAATTTAA	CCTCAAAAAA	AAGCAGCTGC	1560
TTTCAGAGGA	GGAAAGAAAG	AATTTATCAG	CATCTACGGT	ATTAACCTGC	CAAGAATCAT	1620
TTTCCGGTTC	ACTTGGGACT	TTACAGAAAT	GGAAACAACG	TTGTGATTCC	AGAGGACAGA	1680
CTACTAAGCC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAATAGGTTT	1740
ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCATTT	GGAAAGGTCC	1800
CAGTTAACTT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTCA	GTTGTACCTT	1860
GTTTTATGAA	AAGACAAAAA	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAATTTTAAA	GTCTGTTCAA	AATAGTCATT	1980
TCAAGGAACC	TCTGGTGTCA	GATGAAAAGA	GTTCTGAAC	TATTATTACT	GATTCAATAA	2040
CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
AAGAACCAGA	GGTTCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
GTATTAAACA	GAATCCTGCT	GCATCTTCAA	ATCACTGGCA	GATTCCGGAG	TAGCCCGGAA	2220
AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTCTTTCA	GTTCCTCAAA	2280
AGTCACCAAC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTGAAGAC	TCCAGTTGTA	AAGAATGACT	2400
TTCCACCTGC	TTGTCAGTTG	TCAACACCTT	ATGGCCCAAC	TGCCGTGTTT	CAGCAGCAAC	2460
AGCATCAAAAT	ACTTGCCACT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
ATGAATGCAT	TTCCGTTTAA	GGAAGAAATT	ATTCCATATT	AAAGCAGATA	GGAAAGTGGG	2580
GTTCAGCAAA	GGTATTTCAG	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAAATATG	2640
TGAATCTAGA	AGAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
TGAATAAACT	ACAAACAAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAATTCACGG	2760
ACCAGTACAT	CTACATGGTA	ATGGAGTGTG	GAATATTGTA	TCTTAATAGT	TGGCTTAAAA	2820
AGAAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAAAAAATATG	TTAGAGGCAG	2880
TTCAACAAT	CCATCAACAT	GGCATTGTTT	ACAGTGATCT	TAAACCAAGT	AACCTTCTGA	2940
TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAAAATG	CAACCAAGATA	3000
CAACAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAAGCAA	3060
TCAAGAGTAT	GTCTTCTCTC	AGAGAGAAATG	GGAAATCTAA	GTCAAAAGATA	AGCCCAAAAA	3120
GTGATGTTTG	GTCTTATAGG	TGTAATTTGT	ACTATATGAC	TTACGGGAAA	ACACCAATTTC	3180
AGCAGATTAAT	TAATCAGATT	TCTAAATTAC	ATGCCATAAT	TGATCTTAAT	CATGAAATTTG	3240
AATTTCCCGA	TATTCCAGAG	AAAGATCTTC	AAAGTGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
ACCCAAAAAC	GAGGATATCC	ATTCCTGAGC	TCCCTGGCTCA	TOCATATGTT	CAAAATCAAA	3360
CTCATCCAGT	TAACCAAAATG	GCCAAGGGAA	CCACTGAAGA	AATGAAATAT	GTCTGGGGCC	3420
AACCTGTGTG	TCTGAATCTT	CCTAACTCCA	TTTTGAAAGC	TGCTAAAACT	TTATATGAAC	3480
ACTATAGTGG	TGGTGAAGT	CATAATCTT	CATCTCCAAA	GACTTTTGAA	AAAAAAAGGG	3540
GAAAAAAATG	ATTTCAGATT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
GTTTACTCTT	TGAATCCCTG	TGGAATCTA	CATTGGAAGA	CAACATCACT	CTGAAGTGTG	3660
ATCAGCACTA	AAAAATCAGT	GAGATTATCT	TTAAAAAGAA	ACTGTAAAAA	TAGCAACCAAC	3720
TTATGGCACT	GTATATATTG	TAGACTGTGT	TTCTCTGTTT	TATGCTCTTG	TGTAATCTAC	3780
TTGACATCAT	TTTACTCTTG	GAATAGTGGG	TGGATAGCAA	GTATATTCTA	AAAACTTTTG	3840

TAAATAAAGT TTTGTGGCTA AAATGA

A86 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1	11	21	31	41	51	
MNKVRDIKKN	FKNEDLTDEL	SLNKISADTT	DNSGTVNQIM	MANNPEDWL	SLLLKLEKNS	60
VPLSDALLNK	LIGRYSQAI	ALPPDKYQON	ESFARIQVRF	AEKAIQEPD	DARDYFQMAR	120
ANCKKPAFVH	ISFAQFELSQ	GNVKKSKQLL	QKAVERGAVP	LEMLEIALRN	LNLQKKQLLS	180
EEBKQNLAS	TVLTAQESFS	GSLGHLQNRN	NSCDSRGQTT	KARFLYGENM	PPQDAEIGYR	240
NSLRQTNKTK	QSCPFGRVPV	NLLNSPDCDV	KTDDSVVPCF	MKRQTSRSEC	IDLVPVPSKP	300
SGNDSCELRN	LKSVQNSHF	EPLVSEKSS	ELIITDSITL	KNKTESSLLA	KLEETKEYQE	360
FEVPESNQKQ	WQAKRKSECI	NQNPAASSNH	WQIPELARKV	NTEQKHTTFF	QPVFVSXQS	420
PPISTSKWFD	PKSICKTPSS	NTLDDYMSCP	RTPVVGNDFP	PACQLSTPYG	QPACFQQQKH	480
QILATPLQNL	QVLASSANE	CISVKGRIYS	ILKQIGSGGS	SKVFQVLNEK	KQIYAIKYVN	540
LEEADNQTL	SYRNEIAYLN	KLQOHSDKII	RLYDYEITDQ	YIYVMVECGN	IDLNSWLKKK	600
KSIDPWERKS	YWKMLAEAVH	TIHQHGIHVS	DLKPAFLIV	DGMLKLIDFG	IANQMOPDTT	660
SVVKDSQVGT	VNYMPPEAIK	DMSSSRENGK	SKSKISPKSD	VWSLGCILYY	MTYGRTPPQQ	720
IINQISKLHA	IIDPNHEIEP	PDIEKDLQD	VLKCLKRPD	KQRIPIPELL	AMPYVQIQTH	780
PVNMKAGT	EEMKYVLQGL	VGLNSPNSIL	KAATLYEHY	SGGESHNSSS	SKTFEKKRGK	840

A87 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GGGCGCAGCG	GGGCGCGTCT	GCAGCAAGTG	ACCGACGGCC	GGGACGGCCG	CCTGCCCCCT	60
CTGCCACCTG	GGGCGGTGCG	GGCCCGGAGC	CCGGAGCCCG	GGTAGCGCGT	AGAGCCGGCG	120
CGATGCACGT	GGGCGTCACTG	CGAGCTCGCG	CGCCGCACAG	CTTCGTGGCG	CTCTGGGCAC	180
CCCTGTTCCT	GCTGGCTCC	GGCCTGGCCG	ACTTCAGCCT	GGACAACGAG	GTGCACTCGA	240
GCTTCATCCA	CGGCGCCCTC	CGCAGCCAGG	AGCGGCGGGA	GATGCAGCGC	GAGATCCTCT	300
CCATTTTGGG	CTTGCCCCAC	CGCCCGGCGC	CGCACCTCCA	GGGCAAGCAC	AACTCGGCAC	360
CCATGTTTAT	GCTGGACCTG	TACAACGCCA	TGGCGGTGGA	GGAGGGGGCG	GGGCCCCGGG	420
GCCAGGGCTT	CTCTACCCCG	TACAAGGCCG	TCTTCAGTAC	CCAGGGCCCC	CCTCTGGCCA	480
GCTTCGAGGA	TAGCCATTTC	CTCACCGACG	CGACATGGT	CATGAGCTTC	GTCAACCTCG	540
TGGAAATGTA	CAAGGAATTC	TTCACCCAC	GCTACCACTA	TCGAGAGTTC	CGGTTTGATC	600
TTTCCAAGAT	CCCAGAGGGG	GAAGCTGTCA	CGGCAGCCGA	ATTCCGGATC	TACAAGGACT	660
ACATCGGGGA	ACGCTTCGAC	AATGAGACGT	TCCGGATCAG	CGTTTATCAG	GTGCTCCAGG	720
AGCACTTGGG	CAGGGAATCG	GATCTCTTCC	TGCTCGACAG	CGTACCCCTC	TGGGCTCCGG	780
AGGAGGGCTG	GCTGGTGTTC	GACATCACAG	CCACCAAGCA	CCACTGGGTG	GTCAATCCGC	840
GGCACAACCT	GGGCGTCCAG	CTCTGGGTGG	AGACGCTGGA	TGGCAGAGC	ATCAACCCCA	900
AGTTGGCGGG	CCTGATTGGG	CGGCACGGGC	CCCAGAACAA	GCAGCCCTTC	ATGGTGGCTT	960
TCCTCAAGGC	CACGAGGTTC	CACTTCCGCA	GCATCGGTTC	CACGGGGAGC	AAACAGCGCA	1020
GCCAGAACCG	CTCCAGACAG	CCCAAGAAC	AGGAAGCCCT	GCGGATGGCC	AACGTGGCAG	1080
AGAACAGCAG	CACGACCCAG	AGGCAGGCTT	GTAAGAAGCA	CGAGCTGTAT	GTGAGCTTCC	1140
GAGACCTGGG	CTGGCAGGAC	TGGATCATCG	CGCCTGAAGG	CTACGCCGCC	TACTACTGTG	1200
AGGGGAGTGT	TGCCTTCCCT	CTGAATCTCT	ACATGAAGCG	CACCAACCAC	GCCATCGTGC	1260
AGACGCTGGT	CCACTTCATC	AACCGGAAA	CGGTGCCCAA	GCCCTGCTGT	GGGCCCCAGC	1320
AGCTCAATGC	CATCTCCGTC	CTCTACTTCG	ATGACAGCTC	CAACGTCATC	CTGAAGAAAT	1380
ACAGAAACAT	GGTGGTCCGG	GCCTGTGGCT	GCCACTAGCT	CCTCCGAGAA	TTCAGACCCCT	1440
TTGGGGCCAA	GTTTTCCTGG	ATCCTCCATT	GCTCGCCTTG	GCCAGGAACC	AGCAGACCAA	1500
CTGCCCTTTG	TGAGACCTTC	CCCTCCCTAT	CCCCAATTTT	AAAGGTGTGA	GAGTATTAGG	1560
AAACATGAGC	AGCATATGGC	TTTTGATCAG	TTTTTCAGTG	GCAGCATCCA	ATGAACAGAA	1620
TCCTACAAGC	TGTGAGGCA	AAACCTAGCA	GGAAAAAATA	ACAAACGATA	AAGAAAAATG	1680
GCGGGGCCAG	GTCAATGGCT	GGGAAGTCTC	AGCCATGCAC	GGACTCGTTT	CCAGAGGTAA	1740
TTATGAGCGC	CTACAGGCCA	GGCCACCCAG	CGTGGGAGG	AAGGGGGCGT	GGCAAGGGGT	1800
GGGCACATTC	GTGCTGTGTC	GAAAGGAAAA	TTGACCCCGA	AGTTCCGTGA	ATAAATGTCA	1860
CAATAAACGC	AATGAATG					

A88 Protein sequence:

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 Pfam domains: TGFb_propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSRLRAAA PHSFVALWAP LFLLRSALAD FSLDNEVHSS FIHRRRLRSQE RREMQREILS 60
   ILGLPHRRPRP HIQKGKHSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
   LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHHRFREFDL SKIPGEAVT AAEFRYKDY 180
   IRERFDNETF RISVYQVLQE HLGRESDLFL LDSRTLWASE EGWLVFDITA TSNHWVNVNR 240
   HNGLQLQSVL TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFERS IRSTGSKQRS 300
   QNRSKTPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGQWDWIIA PEGYAAYYCE 360
10  GECAPPLNSY MNATNHAIVQ TLVHPINPET VPKPCCAPTQ LNAISVLVFD DSSNVILKKY 420
   RNMVVRACGC H

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A89 DNA SEQUENCE:

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15  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Nucleic Acid Accession #: AC012478
   Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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20  1      11      21      31      41      51
   |      |      |      |      |      |
   ATGCGGCGCG TGCCGCTGCC CGCCCGCTGC CTGCGCTGCG TGCTGCTGCG GCTCCTGGCC 60
   GCTCCGCGCG CCOCGCGCCAG CAGAGCGGAG TCCGTCTCCG CGCGTGCGCC CGAACCCGAG 120
25  CGCGAGTCGC GGCCACCCGC CGCCCGGGG CCCGGGAACA CCACCCGCTT TGGGTCTGGG 180
   GCGGCGGGCG GCAGCGGCAG CTCAGCTGCC AACAGCAGTG GCGACGCCCT GGTGACCCGC 240
   ATTTCCATCC TCCTCCGCGA CCTACCCACC CTCAGGCAG CGGTGATCGT GCGGTTCCGC 300
   TTTACACCCC TCCTCATGCG CTGCGCTGCT CTGCGCTGCT TCAGGTGCGG AAAGAGGTGA 360
   AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
30  CTAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
   TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGCTGCC AGACGCTACT GACAGTTCCT 540
   GTGCCCCAC CTTTCATCTC CGACATTGAC CTTCCAGCAA GATGCACTGG AAGGCGTGAT 600
   GGTGAATACA GACCTGCTAA AACCTGTTTC CCAGCCTGCT GGCATCCTGT GGAAGTGTGG 660
   TCAGCTGCAA CTGCGGTGGT GAAGGACTGG ACCTGGAAGC CCTCTTGCGT CGGAGGTGTT 720
35  GAAACCAAAA CGAACCTTAT GTATAAAACC CCAGCTCCAT CGTGCCTGTC AGGCATCTGC 780
   TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTGTGT TCTGCCACCC 840
   TTTGGGCATC CCTTTAAAGT GCCCCTACT TCTACTCCCC ATGGTTTTCG ACAACTGCAG 900
   CTGAATCTCA TGGAAAGCTT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCTCCACTC 960
   GCCAGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
40  CCTTGGTGGC ACTTCAGCGC CACAGGCTCT CCAATAAAAA CCCTTTACAC ACAAAACCATG 1080
   AGTACCTTGG GCTTGGATGT TTTCTGTGGT GCGCGCCAGC GGGGCACCTT TTGTGAAGAC 1140
   AGAGCAGTGA CTAAGGTTCT CCAGGGTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
   GCCTTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
   ACCCATCTCG TCAGGTTTGG TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
45  AGGGTGTTCG GCGCTCCGCG GCAGTCTCTG CATGCGCGAG GGTGAGCGGG TACGSCAACT 1380
   TGCCCTTTGG TTTTGAAGAT TCTGTTGAGG GCCTATCCTC ACCTTGACCT CTTCTACAAA 1440
   ATCTGCTCC CCTGCTGTGC CGTGGAAACG CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCTTGTGCT CATTTGAGCA GAGCCACAA AAGGCAGCTG CTGCCCACGG GGAGCCTGTC 1560
   AAACGAGGGC TCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
50  GCGAACCTCG AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCAGCTGA GATGTGCACT 1680
   CACCCTGGAG GAGACTTGGA TGGGGTGGCA AATTCTTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GCCAGAAGAT GGTCTGTATG TCTGAGGAAG GGCCACTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860
55  TCCCCCGAC AGCCCTGTT TCTGTCCAGG CCTTGA

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A90 Protein sequence:

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60  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Protein Accession #: PGENESH predicted
   Signal sequence: 1-27
   Transmembrane domains: 94-115, 448-469
   Cellular Localization: not determined

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65  1      11      21      31      41      51
   |      |      |      |      |      |
   MRVPLPAPL LPLLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
   AAGSGSSSS NSSGDALVTR ISILLRLDPT LKAIVIVAPA FTLLLIACLL LRVFRSGKRL 120
70  KKTRKYDIIT TPAERVMAP LNEEDEDED STVPDIKYRV SLPAALRRQL PGQTLTLTP 180
   VPPFFILDID LPARCSGRPD GGIRPGKTCF PAWHFVSVES SAATWGVKDW TWKPSVCGGV 240
   ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VTMELLPLP FGHPPKVPPT STPHGFRQLQ 300
   LNLMEKLDS ALRNRTRAPS ARCLPLVLAE MAAESDLPN PWHFSAATGS PIKTLTYTQM 360
   STLGLDVFCG AGQRTFCED RAVTKVLQGS SFSKQLRWKP ALESQFPFHL RLLRECPPLS 420
75  THPVRLARSD ARGQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAANGFV KRGPSQGLTR HTCPGWGITH 540
   ANLQTIPTDQ GQEGPREDVT HPGGDLDCVA NFYLEEGFPQ DGRGCKRMVLM SEEGPPSLTG 600
   CERLTGSHHF SSKSKSWFL SPRQPLFLSR P

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EWING**A91 DNA SEQUENCE**

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Gene name:      G protein-coupled receptor 64
Unigene number: Hs.184942

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Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80

1 11 21 31 41 51
 AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
 CTGCGGTCGA GGATGGTTTT CTCTGTGAGG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
 GTTTTACTGA CGTTCAGAT ATTCTTGTGC ATCATTGTGC TTCATGTCGT TCTGGTAACA 180
 TCCTCGGAAG AAGATACTGA TAATTCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
 GTCAGTTTTG CCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
 AGCTTACTCC CTTCAAACGA AACAGAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
 GCTTCAGGGG TCAACCCCA GAGAAATATC TGAATTTGT CATCTATTG CAATGACTCA 420
 GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT 480
 CAACATATAA CGAATGGCAC CTTAACTGGA GTCTGTGCTC TAAGTGAATT AAAACGCTCA 540
 GAGCTCAACA AAGCCCTGCA AACCCCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
 GAGGCCCAAA GCACATTAAA TTGTACATTC ACAATAAAC TGAATAATAC AATGAATGCA 660
 TGTGCTGCAA TAGCCGCTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
 TCTGTGAGGA TACCCCTGCCC TTCTTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
 CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840
 TCCATCCAGG TGGTGCTCTG GGCCACTGTG CTTTCCAGG TCCCCAAAGC TACCTCTTTT 900
 GCTGAGCTTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAT AGGGGAGATT 960
 CAACCCCTTC CACCCGCTCC TTCAGTCCCA ATAGCTTCCA GCCCTGCCAT TGACATGCCG 1020
 CCACAGTCTG AAACGATCTC TTCCCCCTAT CCCCCAACCC ATGTCTCCGG CACCCCACTT 1080
 CCTGTGAAGG CCTCATTTTC CTCTCCACCC GTGTCTGCCC CTGCGAATGT CAACACTACC 1140
 AGGCCACCTC CTGTCCAGAG AGACATCGTC AACACAGCA GTATTCTGA TCTTGAGAAC 1200
 CAAGTGTGTC AGATGGAGAA GGCTCTGTCC TTGGGAGGCC TGGAGCCTAA CCTGCGAGGA 1260
 GAAATGATCA ACCAAGTCAG CAGACTCCCT CATTCGCCG CTGACATGCT GGCCCTCTG 1320
 GCTCAAAGAT TGCTGAAAGT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAAACAG 1380
 ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
 TTCAACACAA TACCTTTGTG GGCCCAAGAC CCTGCAATC TTCAGTTTC TCTGGAAACC 1500
 CAAGCTCCTG AGAAGCAGAT TGGCACAATT ACTCTTCTT CATCGCTGAT GAATAATTGA 1560
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 GTTGCAAAAC TGACCGTCAG GAACCTTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
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 ATCTGACTCT ATGAGCTTCT AACAGCTTC GCGTTCTGC TGGACCTATC TAGGACATCT 1920
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 TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCOGAA AATACATCCT TAAATTCTGC 2280
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 CAACGGGAG CCCAGCGAAA AACCAATATT CAAGACCTCA GGAGTATCGC TGGCCTTACA 2580
 TTTTACTGAG GAATAACTTG GGGCTTGGCC TTCTTTGCC TGGGACCGAG TAACGTGACC 2640
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 GTAAACCAAG GAGTGTCCAG CTCTTCAAAT TCCTTACAGT CAAGCAGTAA CTCCTACTAC 2880
 TCCACCACAC TGCTAGTGAA TAATGATGTC TCAGTACAGC CAAGCGGGAA TGGAAATGCT 2940
 TCTACAGAGA GGAATGGGCT CTCTTTTGTG GTTCAGAATG GAGATGTGTG CCTTCAGAT 3000
 TTCACTGAAA AACAGCACAT GTTTAACGAG AAGGAAGATT CCTGCAATGG GAAAGGCGGT 3060
 ATGGCTCTCA GAAGGACTTC AAAGCGGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
 CTTTCTTCTA AATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACTTTTGA 3180
 CACAATGTGA GATGATGAA AATCAACTCA TTTTATTTCT GGCACATCT GGAAGAAGCAT 3240
 AAGCTAATTA AGGCGATGTA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
 TTTAGACATT TCTGATTGAG TTTCTTATCT TTCAATTTAT AAGAAGGTTG GTTTTAAACA 3360
 ATACACTAAG AATGACTCCT ATAAAGAAAA CAAAAAAGG TAGTGAACCT TCAGCTACCT 3420
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 TTGGTGAGTT TAGTTGTGCA TGCCCTTGTG GTATATAAGC TAAATTTCTAG TGACCCATGT 3540
 GTCAAAAATC TTACTTCTAC ATTTTTTTGT ATTTATTTTC TACTGTGTA ATGTATTCTT 3600
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 AAATCCTAAA AGTCTTCTT GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
 TCAAGAAATA ATGATCCGAG CCAGACTGAG AAAATGTAAG CAGACAGTGC CACAGTTAGC 3780
 TCATACAGTG CCTTTAGACA AGTTAGGAAA AGATGCCCCC ACTGGGCGAG CACAGCCCTA 3840
 TGGGTGATGG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
 GTGCAGGACC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCGCAT 3960
 CCCAGTATAG CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
 AGAGGGATGA ACTGTCTATC AGACATGTG TCAGGAAAAA TGTGAACGTA GATGAGGTAC 4080
 ATACACTGCC GCTTCTCAAA TCCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
 CTTCTCTTAA AAAGGTACAT ATATATGAAA AAAATCATA TTGCGTTCT TTAAGAGGCA 4200
 ACTGCAATGT ACATTGTTGA TTGTTATGAC TGGTACACTC TGGCCAGGCC AGAGCTATAA 4260
 TTGTTTCTTA AATGTGCTT GAAGAATGCA CAGTGACAAG GGGAGTAGCT ATTGGGAACA 4320
 GGGAACTGTC CTACACTGCT ATTTGTTGTA CATGTATCGA GCCTTGATTG CTCCTAGTTA 4380
 TATACAGGGT CTATCTTGCT TCCTACCTAC ATCTGCTTGA GCAGTGCCTC AAGTACATCC 4440
 TTATTAGGAA CATTTCAAAC CCCTTTAGT TAAGTCTTTC ACTAAGGTTT TCTGTCATAT 4500
 ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560
 CTGACTGTGC TTTGCAATAT TCTTTTCTG ATTTATTTAA TTTTCTGTGA TTTATATGTT 4620

AAAATCAAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

A92 Protein sequence

5 Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 10 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 15 MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPF PAKLSVVSFA 60
 PSSNEVETTS LNDVTLSELLP SNETEKTKIT IVKTFNASGV KPQRNICNLS SICNDSAPFR 120
 GEIMFPQYDKE STVPQNHIT NGTLTGVLSL SELKRSELNK TLQTLSETYF IMCATAEAQS 180
 TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240
 VCLADHPRGP PFSSSQSIPV VPRATVLSQV PKATSPAEPP DYSPTVTHNPV SPIGEIQPLS 300
 PQPSAPIASS PAIDMPQOSE TISSPMQTH VSGTPPPVKA SFSSPTVSAP ANVNTTSAPP 360
 20 VQTDIVNTSS ISDLNQVLQ MEKALSLGLS EPNLAGEMIN QVSRLLHSPF DMLAPLAQRL 420
 LKVVDDIGLQ LNFSTNTISL TSPSLALAVI RVNASSFNIT TFVAQDPANL QVSLETQAPE 480
 NSIGITFLPS SLMMNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVISSSVANL 540
 TVRNLTIRNVT VTLKHINPSQ DELTVRCVFW DLGRNGRGG WSDNGCSVKD RRLNETICTC 600
 SHLTSFGLVL DLRSFVLPFA QMMALTFTFY IGGLSSIFL SVTLVTYIAF EKIRRDYPSK 660
 25 ILIQLCAALL LNLVFLPDS WIALYKQQL CISAVALFHY PLLVSTFWNG LEAFHMYLAL 720
 VKVFNTYIRK YILKFCIVGW GVPVVVTII LTISPDNYGL GSYGKFPNGS PDDFCWINNN 780
 AVFYITVGV FCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLIG 840
 ITWGFAPFAW GPVNTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKRLRLAE 900
 NSDWSKTATN GLKKQTIVNQ VSSSSNSLQS SSNSTNSTTL LVNNDCSVEHA SGNGNASTER 960
 30 NGVSFSVQNG DVCLHDFTGK QHMFNEKEDS CNKGKRMALR RTSKRGSLHF IEQM

Fibrosis

A93 DNA SEQUENCE

35 Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
 CGCAGAGGA GCCTCGGCCA GGCTAGCCAG GGCGCCCCCA GCCCTCCCC AGGCGCGAG 60
 CGCCCTCGCC GCGGTGCTTG GCCTCCCTC CCAGACTGCA GGGACAGCAC CCGGTAACAG 120
 CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGCGGCTT AGCTGCTACG 180
 45 GGGTCCGGCC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
 ATGCTCTGCG CCTGGAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
 GGGAGCGGGG CCATGCAAG GCATCACGGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
 TGTCACATG GAACATAACT GGCCTGCTGC TAOCGGCTGA GAAGAAACAG CAAGGGAGTC 420
 50 TGTAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
 AGATGCTTTC CAGGATACAC CGGAAAACC TGCAGTCAAG ATGTGAATGA GTGTGGAATG 540
 AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACAGG GAAGCTACAA GTGCTTTTGC 600
 CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
 ATAACTGCTC AGTACAGCTG TGAAGACACA GAAGAAGGCC CACAGTGCCT GTGTCCATCC 720
 55 TCAGGACTCC GCGTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
 GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGGAAG CTACTACTGC 840
 AAATGTCACA TTGGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
 AATGAATGTA CTATGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
 GGGTCTTCA AGTGAATAG CAAGCAGGGA TATAAAGGCA ATGGAATTCG GTGTCTGCT 1020
 60 ATCCCTGAAA ATCTCTGTGA GGAAGTCTC AGAGCACTG GTACCATCA AGACAGAAATC 1080
 AAGAAGTTGC TTGCTCAACA AAACAGCATG AAAAAGAAG CAAAATTAA AATGTTACC 1140
 CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAAGTGC AGCCCTTCAA CTATGAAGAG 1200
 ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
 GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
 65 AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
 CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAAA TATCTCGGTT 1440
 GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
 TGGAAATCCTG CTGATCGAGA TAATGCTATT GGCCTTCTATA TGGCAGTTCC GGCCTTGSCA 1560
 GGTCAACAAG AAGACATGG CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAAGC 1620
 70 AACTTCTGTT TGCTCTTTGA TTACGGCTG GCGGAGACA AAGTCGGGAA ACTTCGAGTG 1680
 TTTGTGAAAA ACRGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGAGTGA GGTGAAAAG 1740
 TGGAGACAG GGAATAATCA GTTGATATCA GGAAGTATG CTACCAAAAG CATCATTTTT 1800
 GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT 1860
 TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTACT ATCTTATAT 1920
 75 TTGACTTGT TTGCTGATT CTGCTTTT TTGATATTGC ATCATAGGAC CTCTGGCATT 1980
 TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
 TCTTGATATA GATATGCCAA TATTGTCTT AAATATCATA TCAGTGTATC TTCTCAGTCA 2100
 TTTCTGAATC TTTCCACATT ATATTATAAA ATATGGAAAT GTCAGTTTAT CTCCCTCTCT 2160
 CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCT TCTACAACAT TTCTAGAAAA 2220
 80 TAGAAAAAAG AGCACAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
 TATGACATCA AAGATAGACT TTTGCCCTAAG TGGCTTAGCT GGGTCTTCA TAGCCAAACT 2340
 TGATATATTA AATCTTTTGT AATAATAATA TCCAAATCAT CAAAAAATA AAAAAA

A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

1 11 21 31 41 51
 15 MPLPLWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRRNSKGV 60
 CEATCEPFGCK FGECEVGNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRVC NTHGSYKFCF 120
 LSGHMLMPDA TCVNSRTCAM INCQYSCEDT EEGPQLCPSS SGLRLAPNGR DCLDIDECAS 180
 GKVICPYNRR CVNTFGSYVC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCFTNTQ 240
 20 GSPKCKCKQG YKGNGLRCSA IPENSVKEVL RAPGTIKDRI KKLLAHKNSM KKKAKIKNVT 300
 PEPTRTPTEK VNLQFPNYEE IVSRGGNSHG GKKGNEEFMK EGLEDEKREE KALKNDIEER 360
 SLRGDVFFPK VNEAGEFGLI LVQRKALTSK LEHKDLNISV DCSFNHIGICD WKQDREDDFD 420
 WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLPDLQPQS NFCLLFYDRL AGDKVKGKLRV 480
 FVKNSNNALA WEKTTSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGKTG ELAVDGVLLV 540
 25 SGLCPDLSLS VDD

GLIOBLASTOMAA95 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1 11 21 31 41 51
 35 AGCAACGACG CCGGGCAGCG GGAGCGGCGG CCGGCCCATG TGGCTGCTGG GGCCTGCTGG 60
 CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCG GSGAACAACT TCACCAATGA 120
 GTGCAACATA CCAGGCCAAT TCATGTGACG CAATGGACGG TGCATCCCGG CGCCTGGCA 180
 40 GTGTGACGGG CTGCGTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTGCAAAATGT GGCACCAACT TCTTCCCTTG TCCAGCGGCG ATCCATTGCA TCATTGGTCG 300
 CTTCCGGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCG CTTTGTCTCA CCGCCCGCTA CCACTGCAAG AACCGCCTCT GTATTGACAA 420
 GAGCTTCATC TGGCATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 45 AAGTTCTCAA GAACCCGGCA GTGGGCAGGT GTTTGTGACT TCAGAGAACC AACTTGTGTA 540
 TTACCCGAGC ATCACCCTATG CCATCATCGG CAGCTCGGTC ATTTTGTGTC TGGTGGTGGC 600
 CCTGCTGGCA CTGCTCTGCG ACCACCAAGG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
 GCACCGGCTG CAGCACCCCTG TGCTGCTGTC CCGCCTGGTG GTCTGAGACC ACCCCACCA 720
 CTGCAACGTC ACCTACAAGC TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 50 GAATGCGTGG GAAGTAGGCT CCCACCCCTC TACTCCGAG GCCTTGCTGG ACCAGAGGCC 840
 TGCGTGGTAT GACCTTCTCT CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGCCC CCCTACCGCT CCGCGTCCGG GAGTGCCAAC AGTGCCAGCT CCCAGGCAGC 960
 CAGCAGCCTC CTGAGCGTGG AAGACACCGG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
 GGGCACTGCT GAGCCACGGG ACTCTGAGCC CAGCCAGGCG ACTGAAGAAG TATAAGTCCC 1080
 55 AGTTATTCCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTC TAAACAATTG 1140
 TGCTCATGGG AAGCTCTTTA AGCACCTGTA AGGATGTCTC AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT GCATTCCTCT CCTCCCCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
 TGACATGATC TGTGTGCGT CTTTCTGTC AGGTCACTCT TCCCTTGGGA CCGAGATCA 1320
 CACCTCATTT TTTCACTTA TTCTGTTTCT GTTGAGAGA CAGCATATAA AACAGTATTG 1380
 60 AATAGGCTG GGAGAGAGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 CGCTGGACCC AATTTCTCTT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTACCCCCCG CAAAAAATTT CCATTGAGC 1560
 ATCAAAACCT GCTTTGCACA ATCCTATTG ATGCCCCCG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAAACCT TGGACGTGAG TAACACCCCT CAGCAGTCGG AACGTTATTT TGGTTTGTG 1680
 65 AAGGACTCTG AAACCATCTA CCCGTGTATA ATCTGCGCTT TAGAAATTTG CCCAAGATG 1740
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCTTAA AATGCAGGCT GCCAAGACCC 1860
 TACACCTGCC CTGGCTCTAC AGCCACTTAC CTGGTTTCTG GACTGTCAAC CTCCAGCTG 1920
 ACCTGCCCGT AGCCAAGGAA TGAGGACCTA ACTTGAGTTG GCCCAAGTC TGACCTGGCT 1980
 70 GTATGCTCCCT GTGGCCCA CAACAGCCTGT CTGCTCATTT CATGCAGCCT CAACACTGGC 2040
 CTCCAAAGTT CCCTTAACAC TTGCAAGTGC CTTTTACCT GTGCATTGGG ACTTGAGGAC 2100
 ACTGGTTTCT ATCACAGGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCCTGGCTCC 2160
 CTGCACTGTG CAGCTCTCTT TCCCAAGGT CCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 75 GGTCAAGGTC AGGCCTCTCC CAACATCCCA GTAGTTTCTC CTCTGAGACA CATGGGCAAG 2280
 AGACAATTG GAGTCAAGAT TTTCCATTG GATCTATTTT AAATCTTTTA GAAATGCATT 2340
 TGAAACAGTG TGTGTGTTT TCCCTTCTA GTTAAGGAGC TATTTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTT TCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAAGAGATC 2460
 ACACCTTGG CCGCTGAGC CCGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCGAG 2520
 ACATTGTGTC ATTTGTGCAC TTTGAGGTTA TTATTTATCA AGTCTTGAA GGAAGCAGAA 2580
 80 AGAGGAGACT CTCCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTTTT 2640
 TTCTCTGTGT CAGTGTGAGT ACAGGGCCCG CCTCCCTGCA GGAATAAGGG GTAAACGTTT 2700
 AGGTGTTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGAGAA CCAGGTAGAG 2760
 CCACTCCGGG CAGCTGTAC CCATTAGAA CTCTTTCCG CAGCTGAAGA AATGTTCACT 2820
 AACCTGTTG ACCTAATTA AAAACAGAGC TGCAGGAAGT GGGCTAAAG TGGCATTGAG 2880

5 TGATCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAAGGA TGTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTTGTTTA AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000
 AACCGAAGAG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAGAAA CTTTTGATGA CAGCCAGAAT GTGTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGTATGGGG CCCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATGT 3300
 AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GCACATTTT ATTATAGATT 3360
 10 TGATTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGSGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC TCTGAAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAA GAGATCCGTG TTTTATTTA GCATTAAATT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTTCACTCT GAAATTGACA 3660
 15 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGGTTGT GTGTGTTGTC TTTTGTGTTT TTGGTTAGGC TTGGTTTGT TTTTAAATT 3780
 TTATACTTC TAATAAATTT GCAGTTTCAT TCTTCTGTTT TGTGCAAAAG GWMCTAMARM 3840
 AAMMAAAAC ANYWTTGGGG GGGCTTGGGC CTGCGAAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGGCGCG GGGCCACGCT AGGTACGGCG ACCACGCGGG CCCAAACGGG ACCCCAGAAG 3960
 20 GAAACCTCG CCAAGAAAAA GTTGGCGAGA ATTCTCCACA CCAGAAAAAA ACGCGCCGG 4020
 GGAAACCGCA GAGTGTTCG TAAACACAC CCGAAGAGAG AACTCAGAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A96 Protein sequence:

25 Gene name: ESTs
 Unigene number: Hs.293616
 ProbeSet Accession #: AW043782
 Protein Accession #: none found
 30 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51
 | | | | |
 MWLLSPLCLL LSSAAESQLL PGNNFTNECN IPGNFMCNSG RCIPIGAWQCD GLPDCFDKSD 60
 EKECKKAKSK CGPTFFPCAS GIHCLIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 40 KNGLCIDKSF ICDQNNQD NSDEESSCESS QEPGSGQVVF TSENQLVYYP SITYAIIGSS 180
 VIFVLVALL ALVLHQQRK NNLMTLPVHR LQHPVLLSRL VVLDHPHHCN VTYNVNNIGQ 240
 YVASQABQNA SEVGSPPSYS EALLDQRPAN YDLPPFPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PQQPGPQEGT AEPRDSEPSQ GTEEV

LUNG

A97 DNA SEQUENCE

50 Gene name: putative GPCR, Weakly similar to dJ365012.1
 Unigene number: Hs.256897
 ProbeSet Accession #: BE001836
 Nucleic Acid Accession #: BE001836
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 ATGGCCGTC AATCTTTTC CTTCACACT GGAATGATG GGCTAGACCC AGACCCAATC 60
 ATGTTAAGTA TGATAGGAT CAGTGGCCCA GCTGGTGTGG AAGACAAGTG GGTCAATCTG 120
 GGTTTAGGCC CACATAGCAC TAAAGTCTT CAACATGCAA TTAGAAGCTC AAATGTTGAC 180
 60 GGAATATTG TTAAGTCTT AAAAGATGTT TCTATTAGAA TTTACTTACT CTTTCATGAA 240
 AACATAGATG CTCTCTCTT OCTGATTAGT GATGGCCATC AGTTAAACCA AGTGCACTCA 300
 GAGAAGTCAA ATTCTGACAC AATCCAGCAA GTAACATATA AACTGATGG CCCAGTCGAA 360
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAG AGATTGAGA 420
 AATTTTCGTA AGCTCTGAA GCCTCCATTA TTATGGTCAC ATGGGCTAAT TAGAATTATC 480
 65 AGAGCAAGG CTACCACAGA CTGCAACAGC CTGAATGGAG TCCTGCAGTG TACCTGTGAA 540
 GACAGCTACA CCTGGTTTCC TCCTCATGCG CTGTATCCCC AGAAGTCTGA CCTTCACACG 600
 GCTGGAGCAC TCCCAAGCTG TGAATGTCTAT CTCAACAACC TCAGCCAGAG TGTCAATTTC 660
 TGTGAGAGAA CAAAGATTG GGGCACTTTC AAAATTAAATG AAAGGTTTAC AAATGACCTT 720
 TTGAATTCAT CTCTGCTAT ATACTCCAAA TATGCAATG GAATTGAAAT TCAACTTAAA 780
 70 AAAGCATATG AAAGAATTCA AGGTTTGTG TCGGTTGAGG TCACCCCAAT TCGAATGGA 840
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 ATTGAACATG TTGCGAGAAA GGCTAAGACA GCCCTTCAAG AGCTGTTTCC ATTAGAAGAC 960
 GGCTCTTTCA GAGTGTTCGG AAAAGCCGAG TGAATGACA TTGCTTTGG ATTGCGGTCC 1020
 AAGGATGATG AATATACCTT GCCCTGACAG AGTGGCTACA GGGGAACAT CACAGCCAAAG 1080
 75 TGTGAGTCTT CTGGGTGGCA GGTCAACAGG GAGACTGTGT TGCTCTCTCT GCTTGAAGAA 1140
 CTGAACAGAA ATTTCAATGAT GATTGTAGGC AATGCCACTG AGGCAGCTGT GTCTCTCTTC 1200
 GTGCAAAATG TTTCTGTCTAT CATTCGGCAA AACCATCAA CCAAGTGGG GAATCTGGCT 1260
 TCGGTGGTGT CGATTCTGAG CAATATTTC TCTCTGTCTC TGGCCAGCCA TTTCAGGGTG 1320
 TCCAATTCAA CAATGGAGGA TGTCTACAGT ATAGCTGACA ATATCTTAA TTCAGCCTCA 1380
 80 GTAACCAACT GGACAGCTCT ACTGGGGGAA GAAAAGTATG CCAGCTCACG GTTACTAGAG 1440
 ACATTAGAAA ACATCAGCAC TCTGTGCTCT CCGACAGCTC TTCTCTGTAA TTTTCTCGG 1500
 AAATTCTATT ACTGGAAAGG GATTCCAGTG AACAAAAGCC AACTCAAAG GGGTTACAGC 1560
 TATCAGATTA AAATGTGTCC CCAAAATACA TCTATTCCCA TCAGAGGCGG TGTGTTAATT 1620
 GGGTCAGAG AATTCCAGAG ATCCCTTCCA GAACTATTA TCAGCATGGC CTCGTGACT 1680
 CTGGGGAACA TTCTACCCGT TTCCAAAAAT GGAATGCTC AGGTCAATGG ACCTGTGATA 1740

	TCCACGGTTA	TTCAAACTA	TTCCATAAAT	GAAGTTTTCC	TATTTTTTTC	CAAGATAGAG	1800
	TCAAACCTGA	GCCAGCCTCA	TTGTGTGTTT	TGGGATTTC	GTCAATTGCA	GTGGAAACGAT	1860
	GCAGGCTGCC	ACCTAGTGAA	TGAAACTCAA	GACATCGTGA	CGTGCCAATG	TACTCACTTG	1920
5	ACCTCCTTCT	CCATATTGAT	GTCACTTTT	GTCCCTCTA	CAATCTTCCC	CGTTGTAAAA	1980
	TGGATCACCT	ATGTGGGACT	GGGTATCTCC	ATTGGAAGTC	TCATTTTATG	CCTGATCATC	2040
	GAGGCTTGT	TTTGGAAGCA	GATTAAAAA	AGCCAAACCT	CTCACACAG	TCGTATTGTC	2100
	ATGGTGAACA	TAGCCCTGTC	CCTCTTGATT	GCTGATGCT	GGTTTATTGT	TGGTGCCACA	2160
	GTGGACACCA	CGGTGAACCC	TTCTGGAGTC	TGCACAGYTG	CTGTGTTCTT	TACACACTTC	2220
10	TTCTACCTCT	CTTTGTTCTT	CTGGATGCTC	ATGCTTGGCA	TCCTGCTGGC	TTACCGGATC	2280
	ATCCTCGTGT	TCCATCACAT	GGCCAGCAT	TTGATGATGG	CTGTTGGATT	TTGCTGGGT	2340
	TATGGGTGCC	CTCTCATTAT	ATCTGTCAAT	ACCAATTGCTG	TCACGCAACC	TAGCAATACC	2400
	TACAAAGGA	AAGATGTGTG	TTGGCTTAAC	TGGTCCAATG	GAAGCAAACC	ACTCCTGGCT	2460
	TTTGTGTGCC	CTGCACTGGC	TATTGTGGCT	GTGAACCTCG	TTGTGTGCT	GCTAGTTCTC	2520
15	ACAAAGCTCT	GGAGGCCGAC	TGTTGGGGAA	AGACTGAGTC	GGGATGACAA	GGCCACCATC	2580
	ATCCCGCTGG	GGAAGAGCCT	CCTCATTCTG	ACCCCTCTGC	TAGGGCTCAC	CTGGGGCTTT	2640
	GGAATAGGAA	CAATGTGGGA	CAGCCAGAA	CTGGCTGGC	ATGTTATTTT	TGCTTTACTC	2700
	AATGCATTC	AGGGATTTTT	TATCTTATGC	TTTGGAAATC	TCTTGACAG	TAAGCTGCGA	2760
	CAACTTCTGT	TCAACAAGTT	GTCTGCCTTA	AGTTCTTGG	AGCAACAGA	AAAGCAAAAC	2820
20	TCATCAGATT	TATCTGCCAA	ACCCAAATTC	TCAAAGCCTT	TCAACCCACT	GCAAAACAAA	2880
	GGCCATTATG	CATTTTCTCA	TACTGGAGAT	TCCTCCGACA	ACATCATGCT	AACTCAGTTT	2940
	GTCTCAATG	AATAA					

A98 PROTEIN SEQUENCE

25	Gene name:	putative GPCR, Weakly similar to dJ365012.1
	Unigene number:	Hs.256897
	Protein Accession #:	none found
	Signal sequence:	1-17
	Pfam domain:	7tm_2 [561-820]
30	Transmembrane domains:	545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
	Cellular Localization:	plasma membrane

	1	11	21	31	41	51	
35	MHALLLCFSV	LNGASGLSL	QSPVEEYQL	LQVTRYDSKE	KRDLRNLFLK	LKPPLLWSHG	60
	LIRIIRAKAT	TDNCSLNGVL	QCTCEDSYTW	FPFSCLDPN	CYLHTAGALP	SCBCHLNLS	120
	QSVNFCERTK	INGTFKINER	FTNDLLNSSS	AIYSKYANGI	EIQLKKAVER	IQGFESVQVT	180
	QFRNGSIVAG	YEVVGSSSAS	ELLSAIEHVA	EKAKTALHLK	FPLEDGSFRV	FGKAQCNDIV	240
40	PGFGSKODEY	TLPCSSGYRG	NITAKCESSG	NQVIRETCVL	SLLEELNKNF	SMIVGNATEA	300
	AVSSFVQNLS	VRIQNPSTT	VGNLASVVIS	LSNISLSLSL	SHFRVSNSTM	EDVISIADNI	360
	LNSASVTNWT	VLLREKEYAS	SRLLETLENI	STLVPPTALP	LNFSRKFIDW	KGIPVNKSQL	420
	KRGYSYQIKM	CQNTSIPIR	GRVLIGSDQF	QRSLPETIIS	MASLTGLNIL	PVSKIGNAUV	480
	NGFVISTVIO	NYSINEVFLF	FSKIESNLSQ	PHCVPWDFSH	LQWMDAGCHL	VNETQDIVTC	540
45	QCTHLTFSFI	LMSPFVPTSI	FPVVKWITYV	GLGISIGSLI	LCLILEALFW	KQIKKSQTS	600
	TERICMNVIA	LSLLIADVWF	IVGATVDITV	NPSGVCTAAV	FFTHFFYLSL	FFWMLMLGIL	660
	LAYRIILVFH	HMAQLHMAV	GFCLGYGCPL	IISVITIAVT	QPSNTYKRED	VCLNWSNGS	720
	KPLLAFFVPA	LAIVAVNFVV	VLLVLTKLWR	PTVGERLSRD	DKATIIRVGK	SLLLILTPLLG	780
	LWGFPGIGTI	VDSQNLAMHV	IFALLNAFQV	RTVTITYCIV	K		

A99 DNA SEQUENCE

	Gene name:	putative G-protein coupled receptor
	Unigene number:	Hs.16085
55	Probeset Accession #:	F07953
	Nucleic Acid Accession #:	NM_016334
	Coding sequence:	104-1471 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
60	AGCACCTGGG	AAAAGGCAGA	CGGTGTGAGG	GGGCCTGTGG	CCCCAGCGTG	CTGTGGCCTC	60
	GGGAGTGGG	AAGTGGAGGC	AGGAGCCTTC	CTTACACTTC	GCCATGAGTT	TCCTGATCGA	120
	CTCCAGCATC	ATGATTACCT	CCCAATACT	ATTTTGTGGA	TTTGGGTGGC	TTTTCTTCAT	180
65	GGGCAATTG	TTTAAAGACT	ATGAGATACG	TCAGTATGTT	GTACAGGTGA	TCTTCTCCGT	240
	GACGTTTGCA	TTTTCTTGCA	CCATGTTTGA	GCTCATCATC	TTTGAATCT	TAGGAGTATT	300
	GAATAGCAGC	TCCCGTTATT	TTCACTGGAA	AATGAACCTG	TGCGTAATTC	TGCTGATCCT	360
	GGTTTTCATG	GTGCCTTTTT	ACATTGGCTA	TTTATTGTGT	AGCAATATCC	GACTACTGCA	420
	TAAACAACGA	CTGCTTTTTT	CCTGTCTCTT	ATGGCTGACC	TTTATGTATT	TCTTCTGGAA	480
70	ACTAGGAGAT	CCCTTTCCCA	TTCTCAGCCC	AAAACATGGG	ATCTTATCCA	TAGAACAGCT	540
	CATCAGCCGG	GTGTGTGTGA	TTGGAGTGAC	TCTCATGGCT	CTTCTTCTCG	GAITTTGGTG	600
	TGTCAACTGC	CCATACACTT	ACATGTCTTA	CTTCTCTCAG	AATGTGACTG	ACACAGATAT	660
	TCTAGCCCTG	GAAAGGCGAC	TGCTGCRAAC	CATGGATATG	ATCATAAGCA	AAAAGAAAAG	720
	GATGGCAATG	CAAGGAGGAA	CAATGTTCCA	GAAGGGGGAA	GTGCATAACA	AACCATCAGG	780
75	TTTCTGGGGA	ATGATAAAAA	GTGTTACCAC	TTCAAGCATCA	GGAAGTGAAA	ATCTTACTCT	840
	TATTCAACAG	GAAGTGGATG	CTTTGGGAAGA	ATTAAGCAGG	CAGCTTTTTT	TGGAACACGC	900
	TGATCTATAT	GCTACCAAGG	AGAGAATAGA	ATACTCCAAA	ACCTTCAAGG	GGAATATATT	960
	TAATTTTCTT	GGTTACTTTT	TCTCTATTTA	CTGTGTTTGG	AAAATTTTCA	TGGCTACCAT	1020
	CAATATTGTT	TTTGATCGAG	TTGGGAAAAC	GGATCCTGTC	ACAAGAGGCA	TTGAGATCAC	1080
80	TGTGAATTAT	CTGGGAATCC	AATTTGATGT	GAAGTTTGG	TCCCAACACA	TTTCTTCAT	1140
	TCTTGTGTGA	ATAATCATCG	TCACATCCAT	CAGAGGATG	CTGACTCACT	TTACCAAGTT	1200
	CTTTTATGCC	ATCTCTAGCA	GTAAGTCCCTC	CAATGTCAAT	GTCCCTGCTAT	TAGCAGATAT	1260
	AATGGGCATG	TACTTTGTCT	CCTCTGTGCT	GCTGATCCGA	ATGAGTATGC	CTTTAGAATA	1320
	CCGACCATA	ATCACTGAAG	TCCTTGGAGA	ACTGCAGTTC	AACCTCTATC	ACCGTTGGTT	1380
	TGATGTGATC	TTCTGTGTCA	GCGCTCTCTC	TAGCATACTC	TTCCCTTATT	TGGCTCACA	1440

	ACAGGCACCA	GAGAAGCAAA	TGGCACCTTG	AACCTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAATTTAGA	TATAAGAGGG	GGGAAAAATG	GAACAGGGGC	CTGACATTTT	1560
	ATAAACAAAC	AAAATGCTAT	GGTAGCATTT	TTACCTTCA	TAGCATACTC	CTTCCCCCTC	1620
5	AGGTGATACT	ATGACCATGA	GTAGCATCAG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGGAGAGGAG	1740
	CCAAGAAACT	AAAGGTGAAA	AATACACTGG	AACCTCTGGG	CAAGACATGT	CTATGGTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTAA	GGTTCACATG	GAAAAGGTTA	TAGCTTTGCC	1860
	TTGAGATTGA	CTCATTAATA	TCAGAGACTG	T			
10	<u>A100 Protein sequence</u>						
	Gene name:		putative G-protein coupled receptor				
	Unigene number:		Hs.16085				
	Protein Accession #:		NP_057418.1				
	Signal sequence:		none found				
15	Transmembrane domains:		5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446				
	Cellular Localization:		plasma membrane				
	1	11	21	31	41	51	
20	MSFLIDSSIM	ITSQILFFGF	GWLFFMRQLP	KDYEIRQYVV	QVIFSVTFAP	SCTMFELIIF	60
	EILGVNLSSS	RYFHWKMLNC	VILLILVFMV	PFYIGYFIVS	NIRLLHKQRL	LFSCLLMLTF	120
	MYFFWKLGGP	FPILSPKHGI	LSIEQLISRV	GVIGVTLMAL	LSGPGAVNCP	YTYMSYFLRN	180
	VTDIDILALE	RRLQLTMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGGFWM	IKSVTTSASG	240
25	SENLTILIQE	VDALIELSRQ	LPLETADLYA	TKERIEYSKT	FKGKYFNPLG	YFFSIYCVWK	300
	IFMATINIVF	DRVGKIDPVT	RGIEITVNYL	GIQPDVKFWS	QHISFILVGI	IIVTSIRGLL	360
	ITLTKFYXAI	SSSKSSNVIV	LLLAQIMGMV	FVSSVLLIRM	SMPLEBYRTII	TEVLGELQFN	420
	FYHRWFDVIF	LVSALSILF	LYLAHKQAPE	KQMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name:		ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]				
	Unigene number:		Hs.19322				
	Probeset Accession #:		AA088458				
	Nucleic Acid Accession #:		AA088458				
35	Coding sequence:		862-1995 (underlined sequences correspond to start and stop codons)				
	1	11	21	31	41	51	
40	GCCCTTGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAAAG	GAGGTGCTGC	TGCAGGGTTT	GGAGATGATG	120
	CGCGGGGGCC	CGGACTGGTA	CCAGCAGCAG	CTGCAACGAG	TGCAGGAGCG	CCAGCGCCGC	180
	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTGCAG	GGAGCCCCCG	CCCATCTGGG	240
	CGGCTACTGC	CCAAGGTACA	AGAGGTGACC	CGGTGCCTGG	GGGAGCTGCT	GGCTGCAGCC	300
	TGTGCCAGCC	GGGCCCTGCC	CCCGTCTCTC	TCCGGGCCCC	CCTGCCCTGC	CCTGACGTCC	360
45	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGGACTC	420
	CTCACCCAGG	AGGTGACCGA	GAAGAGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAAAGTCG	480
	GCCTCTATTA	AGCAGCTGTT	TGAGGCCCGC	GCCTGAGCCC	AGCAGGACGG	GGGAGCTCTG	540
	GATTCCACCT	TCATCTAGTC	CTTGTGGGCC	GCCTGGGGCC	CCAGGGCCAG	CCTGGCACTC	600
	AGCCCTTCGA	GGGTGGGGCC	CCCATCGCAC	CCACCTCTCT	TGGCTGGAGA	CCCCGGGCAG	660
50	GCCACAGCAC	AGTCCCGGAG	TGGGGGCCTT	CCTGCGCCCC	TTGCCAGATG	GGCTCCCCAG	720
	GCCTGCCCCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTTTGGGCTC	CTGGTTGCTG	780
	ACATGGCTCT	GGGGCTCTCT	TGAGTCCGCA	TAGTCCGCGC	CTACTACTGG	CCGCTGTCTG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCCCGG	TTTCCAGCGG	TGCCGGCCCTG	900
	GGTCCCATCT	TCAGGGAAAG	GCATGCCCCA	CGCCAGGCTG	CACCTTCCAA	AACGGGCAGC	960
55	AGAGGGCGCT	AGGCGGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TGGGACGGAC	GGAAGTAGAT	GGAGGGGGTG	GGGAGCGGCT	1080
	GTAAGCGGGG	GGTGGCTGCC	TGGCTGGGGA	GCCTCAGGGA	TAGCGGTGGG	ACTTCAGGTT	1140
	CTGGCCAAAG	CTGAGGGACC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GGGAGAGCTT	1200
	GGCCTGCATC	TGCCCTCCAC	AGACCTCGGG	GTGATGGCCT	TCCCTCTCTT	GGCCGGGAGG	1260
60	TTGCCCCAGG	TTGAGTCCCA	CACAACATCC	TGTGAGCCTG	GCTCCCCAGG	AGGGCCCCCA	1320
	GACAGCTCCC	AGGCACTGCA	TAGGCAAGGC	CTGTTTCCCC	CGACTCAGGA	TTTCCAAGGC	1380
	CTGGGGTCCCT	GCTCACCCCC	CTTTGCTCTC	ACGCCAGGCC	TGTCCCCAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTCCCTCAG	CCCCTGCCCA	GGCCCACTCC	CGCTGGTGCT	1560
65	GGAGTAGGCA	CTGGTGGGGG	GGCCCTGCTC	AGCCCAACCT	GGAGGGTCCC	AGTGTACACA	1620
	GAACCAAGGG	CACGGCAACA	GCATCGATGG	GTCTGTCAGC	CCAGGGCCCC	CGATGCGGGG	1680
	TCAGTGTGTG	TGGGGCGCAG	GGCCTCCGAT	GCGGGGTCAG	TGCGTGGGGG	GGCAGGGGCC	1740
	CCCGATGCGG	GGTCAGTGCG	TGGGGGGCGC	AGGGCCCCCT	CGTGTCCAGG	GCACTTTGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGTCTCAGAG	GAGGGGCCCT	GGCAGGCAGC	GTGGCACTC	1860
70	CCTTCCGAG	CCCAGTCCCA	TGCTAACCTG	CCCACAGCAA	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCACCT	GGTCTGACGG	GGTGTCCGAG	GACAGGCCCA	AGTCAGCCCA	GCATGCAGCT	1980
	GCCCTCCTAC	CCTGAAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCTTGG	2040
	ACCTCCTGGG	CAGGAAAGGG	TGCAGGTCTT	GAGGGCCTGT	GCCCCACAGC	CCCAGCACCC	2100
	AGGTGGACTC	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGCCC	CCCGTCAGCA	2160
75	GGCTGGGGTC	TGCCCAACAG	GGCCTCCCCA	CGTCTGCCTT	TGAGGGTGCC	TGCCATGCCC	2220
	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGGAGACC	GCCCCATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCTCCG	GAAAACTGAC	CTTTAGCCCT	TGGTGTTCGG	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAGTGG	CCCTGGAGAC	2460
80	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCTTG	CCTGGAGCCT	GCCCTAGGAC	GCTGGGGCGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CTCGGCTCT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAAGT	ACATACAGT	2640
	GCGTGACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
	CAGAAGTGTC	CCAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTTGTGTTG	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CCGGGCGTGG	TGTTTCAGCG	2820

CTGGAATCCC AGCACTTGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACAAAAAA AAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAATT ATCAGAGAGA ATATAAAGTA ACAGTGTTTT ATATATCTAA 3060
 5 AGAATAAAA GAGATTTCTG GAAACATGAA AAAAAA

A102 DNA SEQUENCE

10 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

15
 1 | 11 | 21 | 31 | 41 | 51 |
 | | | | | |
 ACCGGGCACC GGACGGCTCG GGTACTTTCT TTTCTTAATTA GGTTCATGCC GTGTGAGCCA 60
 GGAAGGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGC CTACTATCTC TTCGTGGTG 120
 20 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCCGGATGTC 180
 AGAGGTCTCTG AAATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTGGG CCTTGATGAT TTGAAAATAA GTCTCTGTGC ACCAGATGCA 300
 GATGCTGTGG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTCCTC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 25 TCAGGGAGAT ACAGATGTCT CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT ACGCAATGTT TGCCGTGTGCC CAACCTGGGT TCCCAAGCTA TGTGAGTTCA 660
 30 GATAAGCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCCCTCTG GCCACGTGCT TACCTTGACG TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960
 35 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCGCCAAGT CATGGACCAT CCAGGTGGGT 1020
 CTAGTTTCCC TGTGTGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCCTGGCCA 1140
 CTCACGTTCA ATGAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAAAG TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGACGCC 1260
 40 TCCCTGTGTC TGAACCAAGC GGCCGTCCCT TTGATTTCCA ACAAGATCTG CAACCAAGG 1320
 GAGGTGTACG GTGGCATCAT CTCGCCCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGACAGCTG GCCAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG GAGGACCCAG CTTTGGCATC GCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCAAGAGC AGATGGAGAG AGACCTAAAA 1560
 45 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCCCT AGGTGATGAA GACAGCCGA 1620
 TCCTCCCTCG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTCTG GAGCTCTGAG 1680
 TTCGGGCACT AGTAGCAGGC CCGAAAGAGG CACCTTCCCA TCTGATTTCA GCACAACCTT 1740
 CAAGCTGCTT TTTGTTTCTT GTTTTCTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 AGTGCACTGG CGAAATCCCT GCTCACTGCA GCCTCCGCTT CCCTGTTTCA AGCGATTCTC 1860
 50 TTGCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCC GCAACACACC CAACTAATTT 1920
 TTGTATTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAATGA TGTGCTGCTC TCAGCCTCCC ACAGTGTGG GATTACAGGC ATGGGCCACC 2040
 ACGCTAGTCC TCAGCTCCTT TTTGATCTT CACTAAGAAC AAAAGAAGCA GCACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGCT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
 55 ACGAGATAAG CAGTTATGTG ACCTCAAGTG CAAGGCCACC AACAGCCACT CAGAAAAGAC 2220
 GCACCAAGCC CTTTCTTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2280
 CCAAAACCCAC CTTTCTTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCTCAT TTTCATGATT TCTTGTAGC ATTTGGTGTG TGACGTATTA 2400
 60 TTGTCTTTTG ATTCCAATA ATATGTTTCC TTCCCTCAAA AAAAAAAAAA AAAAAAAAAA 2460
 AAAAAAAAAA

A103 Protein sequence:

65 Gene name: TMPRSS3a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 70 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

75 1 | 11 | 21 | 31 | 41 | 51 |
 | | | | | |
 MGENDPPAVE APFSFRSLFG LDDLKISPA PDADAVAAQI LSLPLKFPF IIVIGITALI 60
 LALAIGLGH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GQNAVLQVF 120
 TAASWKTMCs DDWKHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREFPV SIDHLLPDDK 180
 VTALHHSVYV REGCASGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPV QASLQFQGYH 240
 80 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSSE NFPDGVKCVT SGWGATEDGA GDASPLVHNA 360
 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVSDCQGD SGGPLVCQER RLWKLVGATS 420
 FGIGCAEVNK PGVYTRVTSF LDWIEQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (H0T7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

10 ATGCACACCG TGGCTACGTC CGGACCCAAC GCGTCCTGGG GGGCACCGGC CAACGCCCTCC 60

GGCTGCCCGG GCTGTGGGCG CAACGCCCTCG GACGGCCAG TCCTTTCGCC GCGGGCCGTG 120

GACGCTGGC TCGTGGCGCT CTCTCTCGCG GCGCTGATGC TGCTGGGCGT GGTGGGGAAC 180

TCGCTGGTCA TCTACGTCAT CTGCGGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240

ATGCCAACC TGGCGGCCAC GGAOGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300

15 CTGCTGTACC CGCTGCCCGG CTGGGTGCTG GCGACTTCA TGTGCAAGTT CGTCAACTAC 360

ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCATGAG TGTGGACCGC 420

TGCTACGTGA CGGTGTTCCC GTTGGCGGCC CTGCACCGCC GCACGCCCGC CTTGGCGCTG 480

GCTGTGAGCC TCAGCATCTG GGTAGGCTCT GCGCGGTGT CTGCGCGGT GCTCGCCCTG 540

20 CACGCGCTGT CACCGGGGCC GCGCGCTTAC TGCAGTGAGG CCTTCCCGAG CCGCGCCCTG 600

GAGCGCGCTT TCGCACTGTA CAACCTGCTG GCGCTGTACC TGCTGCCGCT GCTCGCCACC 660

TGCGCCTGCT ATGCGGGCAT GCTGCGCCAC CTGGGCCGGG TCGCCGTGCG CCGCGCGCCC 720

GCGGATAGCG CCCTGCAAGG GCAAGTGTCT GCAGAGCGCG CAGGCGCCGT GCGGGCCAAG 780

25 GTCTCGCGCC TGGTGGCGGC CGTGGTCTCT CTCTTCGCGG CTGCTGGGG CCCCATCCAG 840

CTGTTCCTGG TGCTGCAGGC GCTGGGCCCC GCGGGCTCCT GGCACCCAG CAGCTACGCC 900

GCTTACGCGC TTAAGACCTG GGCTCACTGC ATGTCTTACA GCAACTCCGC GCTGAACCCG 960

CTGCTCTACG CCTTCTCTGG CTGCACTTTC CGACAGGCCT TCGCCCGGT CTGCCCCCTG 1020

GCGCGCGGCC CCGCCCGCGC CCGCCCGCGC CCGGACCCCT CGGACCCCGC AGCCCCACAC 1080

30 GCGGAGCTGC ACCGCTTGG GTCCACCCG GCCCGGCCA GGGCGCAGAA GCCAGGAGC 1140

AGTGGGCTGG CCGCGCGCGG GCTGTGCGTC CTGGGGGAGG ACAACGCCCC TCTCTGA

A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (H0T7T175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

1 11 21 31 41 51

45 MHTVATSGPN ASWGAPANAS GCPGCGANAS DGPVPSRAV DAWLVPLPFA ALMLLGLVGN 60

SLVIYVICRH KPMRTVTNFI IANLAATDVT FLLCCVPFTA LLYPLPGWVL GDFMCKFVNY 120

IQQVSUQATC ATLTAHSVDR WYVTVFPLRA LHRRTPLRAL AVSLSIWVGS AAVSAPVLAL 180

HRLSPGPRAY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240

ADSLAQGVVL AERAGAVRAK VSRLVAHVVL LFAACWGIQ LFLVLQALGP AGSMHPRSYA 300

50 AYALKTNWAC MSYSNSALNP LLYAFLGSHF RQAFRRVCPG APRRRPRRRR PGPSDPAAPH 360

AEHLRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

A106 DNA SEQUENCE

Gene name:

integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM_002214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

60 CCCAGAGCGG CCTCCCCCTG TTGCTGGCAT CCCGAGCTTC CTCCTTTCGC AGCCAGGAGC 60

CTGCGACTTC GTCTTTGCCG GCTGCTCCCG AGACGGGGCT GCAGAGCTGC AACTAATGGT 120

GTTCGGCTCC CTGCCCCACT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180

65 TCCCTCGAG CTGCGCGCGG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240

TAGGTTGGTT TCCCCCCAG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300

CTAAGCTGAT TTATGAGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAAG CTCCTTTCTT 360

TGTCGGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCAGTCCGC GCGGGCCCT 420

70 TGGCGTGA AGGAGGTGCT TCTCGCGAG ACCGCGGGAC CCGCGTGC GAGCCGGGAG 480

GGCGTAGGG GCCCTGAGAT GCGAGCGGT GCCCGGGCCC GCTTACCTGC ACCGCTTGCT 540

CCGAGCCGCG GGTCCGCCCT GCTAGGCGCT CGGAAAAGT CCTAGCGACA CTCGCCCGCG 600

GGCCCCGAGG TCGCCCCGGA GGCGAGCCCC CGTCCGGAA GGCAGCCAGG CCGCGGGCGC 660

GGGCGCGGCT GTTTTGCAAT ATGTGCGGCT CCGCCCTGSC TTTTTTACC GCTGCATTGT 720

75 TCTGCTGCA AAACGACCGG CGAGGTCCCG CTCTTCTCT CTGGGAGCG TGGGTGTTT 780

CACCTGTCTT TGAAGTGGG CAAGGTGAAG ACAATAGATG TGCACTTCA AATGACGAT 840

CCTGTGCCAG GTGCCCTGCG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTC 900

TTTCAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTT CAATTAAATA AGCAAAGCT 960

80 GCTCAGTTGA TTCAATAGAA TACCATCTG TGCACTTAT AATACCACT GAAATGAAA 1020

TAAATACCA GGTGACCACT CTATCCAGCT GGTCCAGGA CCGCAAGCTA 1080

ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCTGT GGATCTTTAT TATCTTGTG 1140

ATGCTCAGC ATCAAGTGC AATAATATAG AAAAATTAAT TTCCGTTGGA AACGATTAT 1200

CTAGAAAAAT GGCATTTTTC TCCGTGACT TTCGTTTGG ATTTGGCTCA TACGTTGATA 1260

AAACAGTTTC ACCATACATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCACTGACT 1320

ACAAATTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGCTTTG ACAGAGAACA 1380

TCACAGATT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACAG 1440

5	AAGGAGGTTT	TGACGCCATG	CTTCAGGCAG	CTGTCTGTGA	AAGTCATATC	GGATGGCGAA	1500
	AAGAGGCTAA	AAGATTGCTG	CTGGTGATGA	CAGATCAGAC	GTCTCATCTC	GCTCTTGATA	1560
	GCAAAATGGC	AGGCATAGTG	GTGCCCAATG	ACGGAAACTG	TCATCTGAAA	AACAACGCTCT	1620
	ACGTCAAATC	GACCAACCATG	GAACACCCCT	CACTAGGCCA	ACTTTCAGAG	AAATTAATAG	1680
	ACAACAACAT	TAATGTCTATC	TTTGCACTTC	AAGGAAAACA	ATTTCATTGG	TATAAGGATC	1740
	TTCTACCCCT	CTTGCCAGGC	ACCATTGCTG	GTGAAATAGA	ATCAAAGGCT	GCAAACTCTCA	1800
	ATAAATTTGGT	AGTGGAAAGCC	TATCAGAAGC	TCATTTCAGA	AGTGAAAGTT	CAGGTGGAAA	1860
	ACCAGGTACA	AGGCATCTAT	TTTAACATTA	CCGCCATCTG	TCCAGATGGG	TCCAGAAAGC	1920
10	CAGGCATGGA	AGGATGCAGA	AACGTGACGA	GCAATGATGA	AGTTCTTTTC	AATGTAAACAG	1980
	TTACAATGAA	AAATATGTAT	GTCAACAGGAG	GAAAAACTA	TGCAATAATC	AAACCTATTG	2040
	GTTTTAATGA	AACCGCTAAA	ATTCATATAC	ACAGAAACTG	CAGCTGTCTG	TGTGAGGACA	2100
	ACAGAGGACC	TAAAGGAAAG	TGTGTAGATG	AAACTTTTCT	AGATTCCAAG	TGTTTCCAGT	2160
	GTGATGAGAA	TAAATGTCTAT	TTTGATGAAG	ATCAGTTTTC	TTCTGAGAGT	TGCAAGTCAAC	2220
15	ACAAGGATCA	GCTGTGTTGC	AGTGGTCTGAG	GAGTTTGTGT	TTGTGGGAAA	TGTTTCTGTC	2280
	ACAAAATTAA	GCTTGAAAAA	GTGTATGGAA	AATACTGTGA	AAAGGATGAC	TTTTCTTGTC	2340
	CATATCACC	TGGAATCTG	TGTGCTGGGC	ATGGAGAGTG	TGAAGCAGGC	AGATGCCAAT	2400
	GCTTCAGTGG	CTGGGAAGGT	GATCGATGCC	AGTGCCCTTC	AGCAGCAGCC	CAGCACTGTG	2460
	TCAATTCAAA	GGGCCAAGTG	TGCAGTGGAA	GAGGCACGTG	TGTGTGTGGA	AGGTGTGAGT	2520
20	GCACCGATCC	CAGGAGCATC	GGCCGCTTCT	GTGAACACTG	CCCCACCTGT	TATACAGCCT	2580
	GCAAGGAAAA	CTGGAATTGT	ATGCAATGCC	TTCACTCTCA	CAATTTGTCT	CAGGCTATAC	2640
	TTGATCAGTG	CAAAACCTCA	TGTGCTCTCA	TGGAACAACA	GCATTATGTC	GACCAAACTT	2700
	CAGAATGTTT	CTCCAGCCCA	AGCTACTTGA	GAATATTTT	CATCATTTTC	ATAGTTACAT	2760
	TCTTGATTGG	GTGCTTAAA	GTCTCTGATCA	TTAGACAGGT	GATACTACAA	TGGAATAGTA	2820
25	ATAAATTTGA	GGTCTCATCA	GATTACAGAG	TGTCAGCCTC	AAAAAAGGAT	AAGTTGATTC	2880
	TGCAAAAGTG	TTGCACAAGA	GCAGTCACTC	ACCGACGTGA	GAAGCCTGAA	GAATAAAAA	2940
	TGGATATCAG	CAAAATTAAT	GCTCATGAAA	CTTTCAGGTG	CAACTTCTAA	AAAAAGATTT	3000
	TTAAACACTT	AATGGGAAAC	TGGAATTGTT	AATAATTGCT	CCTAAAGATT	ATAATTTTAA	3060
	AAGTCACAGG	AGGAGACAAA	TTGCTCACGG	TCATGCCAGT	TGCTGTTTGT	ACACTCGAAC	3120
30	GAAGACTGAC	AAGTATCCTC	ATCATGATGT	GACTCACATA	GCTGCTGACT	TTTTCAGAGA	3180
	AAAATGTGTC	TTACTACTGT	TTGAGACTAG	TGTGTTGTGA	GCATTTTACT	GTAATATATA	3240
	ACTTATTTAG	ATCAGCATAG	AATGTAGATC	CTCTGAAGAG	CACTGATTAC	ACTTTACAGG	3300
	TACCTGTTAT	CCCTACGCTT	CCCAGAGAGA	ACAATGCTGT	GAGAGAGTTT	AGCATTGTGT	3360
	CATACAAAGG	GTACAGTAAT	CCCTGCACTG	GACATGTGAG	GAATAAATA	ATCTGGCAAG	3420
35	TATATTCTAA	GGTTGCCAAA	CACCTCAACA	GTGGTGGTT	GAATAGACAA	GAACAGCTAG	3480
	ATGAATAAAT	GATTGCTGTT	TCACCTCTTC	AAGAGGTGAA	CAGATACAAC	CTTAATCTTA	3540
	AAAGATTATT	GCTTTTAAAA	GTGTGTAGTT	TTATGCATGT	GTGTTTATGG	TTTGCTTATT	3600
	TTTGCAAGAT	GGATACTAAT	TCCAGCATTC	TCTCCTCTTT	GCCTTTATGT	TTTGTTTTCT	3660
	TTTTTACAGG	ATAAGTTTAT	GTATGTCAAC	GATGACTGGA	TTAATTAAGT	GCTAAGTTAC	3720
40	TACTGCCATA	AAAACTAAT	AATACAATGT	CACCTTATCA	GAATACTAGT	TTTAAAGCT	3780
	GAATGTTAA						

A107 Protein sequence:

45	Gene name:	Integrin, beta 8
	Unigene number:	Hs.52620
	Probeset Accession #:	AA479726
	Protein Accession #:	NP_002205.1
	Signal sequence:	1-39
50	Transmembrane domains:	682-704
	EGF domain:	552-584
	INB domain:	54-469
	Cellular Localization:	plasma membrane

55	1	11	21	31	41	51	
	MOGSALAFFT	AAFVCLQNDR	RGPSFLWAA	WVPSLVLGIG	QGEDNRCASS	NAASCARCLA	60
60	LGPECGWCVQ	EDFISGGSR	ERCDIVSNLI	SKGCSVDSIE	YPSVHVIIPT	ENBINTQVTP	120
	GEVSIQLRPG	AEANFMLKVH	PLKKYFVDLY	YLVDSASMH	NNIEKINSVG	NDLSRKMAFF	180
	SRDFRLGFGS	YVDKTVSPYI	SIHPERIHNQ	CSQDYNLDCMP	PHGYIHVLSL	TENITEPEKA	240
	VHRQKISGNI	DTPEGGFDAM	LQAAVCESHI	GWRKEAKRLI	LVMTDQTSHL	ALDSKLAGIV	300
	VPNDGNCHLK	NNVYVKSTTM	BHPSLGQLSE	KLIDNNINVI	FAVQKGQFHW	YKDLLPLLP	360
65	TIAGEIESKA	ANLNNLVVEA	YQKLISEVKV	QVENQVQGIY	FNITAIKPDG	SRKPGMEGCR	420
	NVTSNDEVLF	NVTVTMKKCD	VTGGKQYAI	KPIGFNETAK	IIHNRNCSCQ	CEDNRGPKGK	480
	CVDETFLDSK	CFQCDENKCH	FDEDQPSSES	CKSHKQDPVC	SGRGVVCVGK	CSCHKIKLQK	540
	VYGYKCEKDD	FSCPYYHGNL	CAGHGECEAG	RQCFSGWEG	DRQCPSAAA	QRCVNSKGQV	600
	CSGRGTCVCG	RCECTDPRSI	GRFCEHCPTC	YTACKENWNC	MQCLHPHNLS	QAILDQCKTS	660
70	CALMEQQHYV	DQTECFSSP	SYLRIFPIIF	IVTFLIGLLK	VLIIRQVILQ	WNSNKKIKSSS	720
	DYRVASASKD	KLILQSVCTR	AVTYRREKPE	EIKMDISKLN	AHETPRCNF		

A108 DNA sequence

75	Gene name:	ESTs
	Unigene number:	Hs.128899
	Probeset Accession #:	AA983251
	Nucleic Acid Accession #:	AA983251
	Coding sequence:	1-1749 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ATGCTGTCTG	GCTTCTTGAT	GAGTCCCACT	ACCCAGCACA	GAGCACAGTA	CACTCCCGGA	60
	GGAAAGAAAC	TTCCGTGGGA	GGCTTCCATC	GGTGGGCACA	CCTCCCGAGG	GCGAGGCAGC	120
	GACCGGAGGA	GGGAGAGCCG	GCCGGAGGCT	GCCGGGCTCC	TGTGGGACCG	CGCTGCAGCC	180
	GGGGAGGCGG	AGAAGGGGAA	CCGGGGGAG	CCGGCCGCTC	GGATCCGCGC	CCAGCAGCAG	240

5	CGCGGCGCCG	CGCCAGCTGG	GCAGGCTCCC	GGGACTGCGG	CTGGGGGCGC	GCAGGACCCCT	300
	CGCCTGCGTC	CTGGACGTTT	CCGGGGGAGG	GTCCGGTTTC	CAGTGAAACC	TCCAGAGGCT	360
	TCCGGACGAC	AGCCCCGGGG	GCCTTCTGAC	TGCATCCCGA	GATTTCATCC	AGCGAGTGCA	420
	ACTCATAGG	CAGTCCCTAA	GGGACCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCCTGGAC	CTAGGGCCCC	CGCTCGTCCG	CTCCTGGGCG	TGCGGCGAGA	GGGGAGTGGC	540
	CCGCGCGGAA	AGGCGCGCGG	GACAGTCAGT	GACGAGGCCG	GGGGTCCGCG	GGGGCCAAGA	600
	CTTCTCGGAG	ACCGTCTCTG	GCTCTCTGGA	GACGCGCTGT	CCGCGCCCG	GGTGGTGCCA	660
	TGTTGGGCGC	TGCGCGCTCG	TCCGTCTCTT	CATCTTGGAA	CGCCGCTTCG	CTCTGCAGC	720
10	TGCTCTGGG	TGGCTCTGCT	GCGGCGGGGG	CGAGGGCCCA	GCGCGAGAGT	CTGCCACGGC	780
	TGGCTGGAGC	CGCAGGGGCT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTGGACGGC	840
	GGGACGCGCA	CCATCTGCTG	CGCGAGCTGC	GCGTTGCGCT	ACTGCTGCTC	CAGCGCCGAG	900
	GCGCGCTTGG	ACCAGGGGCG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCCTGGC	960
	CGGGCGGACA	AAGACGGGCC	CCGACGGCTC	GGCAGGGGCT	CATGTCTTAG	GGGTACCCAA	1020
15	GGAGACGGCG	AGGGTGGGCC	CCACCCGCTG	AGGGCCTGGC	AGCGGTGCTC	CCCTGAAGGC	1080
	TCCCGGAAAG	GAAAGGAGCT	CCTCAGGGCT	TCCCGGGGCG	TGCTGCCCGC	TGCCAGAGCG	1140
	CGCGGATTCC	CATCTTCTCC	ACGCGCGGCG	CCCTCTCCCG	TGCAGCGGCG	CGCCTTGCCC	1200
	ATCTACGTGC	CGTTCCTCAT	TGTTGGCTCC	TGTTTGTGCG	CCTTTATCAT	CTTGGGGTCC	1260
	CTGTTGGCAG	CTGTTGCTCG	CAGATGTCTC	CGGCCTAAGC	AGGATCCCCA	GCAGAGCCGA	1320
20	GCCCCAGGGG	GTAACCGCTT	GATGGAGACC	ATCCCCATGA	TCCCCAGTGC	CAGCACCTCC	1380
	CGGGGTGCT	CCTCAGCCCA	GTCCAGCACA	GCTGCCAGTT	CCAGCTCCAG	CGCCAACTCC	1440
	GGGGCCCGGG	CGCCCCCAAC	AAGGTACAG	ACCAACTGTT	GCTTGGCCGA	AGGGACCATG	1500
	AACAACGTGT	ATGTCAACAT	GCCCCAGAA	TTCTCTGTGC	TGAACGTGCA	GCAGGCCACC	1560
	CAGATTGTGC	CACATCAAGG	GCAGTATCTG	CATCCCCCAT	ACGTGGGGTA	CACGGTGCAG	1620
25	CACGACTCTG	TGCCCATGAC	AGCTGTGCCA	CTTTTATAGG	ACGGCTGCTC	GCCTGGCTAC	1680
	AGGAGATTTC	AGTCCCGCTT	CCCTCACACC	AACAGTGAAC	AGAAGATGTA	CCCAGCGGTG	1740
	ACTGTATAAC	CSAGAGTCAC	TGTTGGGTTT	CTTTACTGAA	GGGAGACGAA	GGCAGGGGTG	1800
	GATTCTCGAG	GTGGAACTCC	GCACATGTGC	GTGGTATTTA	TGGCAGGATT	CCTTTGGATG	1860
	GCTTCAATTG	CCCCCAGACT	GTATGAAAA	ATCTCCGAAT	TAGCATTTCT	GGATATGTTT	1920
30	CATCCAGGGT	ATCACTGATT	TATGATGGAA	AACCGGCTTC	AGCTGGAGAT	GACTGTGATG	1980
	TGCTGTATGG	GTGTATAACA	AATGCTTGAG	TCCGAAGTGC	CCITGAGATA	TGGTTGACGA	2040
	AAGAATTTTA	TAAACTGATA	AATTAAGGAT	TTTTATTATG	TGTTATTAT	TATTTCTTTT	2100
	TGTTGTGTA	CTGCACAGGA	TCAAAATGCC	TGTTATCTCC	CTTTTACTCG	GACTTTTTTT	2160
	TTTTTTTTTT	TTTTTTTTTA	TCAGACAGGG	TCTTGCTCTG	TGCCCCAGGC	TGGAGTGCAG	2220
35	TGTTGCGATC	TCGGCTCACT	GCAACTTCAG	CCTCCTGGAT	TCAGGCCAACA	CTCCTGCCTC	2280
	AGCCTCCAC	TGGGCTGGGA	TTACAGGTGC	CTGCCCCCAT	GGCTAATTTT	TGTTATTTTT	2340
	TGTAGAGATG	GGGTTTCAAC	ATGTTGGCTG	GGCTGGTCTC	ACTCTCCTGA	CCTCAAGCAA	2400
	TCGCTCTGTC	TCAGCCTCCC	AAAGTGTCTG	GATTACAGGC	GTGAGCCACC	GCCCCCAGCC	2460
	TGAGCCTTTT	TTTTTTTCTA	ATGCATCCAA	GGTTAAGGGG	AAGACGCAAA	TAACAGGACT	2520
40	ATTCTAAAG	GAAACCTGTT	TGAACCTCTG	GAGATCAGTC	ATCAGTCTCA	GTATTCACA	2580
	GGCACACCTT	AATTTCAATG	TAAAAAGATA	TATATATTTT	GTCTATTTT	GTGCTTTTGG	2640
	GGGCTTATTT	TGTGCTTTTT	TACCTTATGT	AGAGATCTTA	TTACAAAGTG	ATTTTCTACA	2700
	TTAAAAAGAG	ACTGAATATA	ATTGTATAGT	TACTTAACTA	ATGAAGACAT	TTCAGAACTC	2760
	TGGGATGATT	TTAATCTTGA	AGTAGTAGGT	GGTATAGTCA	TAAAAACCATT	CATCCCCCTC	2820
45	TGATGTATAT	CTTAATTTTC	TGGCTTTAAG	GTGACATCTG	AGAGGTAATG	CATTCTTTTT	2880
	TATATTGAAA	TCATAAACTA	TCACCCGCTG	CTTCTCTGAG	TTACTTTTAA	TTTTGGCCTG	2940
	TGGTTATGGT	TTGGCGTTTC	CTTCTGTTTG	GTCTTCAGAG	CCCCATGCTC	ATATAGTCTC	3000
	GAGTGCAGGT	AATTAATATA	CTTGTAAATG	AAGATCAGTA	TTTCTGCCTA	GATCTGATAA	3060
	AAAAATTTTC	TTGTCTTAGT	TATAAAAAAT	CAAGAAATG	TGTTACAAAG	ATACTTAGTA	3120
50	TAGCTCTCTA	GCCATAACCT	GAGACTTGGG	ATGAAATTTA	AACCAGATAC	GATTACTTTT	3180
	GCAGATCATA	AGGCTTTTAA	TACTCTTGTT	ATCAAAATGG	CTTATTTTTC	AGGCCACTAAG	3240
	GATTGTAAAG	AGAAAAGCTT	TTCAACGAAG	GATTGCCCTT	CTTCTCCACC	ACTGTTCTTG	3300
	ATTCTCTCTC	CTTTTCAGGC	CTCAACAGGC	ACTGTATTCA	TGCGCAATGT	TCCAAATTAT	3360
	CAAAATCAAG	TGAATTTATT	TGTGTGTTCT	TACTTATAT	AAAAAAGAT	AACCTTAAGG	3420
55	ATGTGCAAGT	ACATTTCCAA	CTGCTAGCAC	AACCAGTATT	TGTAAATTAA	ACAAATGCT	3480
	GTATGATATG	GTCTCTTACA	CATTTATGTC	TATAGATATC	TATCGATCAT	CTTTCTATT	3540
	TGTTTCTATG	CTGAATAATG	TAAACCAAGT	GTTGGCAATT	GGTATCATCA	ATGATACTCA	3600
	TTTTTTAATA	ACCAAGGCA	GGGAAAATC	ATTTTACTTA	TAAATAAATA	TTTTATGATG	3660
	TGAAAAAAA	AAAAAAA	AAAAAAA				

60	A109 Protein sequence						
	Gene name:			ESTs			
	Unigene number:			Hs.128899			
65	Protein Accession #:			none found			
	Signal sequence:			1-11			
	Transmembrane domains:			402-424			
	Cellular Localization:			not determined			
70	1	11	21	31	41	51	
	MLSGFILMSPS	TQHRAQYTPG	GKILPWEASI	GAHTSRGRGS	DRERESRPEA	AGLLWDRAAA	60
	GEAEKGNRGE	PPAWIRAQQQ	PRPPPAQAP	GTAAGGAQDP	RLRPGRSRGR	VRLPVKPPEA	120
	SGRQPRGPD	CIPRPPSASA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
75	PRGRRGTVS	DEARGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAARPS	HPGTPLRSCS	240
	CCWLRCWRRO	RGPSGEYCHG	WLDAQGVWRI	GFQCFERFDG	GDATICOGSC	ALRYCCSSAE	300
	ARLDQGGCDN	DRQQGAGEPG	RADKDGPRRL	GRASCLRGTQ	GDGEGAPPPV	RAWQRCSPEG	360
	SPKGRQLLRA	FPGLLRPRRR	RGFPSSPRGG	PSPLQRPALP	IYVPLIVGS	VVFVFIILGS	420
80	LVAACCCRL	RPKQDPQQR	APGGNRLMET	IFMIPSASTS	RGSSSRQSST	AASSSSSANS	480
	GARAPPTRSQ	TNCDLPEGTM	NNVYVNMPTN	FSVLNCCQAT	QIVPHQGYL	HPPVVGYTVQ	540
	HDSVPMTAVP	PFMDLQPGY	RQIQSPFPHT	NSEQKMTPAV	TV		

A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

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1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGICT CTGCCTCTTA CTGCTCACAG TTTCTTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAGAG GCCTCCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCCTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300
   CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
15 GAAACCACTG ATAAGAATTT ATCACCCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTATCC CCTATTGATA GAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAAAT CAAATTTCAT 600
20 GAAGAAAACC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAATA 660
   TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
   TCTGAAAAAA AAAAAAAAAA AAAAAAAAAA

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25 A111 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

30

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35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSLGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
   PLMVIHLED CQYSQALKKV FAQNEEIQEM AQNKPIMLNL MHETTDKNLS PDGQYVPRIM 120
   FVDPSTLVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

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40

A112 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

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50 1      11      21      31      41      51
   |      |      |      |      |      |
   ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
   AAACCCCGTA TCCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTGG CGAGTATCAT CATTGTGTTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGGACTGTC CCTTGGGGGA GGAAGGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
55 GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCCACTGC AGGTGCTGGA CTCGGCCACA 360
   GGGAACTGTT TCTCTGCTGT TTTGACAAC TTCACAGAAG CTCTGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTGCGATGCG GAACTCAAGT 540
   GGGCCCTGTC TCTCAGGCTC CCTGGTCTCC CTGCACTGTC TTGCCTGTGG GAAGAGCCTG 600
60 AAGACCCCCC GTGTGGTGGG TGGGAGGAG GCCTCTGTGG ATTCTTGCC TTGGCAGGTC 660
   AGCATCCAGT ACGACAAACA GCAGTCTGT GAGGGGAGCA TCCTGGACCC CCACTGGGTC 720
   CTCACGGCAG CCCACTGCTT CAGGAAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
   GGCTCAGACA AACTGGGCAG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
   TTCAACCCCA TGTAACCCAA AGACAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
65 ACTTCTCTAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCAC TCTGGATCAT TGGATGGGCG TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGCAGGCGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
   GCGTACCAGG GGGAGTCAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGCCCGA GCACCCAGG AGTATACACC 1260
   AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTA

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75 A113 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPc domain: 204-429
 Cellular Localization: plasma membrane/ER

80

	1	11	21	31	41	51	
5	MLQDPDSQDP	LNSLDVKPLR	KPRIPMETFR	KVGIPIIIAL	LSLASIIIVV	VLIKVILDKY	60
	YFLCGQPLHF	IPRKQLCDGE	LDCPLGEDDE	HCVKSPPEGP	AVAVRLSKDR	STLQVLDSAT	120
	GNWFSACFDN	FTBALAETAC	RQMGYSKPT	FRABEIGPDQ	DLDVVEITEN	SQELMRNNS	180
	GPCLSGSLVS	LHCLACGKSL	KTPRVVGGBE	ASVDSWPWQV	SIQYDKQHVC	GGSIIDPHWV	240
	LTAHCHFRKH	TDVFNWVKRA	GSDKLGSPFS	LAVAKIIIE	FNPMPKOND	IALMKLQFPL	300
10	TFSGTVRPIC	LPFFDEELTP	ATPLWIIGWG	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
	AYQGEVTEKM	MCAGIEGGV	DTCQGDSSGP	LMYQSDQWHV	VGIVSWGYGC	GGPSTPGVYT	420
	KVSAYLNWY	NVWKAEI					

A114 DNA SEQUENCE:

15	Gene name:	TTK protein kinase
	Unigene number:	Hs.169840
	Probeset Accession #:	M86699
	Nucleic Acid Accession #:	NM_003318
20	Coding sequence:	1026-3551 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
25	GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACCT	TTGTTGGCCA	GGCTGGAGTG	60
	CAATGCACA	ATCTCAGCTT	ACTGCAACCT	CGCCTCCCG	GGTTCAAGCG	ATTCTCCTGC	120
	CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACCTAATT	180
	CTTTCTTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	TGAACCTCCTG	240
	ACCTCAGGTG	ATCCACTTGC	CTTGGCTCTC	CAAAAGTGCTA	GGATTACAGC	CGTGAAACTG	300
	TGCTCTGGCTG	ATTCCTTTTT	TGTTGTTGGA	TTTTTGAAAC	AGGGTCTCCC	TTGGTCGCCC	360
	AGGCTGGAGT	GCAAGTGGTG	GATCTTGGCT	CACATAAACC	TCCACCTCCT	GGTTTCAAGT	420
30	GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	CGGTGCACCA	CCACACCGCG	480
	CTAATTTTGT	TAATTTTATT	AGAGACAGGG	TTTCACCATG	TTGCCAGGC	TGTTCTCAAA	540
	CTCCTGGACT	CAAGGGATCC	GCCTGCCCTC	ACTTCCCAAA	GTCCCGAGAT	TACAGGTGTG	600
	AGTCACCATG	CCTGACCTTA	TAATTCCTTA	GTCAATTTTT	CTGGTCCATT	TCTTCTCTAG	660
	GGTCTTCACA	ACAAATCTGC	ATTAGGCGGT	ACAATAATCC	TTAACTTCAT	GATTCAACAA	720
35	AGGAAGATGA	AGTGATTCTA	GATTTAGAAA	GGGGAAGTAG	TAAGCCCACT	GCACACTCCT	780
	GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
	TTTGGTTTAA	ATTAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	TTGTATGTGA	900
	ATGTAAAGCT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCCCAG	960
40	TGCAGTTTTC	TGTAGAAATG	GAATCCGAGG	ATTTAAGTGG	CAGAGAATTG	ACAATTGATT	1020
	CCATAATGAA	CAAGTAGAGA	GACATTAAAA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
	AACATAAGCT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAATC	GTAAACCAAA	1140
	TTATGATGAT	GGCAAAACAC	CCAGAGGACT	GGTTGAGTTT	GTGTCTCAAA	CTAGAGAAAA	1200
	ACAGTGTCCC	GCTAAGTGAT	GCTCTTTTAA	ATAAATTGAT	TGGTGGTTAC	AGTCAAGCAA	1260
45	TTGAAGCGCT	TCCCCAGAT	AAATATGGCC	AAATGAGAG	TTTTGCTAGA	ATTCAAGTGA	1320
	GATTGTCTGA	ATTAAGAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
	CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
	CACAAGGTAA	TGTCAAAAAA	AGTAAACAAC	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
	TACCACCTAGA	AATGTCTGGA	ATTGCCCTGC	GGAAATTTAA	CCTCCAAAAA	AAGCAGCTGC	1560
50	TTTCAGAGGA	GGAAAGAAG	AATTTATCAG	ACTCTACGGT	ATTAACCTGC	CAAGAACTAT	1620
	TTTCCGGTTC	ACTTGGGCAT	TTACAGAATA	GGAAACAACG	TTGTGATTCC	AGAGGACAGA	1680
	CTACTAAAGC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAAGATGCA	GAATATAGTT	1740
	ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCATTT	GGAAGAGTCC	1800
	CAGTTAACTT	TCTAATATAG	CCAGATTGTG	ATGTGCGAGC	AGATGATTCA	GTGTGACTCT	1860
55	GTTTTATGAA	AGACAAACCC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
	AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAATTTTAA	GTCTGTTCAA	AATAGTCATT	1980
	TCAAGGAACC	TCTGGTGTCA	GATGAAAGA	GTTCTGAAC	TATTATTACT	GATTCAATAA	2040
	CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAGAAACT	AAAGAGTATC	2100
	AAGAACCAGA	GGTTCAGAG	AGTAACCAGA	AACAGTGGCA	AGCTAAGAGA	AAGTCAGAGT	2160
60	GTATTAAACA	GAATCCTGCT	GCACTTCAAA	ATCACTGGCA	GATTCGGGAG	TTAGCCCGAA	2220
	AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTTTTCA	GTTCAAAAAC	2280
	AGTCACCACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
	GCAGCAATAC	CTTGGATGAT	TACATGAGCT	GTTTTAGAAC	TCCAGTTGTA	AAGAAATGACT	2400
	TTCCACCTGC	TGTTCAGTTG	TCAACACCTT	ATGGCCAAAC	TGCTGTGTTT	CAGCAGCAAC	2460
65	AGCATCAAA	ACTTGGCCAT	CCACTTCAAA	ATTTACAGGT	TTTAGCATCT	TCTTCAGCAA	2520
	ATGAATGCAT	TTGGGTTTAA	GGAAAGATTT	ATTCCATATT	AAAGCAGATA	GGAAAGTGGAG	2580
	GTTCAAGCAA	GGTATTTCAG	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAAAATATG	2640
	TGAATTTAGA	AGAAAGCAGAT	AACCAAACTC	TTGATAGTTA	CCGGAACGAA	ATAGCTTATT	2700
	TGAATTAAC	ACAACAACAC	AGTGATAAGA	TCATCCGACT	TTATGATTAT	GAATTCACGG	2760
70	ACCAGTACAT	CTACATGGTA	ATGGAGTGTG	GAATATTGTA	TCTTAATAGT	TGGCTTAAAA	2820
	AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAATAATATG	TTAGAGGCAG	2880
	TTACACAAT	CCATCAACAT	GGCATTGTTC	ACAGTGATCT	TAAACCAAGT	AACCTTCTGA	2940
	TAGTTGATGG	AATGCTAAAG	CTAATTGATT	TTGGGATTGC	AAACCAAAATG	CAACCAAGATA	3000
	CAACAAGTGT	TGTTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAAGCAA	3060
75	TCAAGATAT	GTCTTCTCTC	AGAGAGAAATG	GGAAATCTAA	GTCAAGAGATA	AGCCCCAAAA	3120
	GTGATGTTTG	GTCCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCAATTTC	3180
	AGCAGATAAT	TAATCAGATT	TCTAAATTAC	TGATCTTAAT	TGATCTTAAT	TAATAAATTG	3240
	AAITTTCCCGA	TATTCAGAG	AAAGATCTTC	ARGATGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
	ACCCAAACAA	GAGGATATCC	ATTCTTGAGC	TCTTGGCTCA	TCCATATGTT	CAAAATTCAAA	3360
80	CTCATCCAGT	TAACCAAAATG	GCCAAAGGAA	CCACTGAAGA	AATGAATAT	GTCTCGGGCC	3420
	AACCTGTGTTG	TCTGAATTTCT	CCTAATCTCA	TTTGAAGAGC	TGCTAAATAT	TTATATGAAC	3480
	ACTATAGTGG	TGTTGAAAGT	CATAATTCTT	CACTCTCCAA	GACTTTTGAA	AAAAAAAGGG	3540
	GAAAAAATG	ATTTCAGATT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
	GTTATACTCT	TGAATCCCTG	TGGAAATCTA	CATTTGAAGA	CAACATCACT	CTGAAGTGTG	3660
	ATCAGCAAAA	AAAAATCAGT	GAGATTATCT	TTAAAGAAA	ACTGTAAAAA	TAGCAACCCAC	3720

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAATCTAC 3780
TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAACTTTG 3840
TAAATAAAGT TTTGTGGCTA AAATGA

5

All5 Protein sequence:

Gene name: TTK protein kinase
Unigene number: Hs.169840
Probeset Accession #: M86699
Protein Accession #: NP_003309
Signal sequence: none found
Transmembrane domains: none found
Protein Kinase Domain: 510-775
Cellular Localization: cytoplasmic and nuclear

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1 11 21 31 41 51
| | | | |
MNKVRDIKNN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLLKLEKNS 60
VPLSDALLNK LIGRYSQAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120
ANCKKFAFVH ISFAQFELSQ GNVKKSQQLL QKAVERGAVP LEMLEIALRN LNLQKQQLLS 180
EEEKKNLSAS TVLTAQESSFS GSLGHLQNRN NSCDSRGQTT KARFLYGENM PPQDAEIGYR 240
NSLRQNTKTK QSCPFGRVFV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPKSKP 300
SGMDSCELRN LKSVQNSHPK EPLVSDEKSS ELIITDSITL NKRTSSLLA KLEETKBYQE 360
FEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFF QPVFVSQKQS 420
PPISTGKWFDP KSICKTPSS NTLDDYMSCF RTPVVKNDFP PACQLSTPYG QPACQQQQH 480
QILATPLQNL QVLASSANE CTSVKGRISY ILKQIGSGGS SKVPQVLNEK KQIYAIFYVN 540
LEEDNQTLTD SYRNEIAYLN KLQQHSDKII RLYDYEITDQ YIYVMMECGN IDLNSWLKKK 600
KSIDPWERKS YWRNMLEAVH TIHQHGVHS DLKPFANFLIV DGMKLKIDFG IANQMOPDTT 660
SVVKDSQVGT VNYMPEAIK DMSSSRENGK SKSKISPKSD VMSLGCILYY MTYKTPFPQQ 720
IINQISKLHA IIDPNHEIEF PDIEPKDLQD VLKCCCLKRDP KQRISIPELL AHPYVQIQTH 780
FVNQMAKGT EEMKYVLGQL VGLNSPNSIL KAAKTLYEHY SGGESHNSSS SKTFEKKRKG 840
K

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OVARIAN**All6 DNA SEQUENCE**

Gene name: G protein-coupled receptor 39
Unigene number: Hs.85339
Probeset Accession #: AA349893
Nucleic Acid Accession #: NM_001508
Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
CCGAGTTTGG AGGTGGCCAC CTGGATCAA ATCACCCCTA TTCTGGTGTA CCTGATCATC 120
TTCTGATGAG GCCTTCTGGG GAACAGCGCC ACCATTCCGG TCACCCAGGT GCTGCAGAAG 180
AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240
TTGGTGTTC CTATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTC TCTTCGAGGC CTGCAGCTAC 360
GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC 420
TTCAAGTACA AGGCTGTGTC GGGACCTG CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
GTCACTCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTG 540
GTGAAGGTGC CCAAGCCACG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCAAGAG 600
CAGCCCGAGA CCTCCAAATG GTCCATCTGT ACCAACTCT CCAGCCGCTG GACCGTGTTC 660
CAGTCCAGCA CTCTCGGCGC CTTCGTGGTC TACCTCGTGG TCCTGCTCTC CGTAGCCTTC 720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780
ACCGGCGCTC CGCAGCTGAG GAAGTCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
ACCATCATCT TCCTGAGGCT GATTGTTGTG ACATTGGCCG TATGCTGGAT GCCCAACCAG 900
ATTGCGAGGA TCATGGCTGC GGCCAAACCC AAGCAGCACT GGAAGAGGTC CTACTTCCGG 960
GCGTACATGA TCCTCTCTCC CTTCCTGAG ACCTTTTCT ACCTCAGCTC GGTCAATCAAC 1020
CGCTCCTGT ACACGGTGTG CTGCGAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC 1080
TGCGCGCTGT CGCTGCAGCA CGCCCAACCAG GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
ACCAACGACA GCGCCCGCTT TGTGCGAGCG CCGTGTCTCT TCGCGTCCCG GCGCCAGTCC 1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
TCTAAGTCCC AGTCATTGAG TCTGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAAGC 1320
AATCTGCTG CAGAGAAATG TTTTCAGGAG CATGAAGTTT GA

75

80

All7 Protein sequence:

Gene name: G protein-coupled receptor 39
Unigene number: Hs.85339
Probeset Accession #: AA349893
Protein Accession #: NM_001508, NP_001409
Signal sequence: none found
Pfam domains: 7tm_1 [72-172, 224-344]
Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
Cellular Localization: plasma membrane

1 11 21 31 41 51
| | | | |
MASPSLPQSD CSQIIDHSHV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTQVLQK 60

	KGVLQKEVTD	HMVSLACSDI	LVFLIGMPME	FYSIIWNPLT	TSSYTLSCKL	HTFLFEACSY	120
	ATLLHVLTL	FRYIAICHP	FRYKAVSGPC	QVKLLIGFVW	VTSALVALPL	LFAMGTEYPL	180
	VNPVSHRGLT	CNRSSTRHHE	QPETSNNMSIC	TNLSRRRTVF	QSSIFGAPVV	YLVVLLSVAF	240
5	MCNNMMQVLM	KSKQKSLAGG	TRPPQLRKSE	SEESRTARRQ	TIIFLRLLIV	TLAVCMWPNQ	300
	IRRIMAAAKP	KHDWTRSYFR	AYMILLPFSE	TFYLLSSVIN	PLLYTVSSQQ	FRRVFVQVLC	360
	CRLSLQHANH	EKRLRVHAHS	TTDSARFVQR	PLLFASRRQS	SARRTEKIFL	STFQSEAEPP	420
	SKSQSLSLSE	LEPNNGAKPA	NSAAENGFOE	HEV			
10	<u>A118 DNA sequence</u>						
	Gene name:		bone morphogenetic protein receptor IB (ALK-6)				
	Unigene number:		Hs.87223				
	Probeset Accession #:		AA250737				
	Nucleic Acid Accession #:		NM_001203				
15	Coding sequence:		274-1782 (underlined sequences correspond to start and stop codons)				
	1	11	21	31	41	51	
	CGCGGGCGCG	GGAGTCGGCG	GGGCTCTCGC	GGACGCGGGC	AGTGCGGAGA	CGCGGGCGCT	60
	GAGGACGCGG	GAGCGCGGAG	CGCACGCGCG	GGGTGGAGTT	CAGCCTACTC	TTTCTTAGAT	120
20	GTGAAAGGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180
	CATAACCAT	TGGCTCTGAG	CTATGACAAG	AGAGGAAACA	AAAAGTTAAA	CTTACAAGCC	240
	TGCCATAAGT	GAGAAGCAAA	CTTCTTTGAT	AACATGCTTT	TGCGAAGTGC	AGGAAAATTA	300
	AATGTGGGCA	CCAGAAAGA	GGATGGTGAG	AGTACAGCCC	CCACCCCCCG	TCCAAAGGTC	360
	TTGGCTGTGA	AATGCCACCA	CCATTGTCCA	GAAGACTCAG	TCAACAATAT	TTGCAGCACA	420
25	GACGGATATT	GTTCACGAT	GATAGAAGAG	GATGACTCTG	GGTTGCCTGT	GGTCACTTCT	480
	GGTTGCCTAG	GACTAGAAGG	CTCAGATTTT	CAGTGTGGGG	ACACTCCCAT	TCTCATCAAA	540
	AGAAGATCAA	TGGAATGCTG	CACAGAAAGG	AACGAATGTA	ATAAAGACCT	ACACCTTACA	600
	CTGCTCCAT	TGAAGAACAG	AGATTTTGTT	GATGGACCTA	TACACCCAG	GGCTTTACTT	660
	ATATCTGTGA	CTGTCTGTAG	TTTGCTCTTG	GTCCCTTATCA	TATTATTTTG	TTACTTCCGG	720
30	TATAAAGAC	AAGAAACAG	ACCTCGATAC	AGCATTGGGT	TAGAACAGGA	TGAAACTTAC	780
	ATTCTCTCTG	GAGAATCCCT	GAGAGACTTA	ATTGAGCAGT	CTCAGAGCTC	AGGAAGTGGA	840
	TCAGGCTCCC	CTCTGCTGGT	CCAAAGGACT	ATAGCTAAGC	AGATTTCAGT	GGTGAACAG	900
	ATTGGAAGAG	GTGCTATGG	GGAAGTTTGG	ATGGGAAAGT	GGCGTGGCGA	AAAGGTAGCT	960
	GTGAAAGTGA	TCTTCACCA	AGAGGAAGCC	AGCTGGTTCA	GAGAGACAGA	AATATATCAG	1020
35	ACAGTGTGTA	TGAGGATGTA	AAACATTTTG	GGTTTCATTG	CTGCAGATAT	CAAAGGACA	1080
	GGTCTCTGGA	CCAGTTGTA	CCTAATCACA	GACTATCATG	AAAATGGTTC	CCTTTATGAT	1140
	TATCTGAAGT	CCACCACCT	AGACGCTAAA	TCAATGCTGA	AGTTAGCCTA	CTCTTCTGTC	1200
	AGTGGCTTAT	GTCAATTACA	CACAGAAATC	TTTAGTACTC	AAGGCAAAAC	AGCAATTGCC	1260
	CATCGAGATC	TGAAGAGTAA	AAACATTCTG	GTGAAGAAAA	ATGGAACTTG	CTGTATTGCT	1320
40	GACCTGGGCC	TGGCTGTAAA	ATTTATTAGT	GATACAAATG	AAGTTGACAT	ACCACCTAAC	1380
	ACTCGAGTTG	GCACCAACG	CTATATGCCT	CCAGAAGTGT	TGGACGAGAG	CTTGAACAGA	1440
	AATCACTTCC	AGTCTTACAT	CATGGCTGAC	ATGTATAGTT	TTGGCCTCAT	CCTTTGGGAG	1500
	GTGCTAGGAA	GATGTGTATC	AGGAGGTATA	GTGGAAGAA	ACCAGCTTCC	TTATCATGAC	1560
	CTAGTCCCA	GTGAACCCCT	TTATGAGGAC	ATGAGGGAGA	TTGTGTGATC	CAAGAAGTTA	1620
45	CGCCCTCAT	TCCCAACCG	GTGGAGCAGT	GATGAGTGTC	TAAGGCAGAT	GGGAAACTC	1680
	ATGACAGAAT	GCTGGGCTCA	CAATCCTGCA	TCAAGGCTGA	CAGCCCTGCG	GGTTAAGAAA	1740
	ACACTTGCCA	AAATGTCAGA	GTCCCAGGAC	ATTAAACTCT	GATAGGAGAG	GAAAAGTAAG	1800
	CATCTCTGCA	GAAAGCCAAC	AGGTACTCTT	CTGTTTGTGG	GCAGAGCAAA	AGACATCAAA	1860
	TAAGCATCCA	CAGTACAAGC	CTTGAACATC	GTCCCTGCTC	CCAGTGGGTT	CAGACCTCAC	1920
50	CTTTCAGGGA	GCGACCTGGG	CAAAGACAGA	GAAGCTCCCA	GAAGGAGAGA	TTGATCCGTG	1980
	TCTGTTTGA	GCGCGAGAAA	CCGTTGGGTA	ACTTGTTCAA	GATATGATGC	AT	
55	<u>A119 Protein sequence</u>						
	Gene name:		bone morphogenetic protein receptor IB (ALK-6)				
	Unigene number:		Hs.72472 / Hs.87223				
	Probeset Accession #:		AA250737 / U89326				
	Protein Accession #:		NP_001194				
	Signal sequence:		1-13				
	Transmembrane domains:		128-144				
60	PFAM domains:		activin_receptor [30-111], protein kinase [204-491]				
	Cellular Localization:		plasma membrane				
65	1	11	21	31	41	51	
	MLLSRAGKLN	VGTKKEDGES	TAPTTPRPKVL	RCKCHHHCE	DSVNNICSTD	GYCFTMIEED	60
	DSGLPVVTSG	CLGLEGSDFQ	CRDTPIPHQR	RSIECCTERN	ECNLDLHPTL	PPLKNRDFVD	120
	GPIHRRALLI	SVTVCSLLLV	LIILPCYFRY	KRQETRPYS	IGLEQDEYTI	PPGESLRDLI	180
	BQSQSSGSGS	GLPLLVRQTI	AKQIQMVKQI	KGGRYGEVWM	GKWRGEKVAV	KVFPTTEBAS	240
70	WRETEIYQT	VLMRHENILG	PIAADIKGTG	SWTQLYLITD	YHENGSLVDY	LKSTTLDAKS	300
	MLKLAYSSVS	GLCHLHTEIF	STQGKPAIAH	RDLSKNILV	KKNGTCCCIAD	LGLAVKPID	360
	TNEVDIPPT	RVGTRKYMPP	EVLDESINRN	HFQSYIMADM	YSFGLILMEV	ARRCVSGGIV	420
	EEYQLPYHDL	VPSPSPSYEDM	REIVCIKCLR	PSPPNRRWSSD	ECLRQMGKLM	TECAHNPAS	480
75	RLTALRVKKT	LAKMSQSQDI	KL				
80	<u>A120 DNA SEQUENCE</u>						
	Gene name:		LIV-1 protein, estrogen regulated				
	Unigene number:		Hs.79136				
	Probeset Accession #:		U41060				
	Nucleic Acid Accession #:		NM_012319.2				
	Coding sequence:		138-2405 (underlined sequences correspond to start and stop codons)				
	1	11	21	31	41	51	

	CTCGTGGCCG	ATTGCGCACG	AGACCGCGTG	TTCGCGCCTG	GTAGAGATTT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAAAC	CAAACTCTGC	CGCGTGGCCG	GGCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCGCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCCTG	ACCTTTGCC	180
5	TCTCTGTAC	AAATCCCCTT	CATGAACATA	AAGCAGCTGC	TTTCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTTGAAGGGT	360
	TCAGAAAATT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAATCCAT	ATACACCATG	420
	ACCAACGACCA	TCATCAGAC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
10	AGCATCACTC	AGACCACGAG	CATCACTCTG	ACCATGATCA	TCATCTCTAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAAG	CGAAAAGCTC	TTTGCCGAGA	CCATGACTCA	GATAGTTTCAG	600
	GTAAGATCC	TAGAAAACAG	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCACTGTG	TACAACACTG	720
	TCTCTGAAGG	AATCACTTTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
15	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTCACATC	AAAGAGCCGG	GTGAGCCGGC	840
	TGGCTGGTGA	GAAAAATAAT	GAATCTGTGA	GTGAGCCCGG	AAAAGGGCTT	ATGTATTCCA	900
	GAAACACAAA	TGAAAAATCCT	CAGGAGTGTT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
	GCATGGGCT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
20	TCAACCAAT	TGATGCTAGA	TCTTGTCTGA	TTCATACAAG	TGAAAAGAAG	GCTGAAATCC	1080
	CTCCAAAGAC	CTATTCAATTA	CAAAATAGCCT	GGGTGTTGGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCT	GTCTCTGTCTG	GGGGTTATCT	TAGTGCTCT	CATGAATCGG	GTGTTTTTCA	1200
	AATTTCTCT	GAGTTTCTCT	GTGGCACTGG	CCGTTGGGAC	TTTGAGTGGT	GATGCTTTTT	1260
	TACACCTTCT	TCCACATTCT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
	CAATGAAAT	GAAAGAGGA	CCACTTTTCA	GTCATCTGTC	TTCTCAAAAC	ATAGAAGAAA	1380
25	GTGCTTATT	TGATTCACG	TGGAAGGGTC	TAAACAGCTCT	AGGAGCGCTG	TATTTTCATG	1440
	TTCTTGTGA	ACATGTCCTC	ACATTGATCA	AACAATTTAA	AGATAAGAA	AAAAAGAAATC	1500
	AGAAGAAACC	TGAAAATGAT	GATGATGTGG	AGATTAAGAA	GCAGTTGTCC	AAGTATGAAT	1560
	CTCACTTTCT	AACAATAGAG	GAGAAAGTAG	ATACAGATGA	TCGAAGTGA	GGCTATTTAC	1620
	GAGCAGACTC	ACAAGAGCCC	TCCCACTTTG	ATTCTCAGCA	GCCTCAGTCT	TTGGAAGAAG	1680
30	AAGAGGTCAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
	CTCAGACTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCCGC	GTGCCCACTT	1920
	TGGCTCGAT	GCTGATAATG	GGTGATGGCC	TGCACAATTT	CAGCGATGGC	CTAGCAATTTG	1980
35	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAAGTAC	TTCTGTGCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTCTTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CTTTTATAAT	GCAATGTCAG	CCATGCTGGC	GTATCTTGA	ATGGCAACAG	2160
	GAATTTTCAT	TGGTCATTAT	GCTGAAAATG	TTTCTATGTG	GATATTTGCA	CTTACTGCTG	2220
	GCTTATTCAT	GTATGTTGCT	CTGGTTGATA	TGTTACCTGA	AATGCTGCAC	AATGATGCTA	2280
40	GTGACCATGG	ATGTAGCCGC	TGGGGGTATT	TCTTTTTTACA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTTGGAAT	TATGTTACTT	ATTTCCATAT	TTGAACATAA	AATCGTGTIT	CGTATAAAT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
	TTGTATTGAA	TATTCCTGTC	TGTTACAAAG	TCAGTTAAAG	GTACGTTTIA	ATATTAAAT	2580
45	TATTCATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCACC	GGTATTACCA	GTTTATTATG	2640
	TAAACAAGAG	ATTTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAATAGT	CTTTAATGCT	2700
	TTTTCAAGAA	CTAACACAGT	TATTCCTATA	CTGGATTTTA	GGTCTCTGAA	GAACTGCTGG	2760
	TGTTTAGGAA	TAAAGATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTTA	2820
	AGCAAAGAAA	TAAAGGAGAA	AAGAGAAGAA	TCTGAGAAAT	GGGGAGGCAT	AGATTCTTAT	2880
50	AAAAATCACA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAATTAAG	TATAAAAAGG	2940
	CAGAAATTAGT	ATAGAGTACA	TTCAATAAAC	ATTTTGTGCA	GGATTATTTC	CCGTAATAAC	3000
	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAC	TTTGATATAAT	ACAGAAATCT	3060
	AAATATATTT	AATGAATTTCA	AGCAATATAC	ACTTGACCAA	GAAATTTGAA	TTTCAAAATG	3120
	TTCTGTCGGG	TTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	3180
55	TATTGCCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGTTT	ACCTGGTTTA	3240
	CAAAATATATC	AGAGTAGTAA	AACTTTGATA	TATATGAGGA	TATTAAGACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTCAGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTTG	3360
	GAGCAATTTG	CTTTATATAC	GGTACTGTAG	CCATCTAGG	CCTGCTCTG	GCATTTCTTA	3420
60	GATGTTTCTT	TTTTACACAA	TAAATTCCTT	ATATCAGCTT	G		

A121 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Protein Accession #: NP_036451
 Signal sequence: 1-21
 Pfam domain: Zip[591-743]
 Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
	MARKLSVILI	LTFALSVTNP	LHELKAAAFP	QTTEKISPNI	ESGINVDLAI	STRQYHLQQL	60
	FYRYGENNSL	SVGDFRKLILQ	NIGIDKIKRI	HIHHDHDS	DHEHSDHER	HSDREHSDH	120
75	EYHSDHDS	HNNHAASGN	KRKALCPDHD	SDSSGKDPFN	SQKGAHRPE	HASGRNVKD	180
	SVSASVTST	VYNTVSEGT	FLETIETPRP	GKLPKDVSS	STPPSVTSKS	RVSRLAGRKT	240
	NEVSSEPRKG	FMYSRNTNEN	PQECFNASKL	LTSHGMIQV	PLNATEFNFL	CPALINQIDA	300
	RSCLHTSEK	KAEIPPKTYS	LQIAWVGFP	AIISIPLSL	LGVLVPLMN	RVFFKFLLSF	360
	LVALAVGTLS	GDAFLHLLPH	SHASHHSHS	HEEPAMEMKR	GPLFSLSSQ	NIEESAYFDS	420
80	TWKGLTALGG	LYFMFLVEHV	LTLIKQFKDK	KKKNQKKPEN	DDVEIKKQL	SKYESQLSTN	480
	EEKVDTDRT	EGYLRADSQ	PSHFDSQPPA	VLEEEVEMIA	HAHPQEVYNE	YVPRGCKNKC	540
	HSHFDITLQ	SDDLIHHDH	YHILHHHHH	QNHHPHSHSQ	RYREELKDA	GVATLAWMVI	600
	MGDGLHNFSD	GLAIGAAFTE	GLSSGLSTSV	AVFCHLPHE	LGDFAVLLKA	GMTVKQAVLY	660
	NALSAMLAYL	GMATGIFIGH	YAENVSMWIF	ALTAGLFMVV	ALVDMVPEML	HNDASDHGCS	720

RWGYFFLQNA GMLLFGIML LISIFEKIV FRINF

A122 DNA SEQUENCE

5 Gene name: EGF-like-domain; multiple 6
Unigene number: Hs.12844
Probeset Accession #: N67551
Nucleic Acid Accession #: NM_015507
10 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
COGCAGAGGA GCGTCGGCCA GGCTAGCCAG GCGCGCCCCA GCCCCTCCCC AGGCCGCGAG 60
CGCCCTGCCC GCGGTGCGCTG GCCTCCCTTC CCAGACTGCA GGGACAGCAC CCGGTAACTG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGCTC GCGGCCCTCC CGAGGGGGGC TCAGGAGGAG GAAGGAGGAC CCGTGCGAGA 240
ATGCTCTGCG CCGTGAAGCCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
GGGAACGCGG CCACTGCAAG GCATCAGCGG TTGTTAGCAT CGGCACGTCA GCCTGGGGTC 360
TGTCACATG GAACATAAAT GGCCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAATC 420
TGTAAGCTTA CATGCGAAAC TGGATGTAAG TTTGGTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCTTTC CAGGATACAC CGGGAACACC TGCACTCAAG ATGTGAATGA GTGTGGAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGCCG ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGGAC ATGTGCCATG 660
ATAAAGTCTC AGTGTAAATG TGAAGACACA GAAGAAGGCG CACAGTGCCT GTGTCCATCC 720
TCAGGACTCC GCGTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCTC 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTGACA TTGTTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATTGCTT CAATACCCAA 960
GGTCCCTTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGCACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCCCT AGAGCACCTG GTACCAATCA AGACAGAATC 1080
AAGAAGTTGC TTGCTCACAA AAACAGCATG AAAAAGAAAG CAAAATTAA AAATGTTACC 1140
CCAGAACCCA CAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCCTGATT 1380
CTGGTCCAAA GGAAGCGCT AACTTCCAAA CTGGAACATA AAGATTAAAT TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAATCCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCG GGCCTTGGCA 1560
GGTCACAAGA AAGACATTGG CGAATTGAAA CTCTCCTAC CTGACCTGCA ACCCCAAAGC 1620
AACTTCTGTT TGCTCTTTGA TTACCGGCTG GCGGAGAGCA AAGTCGGGAA ACTTCGAGTG 1680
TTTGTAAGAA ACAGTAACAA TGCCCTGGCA TGGGAGAAGA CCACGATGGA GAGTGAAGAA 1740
TGGAAGACAG GGAATAATCA GTTGATATCA GGAAGTATG CTACCAAAG CATCATTTTT 1800
GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTTGCTTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTATCT GTGGATGACT GAATGTACT ATCTTTATAT 1920
TTGACTTTGT ATGTGAGTTC CCGGTTTTT TTGATATGTC ATCATAGGAC CTCTGGCAAT 1980
TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
TCTTGATAA GATATGCCAA TATTTGCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
TTTCTGAATC TTTCACATT ATATTATAA ATATGGAAT GTCAAGTTAT CTCCCTCTCT 2160
CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACACAT TTCTAGAAAA 2220
TAGAAAAAAA AGCAGAGAGA AATGTTTAA TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
TATGACATCA AAGATAGACT TTTCCTAAG TGGCTTAGCT GGTGCTTTGA TAGCCAAACT 2340
TGTATATTTA AATCTTTTGT AATAATAATA TCCAATCAT CAAAAAATA AAAAAAAA
```

A123 Protein sequence:

55 Gene name: EGF-like-domain; multiple 6
Unigene number: Hs.12844
Probeset Accession #: N67551
Protein Accession #: NP_056322.2
Signal sequence: 1-21
60 Transmembrane domains: none found
MAM domain: 402-546
EGF domain: 80-259
Cellular Localization: secreted

```
1      11      21      31      41      51
|      |      |      |      |      |
MPLPWSLALP LLLSWVAGGF GNAASARHHG LLASARQPGV CHYGTKLACC YGWRNRSKGV 60
CEATCEPGCK FGEVGPNNKC RCFPGYTGKT CSQDVNECGM KPRPCQHRV NTHGSYKFC 120
LSGHMLMPDA TCNVSRTCAM INCQYSCEDT EEPQCLCPG SGLRLAPNGR DCLDIDECAS 180
GKVICFYNRR CVNTFGSYIC KCHIGFELQY ISGRYDCIDI NECTMDSHTC SHHANCENTQ 240
GSFKCKKQGG YKGNGLRCSA IPENSVEVL RAPGTIKDRI KLLAHKNKM KKKAKIKNVT 300
PEPTRTPFK VNLQPFNYEE IVSRGGSNSG GKGNBEKMK EGLEDEKREE KALKNDIEER 360
SLRGDVFPFK VNEAGEFGLI LVQRKALTSK LEHKLNLISV DCSFNHGICD WKQDREDDFD 420
WNPADRDNAI GFYMAVPALA GHKKDIGRLK LLLFDLPQPS NFCLLFYDRL AGDKVGLRV 480
FVKNSNNALA WEKTSSEDEK WKTGKIQLYQ GTDATSKIIF EAERGRGKTG EIAVDGVLLV 540
SGLCPDLSLLS VDD
```

A124 DNA SEQUENCE

80 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
Unigene number: Hs.170195
Probeset Accession #: BE616633
Nucleic Acid Accession #: NM_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

```

5 1      11      21      31      41      51
   |      |      |      |      |      |
   GGGGCGACGG GGGCCCGTCT GCAGCAAGTG ACCGAAGGCC GGAAGCGCGG CCTGCCCTCT 60
   CTGCCACCTG GGGCGGTGCG GGGCCCGAGC CCGAGAGCCG GGTAGCGCGT AGAGCCGGCG 120
   CGATGCACGT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCTGGGCAC 180
   CCCTGTTCTT GCTGCGCTCC GCCCTGGCGG ACTTCAGCCT GGACAACGAG GTGCACTCGA 240
10 GCTTCATCCA CCGGCGCCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCGC GAGATCCTCT 300
   CCATTTTGGG CTTCGCCACG CGCCCGCGCC CGCACCTCCA GGGCAAGCAC AACTCGGCAC 360
   CCATGTTTCAT CTGSGACCTG TACAAGGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGGCG 420
   GCCAGGGCTT CTCCCTACCCG TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGGCCA 480
   GCCTGCAAGA TAGCCATTTC CTCAACGACG CCGACATGGT CATGAGCTTC GTCAACCTCG 540
15 TGGAACTGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGGTTTGATC 600
   TTTCCAAGAT CCCAGAAGGG GAAGCTGTCA CGGAGCCCGA ATTCCGGATC TACAAGGACT 660
   ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
   AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCTTC TGGGCTCTCG 780
   AGGAGGCTGG GCTGGTGTTC GACATCACAG CCACAGCAAA CCACTGGGTG GTCAATCCCG 840
20 GGCACAACCT GGGCCTGCGG CTCTCGGTGG AGACGCTGGA TGGGAGAGAG ATCAACCCCA 900
   AGTTGGCGGG CCTGATTGGG CGGCACGGGC CCCAGAACAA GCAGCCCTTC ATGGTGGCTT 960
   TCTTCAAGGC CACCGAGGTC CACTTCCGCA GCATCCGGTC CACGGGGAGC AACACGCGCA 1020
   GCCAAGAACG CTCCAAGACG CCCAAGAACG AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
   AGAAGACCGG CAGCGACGAG AGGCAGGCCCT GTTAGAAGCA CGAGCTGTAT GTCACTTCC 1140
25 GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCCGCC TACTACTGTG 1200
   AGGGGGAGTG TGCCCTCCCT CTGAACCTCT ACATGAACGC CACCAACCAC GCCATCGTGC 1260
   AGACCGGGT CCACCTTATC AACCCGGAAA CGGTGCCCAA GCCCTGCTGT GCGCCCAAGC 1320
   AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTATC CTGAAGAAAT 1380
   ACAGAAACAT GTCATTCGCG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TCGAACCTTC 1440
30 TTGGGGCCAA GTTTTCTTGG ATCCTCCATT GCTCGCTTGG GCCAGGAACC AGCAGACCAA 1500
   CTGCCCTTTG TGAGACCTTC CCTCCCTAT CCCCAACTTT AAAGGTGTGA GAGTATTAGG 1560
   AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAAAG 1620
   TCCTACAAGC TGTGAGGACA AAACCTAGCA GGAAGAAAAA ACAACGCATA AAGAAAAATG 1680
   GCCGGGCCAG GTCATTCGCG GGGAACTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
35 TTATGAGCGC CTACAGCCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAAGGGGT 1800
   GGGCACATTG GTGCTGTGTC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAATGTCA 1860
   CAATAAAGC AATGAATG

```

40 A125 Protein sequence:
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 Signal sequence: 1-30
 Pfam domains: TGFb_propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

```

50 1      11      21      31      41      51
   |      |      |      |      |      |
   MHVRSIRAA PHSFVALWAP LFLRLSALAD PSLDNEVHSS FIHRRRLRSQ RREMQRILS 60
   ILGLPERPRP HLQCKENSAP MFMLDLYNAM AVEEGGGPGG QGFSYPYKAV FSTQGPPLAS 120
55 LQDSHEFLTD DMVMSFVNLV EHDKEFPFHR VHHREPRFDL SKIPEGEAVT AAEFRYKYD 180
   IRERFDNETF RISVYVQLQE HLGRESDLFL LDSRTLWASE EGMVLFVDITA TSNHVVVNPR 240
   HNLGLQLSVE TLDGQSINPK LAGLIGRHGP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
   QNRSKTPKQK BALRMANVAE NSSSDQRQAC KKHELYVSFR DLGWQDNIIA PEGYAAYICE 360
60 GBCAFPLNSY MNATNHAIVQ TLVHFINPET VEPCCAPTQ LNAISVLYFD DSSNVILKKY 420
   RNMVVRACCG H

```

65 A126 DNA SEQUENCE
 Gene name: integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

```

70 1      11      21      31      41      51
   |      |      |      |      |      |
   CCCAGAGCCG CCTCCCCCTG TGTCTGGCAT CCCGAGCTTC CTCCCTTGCC AGCCAGGACG 60
   CTGCGGACTT GTCTTTGCCC GCTGCTCCGC AGACGGGGCT GCAAGCTGCG AACTAATGGT 120
   GTTGGCTCTC CTGCCACCTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTTT 180
   TCCCTCGAC CTCCCGCGCG TACCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
75 TAGGGTGGTT TCCGCCCGG CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
   CTAAGCTGAT TTATGCAACA GAAGCCACG CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
   TGTCCCGGAG CAGGCTCGCG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCC GCCGGGCCCT 420
   TGGCGTCTGA AGGAGGTGCT TCTCGCGGAG ACCCGGGGAC CCGCGTGCAG GAGCCGGGAG 480
   GGCCTGAGGG GCCCTGAGAT GCCGAGCGGT GCCCGGGGCC GCTTACCTGC ACCGCTTGCT 540
80 CCGAGCCGCG GGGTCCGCTT GCTAGGCTCG CGGAAACGCT CTAAGCGACA CTGCCCCGCG 600
   GGCCTCCGAG TCGCCCGGGA GGCAGAGCCC GCGTCCGGAA GGCAGCCAGG CGCGGGGCGC 660
   GGGGGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGCG TTTTTTTACC GCTGCATTTG 720
   TCTGCTGCA AAACGACCGG CGAGGTCCCG CTCTGTTCTT CTGGGACGCC TGGGTGTTTT 780

```

5 CACTTGTCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCCCTGGC CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900
 TTTCAAGTGG ATCAAGAAGT GAACGTTGTG ATATTGTTTC CAATTTAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA 1020
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTTATGCT GAAAGTTTCT CCTCTGAAGA AATATCCTGT GGATCTTTAT TATCTTGTG 1140
 ATGCTCTCAGC ATCAATGCAC AATAATATAG AAAAAATAAA TTCCGTTGGA AACGATTTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCCGTGACT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260
 10 AAACAGTTTC ACCATCAATT AGCATCCACC CCGAAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTTAGA CTGCATGCCT CCCCATGGAT ACATCCATGT GCTGTCTTGG ACAGAGAACAA 1380
 TCACGTAGGT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACCCAG 1440
 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGTGTATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560
 15 GCAAAATGGC AGGCATAGTG GTGCCCAATG ACGGAACTG TCATCTGAAA AACAACTGCT 1620
 AGTCAAATG GACAACCATG GAACCCCTCT CACTAGGCCA ACTTCAGAG AATTAATAG 1680
 ACAACAATC TAATGTCAT TTTGAGTTT AAGGAAACA ATTCATTGG TATAAGGATC 1740
 TTCTACCCCT CTGTCAGGC ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800
 ATAATTTGGT AGTGGAGGCC TATCAGAAGC TCATTTTCAA AGTGAAGATT CAGGTGSAAG 1860
 20 ACCAGGTACA AGCATCTTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
 CAGGATGGA AGGATGCAGA AAGTGACGA GCAATGATGA AGTCTTTTC AATGTAAACAG 1980
 TTCAATGAA AATATGTCAT GTCAAGGAG GAAAAAATA TGCAATATC AACCTATTG 2040
 GTTTAATGA AACCGCTAAA ATTCATATAC ACAGAACTG CAGCTGTCTG TGTGAGGACA 2100
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTTC AGATTCCAAG TGTCTCCAGT 2160
 25 GTGATGAGAA TAAATGTCAT TTTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220
 ACAAGGATCA GCCTGTTTGC AGTGGTGGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280
 ACAAAATTA GCTTGGAAAA GTGTATGGA AATACGTGA AAGGATGAC TTTCTTGTG 2340
 CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
 30 TCAATTCAAA GGGCCAAAGT TGCAAGTGA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
 GCACGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
 GCAAGGAAA CTGGAATTGT ATGCAATGCC TTCACCTCA CAATTTGCTC CAGGCTATAC 2640
 TTGATCAGTG CAAAACCTCA TGTGCTCTCA TGGAAACACA GCATTATGTC GACCAAACTT 2700
 CAGAATGTTT CTCACGCCCA AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
 35 TCTGATGTT GTTGCTTAAA GTCCCTGATCA TTAGACAGGT GATACTACAA TGGAAATAGTA 2820
 ATAAATTAAT GTCTCATCA GATTACAGAG TGTGAGCTC AAAAAAGGAT AAGTTGATTC 2880
 TGCAAGTGT TTGCACAAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTCTTAA AAAAAAGATT 3000
 TTAACACTT AATGGGAAAC TGGAAATGTT AATAATTGCT CTAAGAGATT ATAATTTTAA 3060
 40 AAGTCACAG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGGTTGT AACTCGAAC 3120
 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
 AAAATGTGTC TTAATCTGT TTGAGACTAG TGTGTTGTA GCACITTAAT GTAATATATA 3240
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
 TACCTGTTAT CCCTACGCTT CCCAGAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360
 45 CACTACAAGG GTACAGTAAT CCCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAAG 3420
 TATATTCTAA GGTTCGCAAA CACTTCAACA GTTGGTGGTT GAATAGACAA GAACAGCTAG 3480
 ATGAATAAAT GATTCGTGTT TCACCTTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
 AAGATTATT GCTTTTAAA GTGTGATGTT TTATGCATGT GTGTTTATGG TTTGCTTATT 3600
 TTTGCAAGAT GGATACTAAT TCCAGCATTC TCTCTCTTT GCCTTTATGT TTTGTTTCT 3660
 50 TTTTACAGG ATAAGTTTAT GTATGTACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
 TACTGCCATA AAAAATAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
 GAATGTAA

55 **A127 Protein sequence:**
 Gene name: Integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Protein Accession #: NP_002205.1
 60 Signal sequence: 1-39
 Transmembrane domains: 682-704
 EGF domain: 552-584
 INB domain: 54-469
 Cellular Localization: plasma membrane

65
 1 11 21 31 41 51
 70 MCGSALAFPT AAFVCLQND RGPASFLWAA WVFSVLVLGL QGEDNRCASS NAASCARCLA 60
 LGPECGWCQV EDFISGGSRS ERCDIVSNLI SKGCSVDSIE YPSVHVIIPT ENEINTQVTP 120
 GEVSIQLRPG AEANFMLKVH PLKYPVDLY YLVDVSASMH NNIEKLSVVG NDLSRMAFF 180
 SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDYNLDCMP PHGYIHVLSL TENITEFEKA 240
 VHRQKISGNI DTPEGGFDAM LQAAVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLAGIV 300
 75 VPDNGNCHLK NNIVVKSTTM EHPSLGQLSE KLIDNNINVI FAVQKQFHW YKDLLPFLPG 360
 TIAGEIESKA ANLNLVVEA YQKLISEVKV QVENQVQGIY FNITAIICPDG SRKPGMEGCR 420
 NVTSNDEVLF NVVTIMKKCD VTGKKNYAI KPIGFNETAK IHIHRNCSQ CENDRGPKGK 480
 CVDETFLDSK CFQCDENKCH FDEDQFSSES CKSHKDQPV C SGRGVCVCGK CSCHKIKLKG 540
 VYGKYCEKDD FSCPYHNGNL CAGHGECEAG RQCFSGWEG DRQCPSAAA QHCNVNSKQV 600
 80 CSGRGTVCVG RCECTDPRS GRFCEHCPTC YTACKENWNC MQCLHFNLS QALLDQCKTS 660
 CALMEQOHYV DQTECFSSP SYLRIFFLIF IVTFLIGLLK VLIIRQVILQ WNSNKKIKSS 720
 DYRSASKKD KLILQSVCTR AVTYRREKPE EIKMDISKLN AHETPRCNF

A128 DNA SEQUENCE

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942
 Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5

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1      11      21      31      41      51
10    AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
      CTCGGGTGCA GGATGGTTTT CTCTGTGTCAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
      GTTTTACTGA CGTTCAAGAT ATTCCTTGTC ATCATTGTGC TTATGTCGT TCTGGTAACA 180
      TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTCAACCAC CACCTGCTAA ATTATCTGTT 240
      GTCAGTTTTG CCCCTCCTC CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTA 300
      AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAAATCA CTATAGTAAA AACCTTCAAT 360
15    GCTTCAGGCG TCAAAACCCA GAGAAATATC TGCAATTGTG CATCTATTG CAATGACTCA 420
      GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCCAGAAT 480
      CAACATATAA GGAATGGCAC CTAACTGGGA GTCCTGTCTC TAAGTGAATT AAAACGCTCA 540
      GAGCTCAACA AAACCTTGCA AACCTTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
      GAGGCCCAAA GCACATTAAA TTGTACATTG ACAATAAAAC TGAATAATAC AATGAATGCA 660
20    TGTGCTGCAA TAGCCGCTTT GGAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
      TCTGTACAGG TACCTGCCCC TTCTTCCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
      CAGGATCCCA TTGCTGTCTT TGCTGACCAT CCACGTGGCC CACCATTTTC TTCCAGCCAA 840
      TCCATCCCAG TGGTGCTCTG GGCCACTGTG CTTCCTCCAG TCCCCAAAGC TACCTCTTTT 900
      GCTGAGCTTC GATGATTATC ACCTGTGACC CACAATGTTC CTCTCCAAT AGGGGAGATT 960
25    CAACCCCTTT CACCCAGGCC TTCAGCTCCC ATAGCTTCCA GCCCTGCCAT TGACATGCCC 1020
      CCACAGTCTG AAACGATCTC TTCCCCTATG CCCCACACCC ATGTCTCCGG CACCCACCTC 1080
      CCGTGAAAG CTCAATTTTC CTCTCCACC GTGTCTGCCC CTGCGAATGT AACACTACCT 1140
      AGCGCACTCT CTGTCCAGAC AGACATGCTC AACACCAGCA GTATTCTGTA TCTTGAGAAC 1200
      CAAGTGTGTC AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCTTAA CCTCGCAGGA 1260
30    GAAATGATCA ACCAAGTCAG CAGACTCCTT CATTCCCCGC CTGACATGCT GGCCCTCTG 1320
      GCTCAAGATG TGCTGAAGAT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAAACAG 1380
      ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
      TTCAACCAA CTACCTTTGT GGCCCAAGAC CCTGCAAAATC TTCAGGTTTC TCTGGAACCC 1500
      CAAGCTGCTC GATGAGTATG TGGCACAATT ACTCTTCCTT CATCGCTGAT GAATAATTTA 1560
35    CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTTTTGA AACACCTGCT 1620
      TTGTTTCAGG ATCTTCCCTT GGAGAACCTC TCTCTGATCA GCTACGTGAT ATCATOGAGT 1680
      GTTGCAAACT TGAACGTCAG GAACCTTGCA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
      AACCCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGCT 1800
      GGCAGAGGAG CTGTGTGAGA CAATGGCTGC TCTGTCAAAG ACAGGAGATT GAATGAACCC 1860
40    ATCTGTACCT GTAGCCATCT AACAGCTTC GCGGTCTGTC TGAACCTATC TAGGACATCT 1920
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      TCAATTTTTT TGTCTGTCAG TCTTGTAAAC TACATAGCTT TTGAAAAGAT CCGGAGGGAT 2040
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      CTCTGCTGCT GATGAGTTAG TCTGTATAAG ATGCAAGGCC TCTGCTCTC AGTGGCTGTA 2160
45    TTTCTTCATT ATTTCTCTT GGTCTCATC ACATGATGAG GCCTAGAAGC ATTCATATG 2220
      TACCTGGCCC TTGTCAAAGT ATTTAATACT TACATCCGAA AATACATCCT TAAATCTGCT 2280
      ATTGTGCGTT GGGGGGTACC AGCTGTGTTT GTGAACATCA TCCTGACTAT ATCCCGAGAT 2340
      AACTATGGGC TTGGATCTTA TGGGAAATTC CCAATGGTTT CACCGGATGA CTCTGCTGCT 2400
      ATCAACAACA CTGACGATTT CTACATTACG GTGTGGGAT ATTTCTGTGT GATATTTTTG 2460
50    CTGAACGTCA GCATGTTTAT TGTGGTCTGT GTTCAGCTCT GTGCAATTAA AAAGAAGAAG 2520
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      CACAATGTGA GATGTATGAA AATCAACTCA TTTTATTCTC GGCAACATCT GGAGAAGCAT 3240
      AAGCTAATTA AGGGCGATGA TTATTATTAC AAGAAGAAAC CAAGACATTA CACCATGGTT 3300
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      TTATTAGGAA CATTTCAAAC CCTTTTAGT TAAGTCTTTC ACTAAGGTTT TCTTGATATC 4500
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CTGACTTGTC TTGCAATAT TTCTTTCTCG ATTATTTAA TTTTCTGTGA TTTATATGTT 4620
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5 A129 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

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 GEIMFQYDKE STVPQNHQIT NGTLTGVLSL SELKRSELAK TLQTLSETYF IMCATAEAQS 180
 TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240
 VCLADHPRGP PPSSSQIPV VPRATVLSQV PKATSFAEPF DYSFVTHNVP SPIGEIQPLS 300
 PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTPPPVKA SPSSPTVSAP ANVNTTSAPP 360
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 NSIGTITLPS SLMNPLPAHD MELASRVQFN EFETPALFQD PSLENLSLIS YVSSSVANL 540
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 SHLTSFQVLL DLSRTSVLPA QMMALTFITY IGCGLSIFL SVTLVYTIAP EKIRRDYPSK 660
 ILIQLCAALL LNLVFLLLS WIALYKMQGL CISVAVFLHY PLLVSTWVG LEAFHMYLAL 720
 VKVFNTYIRK YILKFCIVGW GVPVAVVTII LTISPDPNYGL GSYGKPFNGS PDDPCWINNN 780
 AVFYITLVGY FCVIFLLNVS MFIVVLVQLC RIKKKQLGA QRKTSIQDLR SIAGLTFLLG 840
 ITWGAFFAW GPNVNTFMYL FAIFNTLQGF FIFIFYCVAK ENVRKQWRRY LCCGKRLAE 900
 NSDWSKIATN GLKKQTVNQV VSSSSNSLQS SSNSTNSTTL LVNNDCSVHA SGNGNASTER 960
 NGVSPSVQNG DVCLHDFTGK QHMFNEKEDS CNGKGRMALR RTSKRGSLEH IEQM

35 A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Probeset Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
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 GGCCCCCTAC TTGGGGCACC ATGGACACCT CCCGCTCGG TGTGCTCCTG TCCTTGCCCTG 240
 TGCTGCTGCA GCTGGGAGAC GGGGGCAGCT CTCCAGGTC TGGTGTGTG CTGAGGGGCT 300
 GCCCACACCA CTGTCAATTG GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG 360
 ACCTGGGGCT CTGGAGCTG CCTTCCAACC TCAGCGTCTT CACCTCTTAC CTAGACCTCA 420
 GTATGAACAA CATCAGTCAG CTGCTCCCGA ATCCCTGCC CAGTCTCCG TCTCTGGAG 480
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 CCTGAACAA AATACACCAC ATACCAAGCT ATGCTTTTGG AAACCTCTCC AGCTTGGTAG 840
 TTCTACATCT CCATAACAAT AGAATCCACT CCCTGGGAAA GAAATGCTTT GATGGGCTCC 900
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 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

A131 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

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1 11 21 31 41 51
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 LQNNQLRHVP TEALQNLRLSL QSLRLDANHI SYVPPSCFSG LHSRLHLWLD DNALTEIPVQ 180
 AFRSLALQA MTIALNKIHH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLETL 240
 LNYNLDLDFP TAARTLSNLK ELGPHSNIR SIPEKAFVGN PSLITIHFYD NPIQFVGRSA 300
 FOHLPELRTL TLNGASQITE FPDLTGTANL ESLTLTGAQI SSLPQTVCNQ LPNLQVLDLS 360
 YNLEDLPSF SVQCKLKQKD LRHNEIYEIK VDTFQQLLSL RSLNLAWNKI AIHFNAPST 420
 LPSLIKLDLS SNLSSFPPI GLHGLTHLKL TGNHALQSLI SSENFPPELV IEMPYAYQCC 480
 AFGVCNAYK ISNQWNKGDN SSMDDLHKRD AGMFAQQDER DLEDFLLDFE EDLRALHSVQ 540
 CSPSPGPPKP CEHLLDGLWLY RIGVNTIAVL ALTCLALVTS TVFRSPLYIS PIKLLIGVIA 600
 AVNMLTGVSS AVLGAVDATF FGSFARHGA WENGVGCHVI GFLSIFASES SVFLLTLAAL 660
 ERGFSVKYSA SFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGE 720
 STMGYMAVLI LLNSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC 780
 PVAFLSPSSL INLTFISPEV IKPILLVVVP LPACLNPLLY ILFNHFKED LVSLRKQTYV 840
 WTRSKHPSLM SINSDDVEKQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
 VAFVPLCL

A132 DNA SEQUENCE

Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Probeset Accession #: U25128
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
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 ATACTCTCTAT GCTTGAGTTC AAAGGCTGAA AATTCACTTA AGGTGTTACT TAATAATAGT 1920
 TTTTAGGCTC CATGAATTGG CTCTGTAAA TACTAACGAC ATGAAAATAC AAGTGTCAAT 1980

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T

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A133 PROTEIN SEQUENCE

Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Protein Accession #: NP_005039.1
 Signal sequence: 1-25
 Pfam domain: 7tm_2 [141-420]
 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MAGLGASLHV WGLWMLGSLC LARAQLDSDG TITIEQIVL VLKAKVQCEL NITAOQEGB 60
 GNCFPEWDGL ICHFRGTGVK ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMHSINKTWA 120
 NYSDCLRFLO PDISIGKQEP FERLYVMYTV GYSISFGSLA VAILIIGYFR RLHCTRNYIH 180
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 LADARCWELS AGDIKKIYQA PILAAIGLNF ILFLNTVRVL ATKIWNNAV GHDTRKQYRK 360
 LAKSTLVVLV VFGVHYIVFV CLPHSPTGLG WEIRMHCELF FNSPQGFVVS ILYCYCNGEV 420
 QAEVKQWMSR WNLSDVMKRT PPCGSRRCGS VLTITVTHSTS SQSQVAASTR MVLISGKAOK 480
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 GCGGETEDVL

A134 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251.
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCGCGCT GATTCGCGC CCAGCAGCAG 240
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 CTGGTGGCAG CCTGTGCTG CAGATGTCTC CGGCCTAAGC AGGATCCCCA GCAGAGCCGA 1320
 GCCCCAGGGG GTAACCGCTT GATGAGAGAC ATCCCATGTA TCCCGAGTGC CAGCACCTCC 1380
 CGGGGGTGTG CCTCAGCCCA GTCCAGCACA GCTGCCAGTT CCAGCTCCGA CGCCAACTCC 1440
 GGGGCGCGGG CGCCCCCAAC AAGGTACAG ACCCACTGTT GCTTGCCGGA AGGGACCATG 1500
 AACCAAGTGT ATGTCAACAT GCCCAAGAA TTCTCTGTGC TGAACGTGCA CAGGCGCACG 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCCAT ACGTGGGGTA CACGGTGCAG 1620
 CAGACTCTGT TGCCCATGAC AGCTGTGCCA CCTTTCTAGG ACGGCCTGCA GCCTGGCTAC 1680
 AGGCAGATTC AGTCCCCCTT CCCTCACACC AACAGTGAAC AGAAGATGTA CCCAGCGGTG 1740
 ACTGTATAAC CGAGAGTCAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTGAG GTGCAAGTCC GCACATGTGG GTGGTATTTA TGGCAGATT CCTTTGATG 1860
 GCTTCATTTG CCCCAGACT GTATGAAAAC ATCTCCGAAT TAGCATTTCT GGATATGTTT 1920
 CATCCAGGGT ATCATTGATT TATGATGGAA AACCGGCTCT AGCTGGAGAT GACTGTGATG 1980
 TTGCTGATGG GTGTATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGACGA 2040
 AAGAAATTTA TAACTGATA AATTAAGGAT TTTTATTATG TTGTTATPAT TATTTCTTTT 2100
 TTGTTGTTGA CTGACAGGA TCAAAATGCC TGTATCTTCC CTTTACTTGG GACTTTTITT 2160
 TTTTTTTTTT TTTTTTTTAA TCAGACAGGG TCTTGCTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGGGATC TGGGCTCACT GCACTTCAG CCTCTGGAT TCAGGCAACA CTCCTGCCTC 2280
 AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCAT GGCTAATTTT TTGATTTTTT 2340

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TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
TCGCGCTGTC TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
TGAGCCTTTT TTTTCTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAA TAACAGGACT 2520
ATTCTAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCCACA 2580
GGCACACCTT AATTTCATTG TAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
GGGCTATTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTACA 2700
TTAAAAGAG ACTGAAATAA ATTGTATAGT TACTTAACTA ATGAAGACAT TTCAGAACTC 2760
TGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCACTT CATCCCTTC 2820
TTGATGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880
TATATTGAAA TCATAAATA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
TGGTTATGGT TTGGCGTTTC CTCTCTGTTG GTTTTCAGAG CCCATGTCT ATATAGTCT 3000
GAGTGCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCCTA GATCTGATAA 3060
AAAAATTTTC TTGCTTAGT TATAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
TAGCTCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTT 3180
GCAGATCATA AGGCTTTTAT TACTCTTGT ATCAAAATGG CTTATTTTTC AGGCACTAAG 3240
GATTGTAAAG AGAAAAGCTT TTCAACGAAG GATTCGCTTT CTCTCCAC ACTGTTCTTG 3300
ATTCTCTCTC TCTTTCAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
CAATCTCAAG TGAATTTAT TTGTGTCTCT TTACTTATAT AAAAAAGAT AACTTTAAGG 3420
ATGTGCAAGT ACATTTCCAA CTGCTAGCAC AACCAGTATT TTGTAATTA ACAAATCGCT 3480
GTATGTATG GTCTTCTACA CATTATATG TATAGATATC TATCGATCAT CTTTCTATTC 3540
TGTTCATGA CTGAATAATG TAAAACCAAG GTTGGCAATT GGTATCATCA ATGATACTCA 3600
TTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAAAA AAAAAAATA AAAAAAATA

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A135 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

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1 11 21 31 41 51
| | | | |
MLSGFLMSPS TQHRAQYTPG GKLPWEASI GAHTSRGRGS DRERESRPEA AGLLNDRAAA 60
GEAEKGNRGE PPANIRAQQQ PRPPAPGQAP GTAAGGAQDP RLRPGRSRGR VRLPVKPPEA 120
SGRQPRGPD CIPRFPSASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSG 180
PRGKRRTVS DEARGSPGPR LLGDRPALSG DALSAFVRVP CGALAARPSF HPGTPLRSCS 240
CCWLRCAWRG RGPSSGEYCHG WLDAQGVNRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
ARLDQGGCDN DRQQGAGEPG RADKDGPRRL GRASCLRGTQ GDGEGAPFV RAWQRCSPG 360
SPKGRQLLRA PGLLPFRARR RGPSSSPRGG PSPLQRPALP IYVPLIVGS VFVAFIILGS 420
LVAACCCRCL RPKQDPQQR APGGRNLMET IPMIPASSTS RGSRRQSST AASSSSSSNS 480
GARAPFTRSQ TNCCLPBGTM NNVYVNMPTN FSVLNCQQAT QIVPHQGGYL HPFYVGYTVQ 540
HDSVPMTAVP PFMDLQPGY RQIQSPFPHT NSEQMKYPAV TV

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A136 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTAA AGAGAGTGGA 60
GCTTGGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
CAGCAAAAGT ACACACACCT GGTGTCAATT CAAAACAAG AAGAGATTGA GTACCTAAAC 180
TCCATATTGA GCTATTACCC AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
TGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
GAACCCAACA ATAGGCAAAA AGATGAGGAC TGCGTGGAGA TCTACATCAA GAGAGAAAAA 360
GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
GCTGCTGTA CCAATACATC CTGCACTGGC CACGCTGAAT GTGTAGAGAC CATCAATAAT 480
TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAAT TGTGAACCTG 540
ACAGCCCTGG AATCCCTGGA GCATGGAAGC CTGCTTGGCA GTCAACCACT GGGAACTTC 600
AGCTACAATT CTTCCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
ACCATGCGAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCCCTGA 780
AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGGA ACTAATGGGA 840
GCCAGAGGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTT CAGCCATTCC 960
CCTGCTGAGG AGTTTCACTT CAAATCATCC TGCAACTTCA CTTGTGAGGA AGGCTTCATG 1020
TTGCAGGAC CAGCCCAAGT TGAATGCACC ACTCAAGGCG AGTGGACACA GCAAATCCCA 1080
GTTTGTGAAG CTTTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
CTTCTAGTGT CTCTGCGCAG TTTCCGTTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200
GGTTTTGTGT TGAAGGGATC CAAAGGCTC CAATGTGGCC CCACAGGGA GTGGGACAAC 1260
GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCC GAAGGGTTTG 1320
GTGAGGTGTG CTATTCCCC TATTGGAGAA TTCACTTACA AGTCTCTTG TGCCTTCAGC 1380
TGTGAGGAGG GATTTGAATT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
TGGACAGAAG AGGTTCCCTC CTGCCAAGTG GTAAAATGTT CAAGCCTGGC AGTTCGGGA 1500
AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGGCA CTGTGTGCAA GTTCGCCCTG 1560
CCTGAAGGAT GGAACGCTCAA TGGCTCTGCA GCTGGACAT GTGGAGCCAC AGGACACTGG 1620
TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
CTTCTGCTG CTGAGCTCTC CCTCTGACA TTAGCACCAT TTCTCCTCTG GCTTCGGAAA 1740

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TGCTTACGGA AAGCAAAGAA ATTTGTTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

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A137 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

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1	11	21	31	41	51	
MIASQFLSAL	TLVLLIKESG	ANSYNTSTEA	MTYDEASAYC	QQRVTHLVAI	QNKEEIEYLN	60
SILSYSPSY	WIGIRKVMNV	WVWVGTOKPL	TEEAKNWAPG	EPNNRQKDED	CVBIYIKREK	120
DVGMWNDERC	SKKHLALCYT	AACINTSCSG	HGECVETINN	YTCKCDPGFS	GLKCEQIVNC	180
TALESPEHGS	LVCSHPLGNF	SYNSSCSISC	DRGYLPSSME	TMQCMSSGEW	SAPIPACNVV	240
ECDAVTNPAN	GFVECFQNP	SFPWNTTCTF	DCEBGFELMG	AQSLQCTSSG	NWDNEKPTCK	300
AVTCRAVRQP	QNGSVRCSHS	PAGEFTFKSS	CNFTCEEFGM	LQGPAAVECT	TQGQWTQQIP	360
VCEAFQCTAL	SNPERGYMNC	LPSASGSFRY	GSSCFSCCEQ	GFVLKGSKRL	QCGPTGEWDN	420
EKPTCEAVRC	DAVHQPFGKL	VRCASHPIGE	FTYKSSCAFS	CEEGFELYGS	TQLECTSQGQ	480
WTEEVPSQVQ	VKCSLAVPG	KINMSCSGEP	VFGTVCKFAC	PEGWTLNGSA	ARTCGATGHW	540
SGLLPTCEAP	TESNIPLVAG	LSAAGLSLLT	LAPFLLNLRK	CLRKAKKFPV	ASSCQSLESD	600
GSYQKPSYLL						

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A138 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51	
CGGCACCAAG	AGCACTGGCC	AAGTCAGCTT	CTTCTGAGAG	AGTCTCTAGA	AGACATGATG	60
CTACACTCAG	CTTTGGGTCT	CTGCTCTTTA	CTGTCACAG	TTTCTTCCAA	CCTTGCCATT	120
GCAATAAAAA	AGGAAAAGAG	GCCTCCTCAG	ACACTCTCAA	GAGGATGGGG	AGATGACATC	180
ACTTGGGTAC	AAACTTATGA	AGAAGGTCTC	TTTTATGCTC	AAAAAAGTAA	GAAGCCATTA	240
ATGGTATTTC	ATCACCTGGA	GGATTGTCAA	TACTCTCAAG	CACTAAAGAA	AGTATTTGCC	300
CAAAATGAAG	AAATACAAGA	AATGGCTCAG	AATAAGTTCA	TCATGCTAAA	CCTTATGCAT	360
GAAACCACTG	ATAAGAAATT	ATCACCTGAT	GGCAATATG	TGCCTAGAAT	CATGTTTGTA	420
GACCTTCTCT	TAACAGTTAG	AGCTGACATA	GCTGGAAGAT	ACTCTAACAG	ATTGTACACA	480
TATGAGCCTC	GGGATTTACC	CCTATTGATA	GAAGACATGA	AGAAAGCATT	AAGACTTATT	540
CAGTCAGAGC	TATAAGAGAT	GATAGAAAAA	AGCCTTCACT	TCAAAGAAGT	CAAATTTTCA	600
GAAGAAACCC	TCTGGCACAT	TGACAAATAC	TAAATGTGCA	AGTATATAGA	TTTTTGTATA	660
TTACTATTTA	GTTTTTTTAA	TGTGTTTGCA	ATAGTCTTAT	TAAAAATAAT	GTTTTTTAAA	720
TCTGAAAAAA	AAAAAAAATA	AAAAAAAATA				

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A139 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

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1	11	21	31	41	51	
MMLHSALGLC	LLLVTVSSNL	AIAIKKEKRP	PQTLRSGWGD	DITWVQTYEE	GLFYAQKSKK	60
PLMVIHLED	CQYSQALKKV	FAQNBEIQEM	AQNKFIMLNL	MHETTDKNLS	PDGQYVPRIM	120
FVDPSLTVRA	DIAGRYSNRL	YTYEPRDLPL	LIENMKKALR	LIQSEL		

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A140 DNA SEQUENCE

Gene name: TMPRSS3a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Nucleic Acid Accession #: AB038157
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51	
ACGGGGCACC	GGACGGCTCG	GGTACTTTGG	TTCTTAATTA	GGTCATGCCC	GTGTGAGCCA	60
GGAAAGGGCT	GTGTTTATGG	GAAGCCAGTA	ACACTGTGGC	CTACTATCTC	TTCCGTGGTG	120
CCATCTACAT	TTTTGGGACT	CGGGAATTAT	GAGGTAGAGG	TGGAGGCGGA	GCCGGATGTC	180
AGAGGTCTCT	AAATAGTCA	CATGGGGGAA	AATGATCCGC	CTGCTGTGTA	AGCCCCCTTC	240

5 TCATTCCGAT CGCTTTTGG CCTTGATGAT TTGAAAAATA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGGAAGT ACAGATGTGG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
 AAGGGTCACT AGCAAAATGT TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTCCATCGAT 720
 10 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCCCTCG GCCACGTGGT TACCTTGCGA TGCACAGCCT GTGGTCATAG AAGGGGCTAC 840
 AGCTCAGCCA TGGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
 CTTCACTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTC GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
 15 CTAGTTTCCC TGTTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCA 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCAGGGCCA 1140
 CTCAGCTTGC ATGAATATGT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACTTCCCC 1200
 GATGGAAGAG TGTGCTGGAC GTCAGGATGG GGGGCCACAG AGGATGAGC AGGTGACGCC 1260
 TCCCTGTGCC TGAACCAAGC GGCCTGCTCT TTGATTTCCA ACAAGATCTG CAACCAACAG 1320
 20 GACGCTGACG GTGGCATCAT CTCCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCCTGCTGTG GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGC TGTGTTTCTT CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
 TACACCCGTG TCACCTCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
 ACCTGAGAGG GAGGGGGACA AGTAGCCACC TGAGTTCTTG AGGTGATGAA GACAGCCCGA 1620
 25 TCCTCCCTCG TAGTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTGG GAGCTCTGAG 1680
 TTCCGGCACC AGTAGCAGGC CCGAAGAGG CACCTTCCA TCTGATTCCA GCACAACCTT 1740
 CAAGCTGCTT TTTGTTTCTT GTTTTCTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
 AGTGACAGTG CGAAATCCCT GCTCACTGCA CCCTCGCTT CCCTGGTTCA AGCGATTCTC 1860
 TTGCTCTAGC TTCCCGAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCT CAACTAATTT 1920
 30 TTGATTCTTT AGTAGAGACA GGGTTTCACT ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
 CCTCAAATGA TGTGCTGCTC TCAGCTCCTC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
 AGCCTAGGCC TCACGCTCCT TCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 AGGGCGGCTT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
 ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
 35 GCACCAAGCC AGAAGTGACG AACTGCAGTC ACTGCACTG TTCTATCTTA GGGACCCAGAA 2280
 CCAAACCCAC CCTTCTACT TCCAAGACTT ATTTTACAT GTGGGAGGT TAATCTAGGA 2340
 ATGACTCGTT TAAGCTCTAT TTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
 TTGCTCTTTG ATTTCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAATA AAAAAAATA 2460
 AAAAAAATA

40 **A141 Protein sequence:**
 Gene name: TMPSR33a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 45 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

50
 1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLPLKFFP IIVIGIILI 60
 55 LALAIGLGIH FDCSGKYRRC SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVILQVF 120
 TAASWKTMCs DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHHSVIV REGCASHVIV TLQCTACGHR RGYSSRIVGG NMSLLSQWPW QASLQFGYH 240
 LCGGSVITPL WIITAARCVY DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMLK AGPLTFNEMI QPVCLPNSSE NFPGDKVCWT SGWGATEDGA GDASPVLNHA 360
 60 AVPLISNKIC NHRDVYGGII SPSMLCAGYL TGGVDSQGGD SGGPLVCQER RLWLKLVGATS 420
 FGIQCAEVNK PGVYTRVTSF LDWIHEQMER DLKT

65 **A142 DNA SEQUENCE**
 Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

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 1 11 21 31 41 51
 | | | | |
 CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
 75 CTGAGATCTCT TGCCTAGCT ACATCTCAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
 CGGCTGCTCC TATTGCTGAG CTGCCCTGCC AAAACAGGAG TCTGGGTGA TATCATCATG 180
 AGACCCAGCT GTGCTCTCGG ATGGTTTAC CACAAGTCCA ATTGCTATGG TTAATTCAGG 240
 AAGCTGAGGA ACTGGTCTGA TGCCGAGCTC GAGTGTCACT CTTACGAAA CCGAGCCAC 300
 CTGGCATCTA TCCTGAGTTT AAAGGAAGCC AGCACCATAG CAGAGTACAT AAGTGGCTAT 360
 80 CAGAGAAGCC AGCCGATATG GATTGGCTG CAGACCCAC AGAAGAGGCA GCAAGTGGCAG 420
 TGGATTGATG GGGCCATGTA TCTGTACAGA TCCTGGTCTG GCAAGTCCAT GGGTGGGAA 480
 AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTTGGAGCAG CAACGAATGC 540
 AACAAAGGCC AACACTTCTT GTGCAAGTAC CGACCATAGA GCAAGAATCA AGATTCTGCT 600
 AACTCTGCA CCAGCCCGT CCTCTTCTT TCTGTAGCG TGGCTAAATC TGCTCATTTAT 660
 TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGGCC CTACTACACT GGCTTTTTTA 720

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GGCTTAGAGA CAGAACTTT AGCATTGGGC CAGTAGTGG CTCTAGCTC TAAATGTTG 780
CCCCGCCATC CCTTCCACA GTATCCTTCT TCCCTCCTCC CTGTCTCTG GCTGTCTCGA 840
GCAGTCTAGA AGAGTGATC TCCAGCCTAT GAAACAGCTG GGTCTTTGGC CATAAGAAGT 900
AAAGATTTGA AGACAGAAGG AAGAACTCA GGAGTAAGCT TCTAGACCCC TTCAGCTTCT 960
ACACCCTTCT GCCCTCTCTC CATTCGCTGC ACCCCACCCC AGCCACTCAA CTCCTGCTTG 1020
TTTTCTCTTT GCCCATAGGA AGGTTTACCA GTAGAATCCT TGCTAGTTTG ATGTGGGCCA 1080
TACATTCCTT TAATAAACCA TTGTGTACAT AAGAGAAAAA AAAAAAAAAA AAAAAAAAAA
  
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A143 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

1 11 21 31 41 51
 MASRSMRLLL LLSCLAKTGV LGDIIMRPSC APGWYFHKSN CYGYFRKLKN WSDALEECQS 60
 YNGGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQWQWIDG AMYLYRSWSG 120
 KSMGGNKHCA EMSSNNFLT WSSNECNKQ HFLCKYRP

A144 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

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GGGGAACACC GGGCCGCGGT GCGGCGAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
TCCCTCGTGG ACCCTCTCGCG TCTCTCCTCC TTCTCCAGGT TTGCTGGCTG CAGTGGCGGG 120
CCTCCGAGCC GTGCCGGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGAGGGCG 180
CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AAGTATTTCAT GGGCTGCCCT GGGCAAGAGC 240
CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGCG GAATGGCGAG ACAGTCCAGG 300
AAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
GRAGACAAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
ACAGCATCAC GGGGCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCGCT GTAGAGAAGG 540
AGACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GGAGATGGCC AAGTATGAGC 600
TCTTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGG GGACCCCATG AACATCTCCA 660
TCATCGTAGC CGACCAGAAAT GACCACAAGC CCAAGTTTAC CCAGGACACC TTCGAGGGGA 720
GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
ATGATGAGCT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCRA 840
AGGACCACA CGACCTCATG TTCACAATTC ACCGGAGCAC AGGCACCATC AGGCTCATCT 900
CCAGTGGCCT GGACCGGGA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
ACAATGCTCC CATGTTTGAC CCCAGAAAT ACAGAGGCCA TGTGCCTGAG AATGCAATGG 1080
GCCATCAAGT CGTTGAGGTC ACGGTCACTG ATCTGGACGC CCCCACTCA CCAGCGTGGC 1140
GTGCCACCTA CCTTATCATG GCGGTGACG ACGGGGACCA TTTTACCATT ACCACCCACC 1200
CTGAGAGCAA CCAGGCGCAT CTGACAACCA GGAAGGGTTT GGATTTTGAG GCCAAAAACC 1260
AGCACCACTG GTACGTTGAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACCT 1320
CCACAGCCAC CATAGTGATC CAGGTGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGCG GGAGCCTGTG TGTGTCTACA 1440
CTGCAGAGA CCTGACAAAG GAGAATCAA AGATCAGCTA CCGCATCCTG AGAGACCCAG 1500
CAGGCTGGCT AGCCATGGA CAGACAGTG GGCAGGTCA AGCTGTGGGC ACCCTGACCC 1560
GTGAGGATGA GCAATTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGGACA 1620
ATGGAAGGCC TCCACCAACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
ACCATGGCCC AGTCCCTGAG CCCCGTCAAG TCACCATCTG CAACCAAGC CCGTGTGGCC 1740
ACGTGCTGAA CATCAGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTC CAGGCCACG 1800
TCACAGATA CTCAGACATC TACTGGACG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
TCTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGACCTT TCTCTGTCTG 1920
ACCATGGCAA CAAGAGCAG CTGACGTTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
ATGTGAAAC CTGCCCTGGA CCCTGGAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
TCTTGCTCT GCTGTTCTCT CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGAAGA 2100
TCAAGGAGCC CCTCCTACTC CCAGAAGAT ACACCGTGA CAAGCTCTT TACTATGGCG 2160
AAGAGGGGGG TGGGGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
AGGCCAGGCC GGAGGTGGTT CTCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
AGGCGGCTAA CACAGACCCC ACAGCCCGCG CCTACGACAC CCTCTGGTG TTGACTATG 2400
AGGCGAGCGG CTCGACGCC GCGTCCCTGA GCTCCCTCAC CTCCCTCGCG TCCGACCAAG 2460
ACCAAGATTA CGATTATCTG AACGAGTGGG GCAGCCGCTT CAAGAAGCTG GCAGACATGT 2520
ACGCTGGCGG GGAGGACGAC TAGGCGGCCT GCCTGACAGG CTGGGGACCA AACGTGAGG 2580
CACAGGCTAT CTCCAAGGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTC 2640
GGAGTGGGCC GTAGCAACTT GCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
TCTTTAGCCT TTCAGGATGG AGGAATGTGG GCAATTTGAC TTCAGCACTG AAAACCTCTC 2760
CACCTGGGCC AGGTTTGCCT CAGAGGCCAA GTTTCAGAA GCCTCTTACC TGCCGTAAAA 2820
TGCTCAACCC TGTGTCTCTG GCCTGGGCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTITTTTT AATGCTATCT 2940
  
```

TCAAAACGTT AGAGAAAGTT CTTCAAAAGT GCAGCCCAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATT CTGGTTTCCA GACCCCAATG CCTCCCATC GGATGGATCT CTGCGTTTTT 3060
 ATACTGAGTG TGCCTAGGTT GCCCCTTATT TTTTATTTTC CTTGTTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACATCGTG TATATGTACT AGAAGCTTTT TATTAAAGAA A

A145 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675

Cellular localization: plasma membrane

1 11 21 31 41 51
 MGLPRGPLAS LLLLQVCWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMCPCG 60
 QEPALFSTDN DFDTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
 KGFPPQRLNQ LKSNKDRDTK IFYSITGPGA DSPPEGVFAV EKETGWLLEN KPLDREEIAK 180
 YELFGHAVSE NGASVEDPMN ISIIVTQDND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTYN GVVAISIHSQ EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
 TDMGDGSGTT TAVAVVEILD ANDNAFMFDP QKYEAHVPEV AVGHEVQRLT VTDLDPNSP 360
 AWRATYLMG GDDGDHFTIT THPESNQGLL TTRKGLDPEA KNQHTLYVEV TNEAPFVLKL 420
 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
 DPAGWLANDP DSQVTAAGT LDREDEQFVR NNIYEVMLA MDNGSPPTTG TGTLLLTLD 540
 VNDHGVPPEP RQITICNQSP VRHVLNITDK DLSPHTSPFQ AQLTDDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGHVETCPGP WGGGFIPLVL 660
 GAVLALLFL LVLILLVRKK RKIKEPLLLP EDDTRDNVYF YGEEGGGEED QDYDTQLHR 720
 GLEARPEVVL RNDVAPTIIIP TPMYRPRPAN PDEIGNFIE NLKAANTDPT APPYDTLLVF 780
 DYEGSGSDAA SLSSLTSSAS DQDQDYDYLW EWGSRFKKLA DMYGGEED

A146 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGAATTCCTT TTTTCTTTT TTTGAGATGG AGTTTCACTC TTGTTGGCCA GGCTGGAGTG 60
 CAATGGCACA ATCTCAGCTT ACTGCAACCT CGCCTCTCCG GGTTCAGCG ATTCTCTGTC 120
 CTGAGCTCTT CAAGTAGCTG GGAATTACAG CATGTGCCAC CACCCCTGGC TAACATAATT 180
 CTTTCTTATT TAGTAGAGAT GGGGTTTCAC CATGTTGGTC AGGCTGGTCT TGAACCTCTG 240
 ACCTCAGGTG ATCCACTTGC CTGGGCTCC CAAAGTGCTA GGATTACAG CGTGAAGACT 300
 TGCTGGCTG ATTCTTTT TGTGTTGGA TTTTGAAGC AGGGTCTCCC TTGGTCGCC 360
 AGGCTGGAGT CGAGTGGTGC GATCTGGCT CACTATAACC TCCACCTCCT GGTTCACAGT 420
 GATCCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG CGGTGCACCA CCACACCCGG 480
 CTAATTTTGT TATTTTATT AGAGACAGGG TTTCAACATG TTGCCAGGC TGTCTCTCAA 540
 CTCTGGACT CAAGGGATCC GCCTGCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG 600
 AGTCACCATG CCTGACCTTA TAATCTTAA GTCAATTTT CTGCTCCATT TCTTCCCTAG 660
 GGTCTCTACA ACAATCTGC ATTAGCGGT ACAATAATCC TTAATTCAT GATTACACAA 720
 AGGAAGATGA AGTGATTCAT GATTAGAAA GGGGAAGTAG TAAGCCCACT GCACATCTCT 780
 GGATGATGAT CCTAAATCCA GATACAGTAA AAATGGGGTA TGGGAAGGTA GAATACAAAA 840
 TTTGGTTTAA ATTAATATC TAAATATCTA AAAACATTTT TGGATACAT GTTGATGTGA 900
 ATGTAAGACT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960
 TGCAGTTTTC TGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAATTG ACAATTGATT 1020
 CCATAATGAA CAAGTGAGAG GACATTAAAA ATAAGTTTAA AAATGAAGAC CTTACTGATG 1080
 AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCCGGAACT GTTAAACCAA 1140
 TTATGATGAT GGCAACAAC CCAGAGGACT GGTGAGTTT GTTGCTCAA CTAGAGAAAA 1200
 ACAGTGTTC GCTAAGTGAT GCTCTTTTAA ATAAATTGAT TGGTCGTTAC AGTCAAGCAA 1260
 TTGAAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAAGTGA 1320
 GATTGCTGA ATTAAGAGC ATTCAAGAGC CAGATGATGC ACGTGACTAC TTTCAAATGG 1380
 CCAGAGCAAA CTGCAAGAAA TTTGCTTTG TCTATATATC TTTTGCAAA TTTGAACGTG 1440
 CACAAGGTAA TGTCAAAAA AGTAAACAAC TTCTTCAAAA AGCTGTAGAA CGTGAGCAG 1500
 TACCCTAGAG AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560
 TTTTCAAGGA GGAAGAAGAG AATTATATCAG CATCTACGGT ATTAAGTACC CAAGAATCAT 1620
 TTTCCGGTTC ACTTGGGCAT TTACAGAATA GGAACAACAG TTGTGATTCC AGAGGACAGA 1680
 CTACTAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAGATGCA GAAATAGGTT 1740
 ACCGGAATTC ATTGAGACAA ACTAACAAAA CTAAACAGTC ATGCCCATTT GGAAGAGTCC 1800
 CAGTTAACCT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATPCA GTTGATCTT 1860
 GTTTATGAA AAGACAAACC TCTAGATCAG AATGCCGAGA TTTGGTTGTG CCTGGATCTA 1920
 AACCAAGTGG AATGATTTC TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCATT 1980
 TCAAGGAACC TCTGGTGCA GATGAAAAGA GTTCTGAATC TATTATTACT GATTCAATAA 2040
 CCCTGAAGAA TAAACCGGAA TCAAGTCTTC TAGCTAATTT AGAAGAAACT AAAGAGTATC 2100
 AAGAACCAAG GTTCCAGAG AGTAACCAAG AACAGTGGCA AGCTAAGAGA AAGTCAGAGT 2160
 GTATTAAACA GAATCTCTGCT GCATCTCTAA ATCACTGGCA GATTCGGGAG TTAGCCCGAA 2220
 AAGTTAATCA AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAA 2280
 AGTCACCAAC AATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTGTG AAGACACCAA 2340

5 GCAGCAATAC CTGATGAT TACATGAGCT GTTTTAGAAC TCCAGTTGTA AAGAATGACT 2400
 TTCCACCTGC TTGTGAGTTG TCAACACCTT ATGGCCAACC TGCCTGTTTC CAGCAGCAAC 2460
 AGCATCAAT ACTTGCCACT CCACTTCAAA ATTTACAGGT TTTAGCATCT TCCTCAGCAA 2520
 ATGAATGCAT TTCGTTTAAA GGAAGAATTT ATTCCATATT AAAGCAGATA GGAAGTGGAG 2580
 GTTCAAGCAA GGTATTTTCT GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
 TGAACCTAGA AGAAGCAGAT AACCAAACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700
 TGAATAAACT ACAACAACAC AGTGATAAGA TCATCCGACT TTATGATTAT GAAATCACGG 2760
 ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCCTTAATAGT TGGCTTAAAA 2820
 AGAAAAATC CATTCATCCA TGGGAACGCA AGAGTTACTG GAAAAATATG TTAGAGGCAG 2880
 TTCAACAAT CCATCAACAT GGCATTGTTT ACAGTGATCT TAAACAGCT AACTTCTCGA 2940
 TAGTTGATGG AATGCTAAG CTAATTGATT TTGGGATTGC AAACCAATG CAACAGATA 3000
 CAACAAGTGT TGTAAAGAT TCTCAGTTG GCACAGTTAA TTATATGCCA CCAGAAGCAA 3060
 TCAAGATAT GTCTTCTCC AGAGAGAATG GGAATCTAA GTCAAGATA AGCCCCAAA 3120
 GTGATGTTTG GTCTTAGGA TGTATTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180
 AGCAGATAAT TAATCAGATT TCTAAATTAC ATGCCATAAT TGATCCTAAT CATGAAATTG 3240
 AATTTCCCGA AATTCCAGAG AAGATCTTC AAGATGTGTT AAGATGTGTT TTAATAAGGG 3300
 ACCCAAAACA GAGGATATCC ATTCTGAGC TCCTGGCTCA TCCATATGTT CAAATTCAAA 3360
 CTCATCCAGT TAACCAATG GCCAAGGGAA CCACTGAAGA AATGAAATAT GTTCTGGGCC 3420
 AACTTGTGG TCTGATTCT CTTAACTCCA TTTTGAAAGC TGCTAAACT TTATATGAAC 3480
 ACTATAGTGG TGGTGAAGT CATAATTCTT CATCTCCCAA GACTTTTGAA AAAAAAGGG 3540
 GAAAAAATG AATTGCAGT ATTGTAATG TCAGATAGGA GGTATAAAT ATATTGGAGT 3600
 GTTATACTCT TGAATCCCTG TGGAAATCTA CATTGAAGA CAACATCACT CTGAAGTGT 3660
 ATCAGCAAAA AAAATTCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAAA TAGCAACAC 3720
 TTATGGCACT GTATATATG TAGACTTGT TTCTCTGTTT TATGCTCTTG TGAATCTAC 3780
 25 TTGACATCAT TTTACTCTG GAATAGTGG TGGATAGCAA GTATATCTA AAAAACTTG 3840
 TAAATAAAGT TTTGCGCTA AATGA

30 A147 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 35 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

40 1 11 21 31 41 51
 MNKVRDIKKN FKNEDLTDEL SLNKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS 60
 VPLSDALLNK LIGRYSQAIE ALPPDKYQGN ESFARIQVRF AELKAIQSPD DARDYQMAR 120
 ANCKKPAFVH ISFAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180
 45 EEEKINLSAS TVLTQAESFS GSLGHLQNRN NSCDNRGQTT KARFLYGENM PPQDAEIGYR 240
 NSLRQTNTK QSCPFGRVPV NLLNSPDCDV KTDSDVVPFC MKRQTSRSEC RDLVVPGSKP 300
 SGNDSCELRN LKSVQNSHFH EPLVSDKSS ELIITDSITL KNTBSSLLA KLEETKEYQE 360
 PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPBELARKV NTEQKHTTPE QPVFVSQKQS 420
 PPISSTKWF DPKSICKTPSS NTLDDYMSCP RTPVVKNDFF PACQLSTPYG QPACFQQQNH 480
 50 QILATPLQNL QVLASSANE CISVKGRYS ILKQIGSGGS SKVFQVLNEK KQIYAIFYNV 540
 LEEADNQTL DSYRNEIAYLN KLQHSKDKII RLYDYEITDQ YIYVMMECN IDLNSWLKKK 600
 KSIDPWERKS YWKNMLEAVH TIHQHGIHVS DLKPNANFLIV DGMKLIDFG IANQMOPDIT 660
 SVVKDSQVGT VNYMPEPAIK DMSSSRENGK SKSKISPKSD VWSLGCILYY MTYQKTPFPQ 720
 IINQISKLHA IIDPNHIEF PDIPEKDLQD VLKCCCLKRDP KQRISIPELL AHPYVQIQTH 780
 55 PYNQMAKGT EEMKYVLGQL VGLNSPNSIL KAAKTLYERY SGGESHNSSS SKTFEKKRGK 840
 K

A148 DNA SEQUENCE

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 60 Probeset Accession #: NM_012152
 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 CTCTCTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAAGCACA TGGACTTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
 70 GGAACAAAGC TTGTGATTGT TTTGTGTGTT GGGACGTTTT TCTGCTGTTT TATTTTTTTT 180
 TCTAATCTCT TGGTCATCGC GGCAGTGATC AAAAACAGAA AATTTCATTT CCCCTTCTAC 240
 TACCTGTGG CTAATTTAGC TGCTGCGGAT TTCTTCTGCT GAAATGCTTA TGTATTCTGT 300
 ATGTTTAAAC CAGGCCAGT TTCAAAACT TTAGCTGTCA ACCGCTGGTT TCTCGTCTAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGTTTAT CGCCGTGGAG 420
 75 AGGCACATGT CAATCTAGG GATGCGGTC CATAGCAACC TGACCAAAAA GAGGCTGACA 480
 CTGCTCATTT TGCTGTCTG GGCATGCGC ATTTTATAGG GGGCGGTCCC CACACTGGGC 540
 TGGAAATGCC TCTGCAACAT CTCTGCTGCT TCTTCCCTGG CCCCATTTA CAGCAGGAGT 600
 TACCTTGTGT TCTGACAGT GTCCAACCTC ATGGCCCTTC TCATCATGGT TGTGTTGTAC 660
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAAGCTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCATGT GCCGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780
 80 GCGTTTGTGG TATGCTGGAC CCGGGGCTG GTGGTTCTGC TCCTGACGG CCTGAACCTG 840
 AGGCAGTGTG GCGTGCAGCA TGTGAAAAGG TGGTTCTGCT TGCTGGCGCT GCTCAACTCC 900
 GTCGTGAACC CCATCATCTA CTCTTACAAG GACGAGGACA TGTATGGCAC CATGAAGAAG 960
 ATGATCTGCT GCTTCTCTCA GGAGAACCCA GAGAGGCGTC CCTCTGCGAT CCCCCTCCAC 1020
 GTCCTCAGCA GGAGTGACAC AGGCAGCCAG TACATAGAGG ATAGTATTAG CCAAGGTGCA 1080

GTCTGCAATA AAAGCACTTC CTAAACTCTG GATGCCTCTC GGCCACCCA GGTGATGACT 1140
GTCTTAGG

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A149 Protein sequence:

Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
Unigene number: Hs.258583
Probeset Accession #: NM_012152
Protein Accession #: NP_036284
Signal sequence: none found
Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295
Cellular Localization: plasma membrane

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1	11	21	31	41	51	
MNECHYDKHM	DEFFYNRSNTD	TVDDWTGKTL	VIVLCVGTFF	CLFIFFSNSL	VIAAVIKNRK	60
FHFPPFYLLA	NLAAADFFAG	IAYVPLMFNT	GPVSKTLTVN	RWFLRQGLLD	SSLTASLTNL	120
LVIIVERHMS	IMRRRVHSNL	TKKRVTLIL	LVNAIAIFMG	AVPTLGNWCL	CNISACSSLA	180
PIYSRSYLVE	WTVSNLMAFL	IMVVVYLRIY	VYVKKRTINVL	SPHTSGSISR	RRTPMKLMKT	240
VMTVLGAFVV	CWTPGLVVLL	LDGLNCRQCG	VQHKRWFL	LALLNSVVP	IISYKDEDM	300
YGTMKKMICC	FSQENPERRP	SRIPSTVLSR	SDTGSQYIED	SISQGAVCNK	STS	

25

ProstateA150 DNA SEQUENCE

Gene name: ESTs
Unigene number: Hs.293616
Probeset Accession #: AW043782
Nucleic Acid Accession #: none found
Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

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1	11	21	31	41	51	
AGCAACGACG	CGGGCAGCG	GGAGCGGCGG	CGCGCCATG	TGGCTGCTGG	GGCCGCTGTG	60
CCTGCTGCTG	AGCAGCGCGG	CGGAGAGCCA	GCTGCTCCCC	GGGAACAAC	TCACCAATGA	120
GTGCAACATA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	GCGCCTGGCA	180
GTGTGACGGG	CTGCCCTGACT	GCTTOGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTCGAAATGT	GGCCCAACCT	TCTTCCCCTG	TGCCAGCGGC	ATCCATTGCA	TCATTGGTCG	300
CTTCGGGTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCCCTCTG	CTTTGCTCCA	CGCCCCGCTA	CCAATGCAAG	AACGGCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTTCTCAA	GAACCCCGCA	GTGGCAGGT	GTTTGTGACT	TCAGAGAACC	AACTTGTTGA	540
TTACCCGAGC	ATCACTATG	CCATCATCGG	CAGCTCCGTC	ATTTTGTGTC	TGGTGGTGGC	600
CCTGCTGGCA	CTGGTCTTGC	ACCACGAGCG	GAAGCGGAAC	AACCTCATGA	CGCTGCCGT	660
GCACCGGCTG	CAGCACCCCTG	TGCTGCTGTC	CGCGCTGGTG	GTCTGGGACC	ACCCCAACCA	720
CTGCAAGCTC	ACCTTACAAG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGCGGAGGCA	780
GAATGCGCTG	GAAGTAGGCT	CCCCACCCCTC	CTACTCCGAG	GCCTTGCTGG	ACCAGAGGCC	840
TGCGTGTAT	GACCTTCCCT	CACCGCCCTA	CTCTTCTGAC	ACGGAATCTC	TGAACCAAGC	900
CGACTGCCCC	CCCTACCGCT	CCCGTCCGCG	GAGTGCCAAC	AGTGCCAGCT	CCAGGCGAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACCAG	CCACAGCCCC	GGGCGAGCCTG	GCCCCCAGGA	1020
GGGCACTGCT	GAGCCCAAGG	ACTCTGAGCC	CAGCCAGGCG	ACTGAAGAAG	TATAAGTCCC	1080
AGTTATTCCA	AAGTCCATAT	GGGTAAATCT	GCTCTGACTT	GTGGCCATTC	TAACAAATTG	1140
TGCTCATGGG	AAGCTCTTTA	AGCACCTGTA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACTATCTCT	GCATTCCCTC	CCTCCCCCAG	ACTTCAGAGA	TGTTTTCTCG	CGCTCTCAGT	1260
TGACATGATC	TGTTGTGCGT	CTTTTCTGTC	AGGTCACTCT	TCCCTTGGGA	CCGAGATCA	1320
CACCCCTCAT	TTTCACATTA	TTCTGTTTCT	GTGGGAGAGA	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTGG	ATGCTCAGAA	GTGCGAGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTGGGGGA	TTTGGGTTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCACTGGATG	GTCAACCCCG	CAGAAATATT	CCATTGTAGC	1560
ATCAAAACCT	GCTTTGCACA	ATCCTATTTG	ATGCCCCCAG	TTCAAGCAGG	TCAGTGGCCA	1620
AAGAAACTT	TGGACGTGAG	TAACACCCCT	CAGCAGTGCG	AACGTTATTT	TGTTTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATTCTGGCTT	TAGAAATTGG	CCCAAGAAATG	1740
CTCATTCTGA	GAGCTTTCCT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCAGG	1800
GAGCCCCCTC	CATGAGTTTA	TCCAAGTTCT	CAGCTCTTAA	AATGCAGGCT	GCCAAGACCC	1860
TACACCTGCC	CTGGCTCTAC	AGCCACTTAC	CTGGTTTCTG	GACTGTACCC	CTCCAGCTG	1920
ACCTGCCCGT	AGCCCAAGGAA	TGAGGACCTA	ACTTGAGTTG	GCCCCAAGTC	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCACCA	CCCAGCCTGT	CTTGCTCAT	CATGCAGCCT	CAACACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAAAGTC	CTTTTACCT	GTGCAATTGG	ACTTGAGGAC	2100
ACTGGTTTCT	ATCACAGGTG	AGAGCCATGT	TCAATACCTC	CAGCAAGCTC	TCTGGCTCC	2160
CTGCACGTG	CACGCTCCCT	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	AGGCCTCTCC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CATGGGCAAG	2280
AGACAATTG	GAGTCAAGAT	TTTCCATTG	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAACAGGTG	TGTTTGTGTT	TTCCCTTCTA	GTTAAGGGAC	TATTTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTGTGTT	TTCTTTTAA	AAGGTCCTAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCCCTGC	CCCGCTGAGC	CCCGTGATAA	CAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTGTGTC	ATTGTTGAC	TTTGAGGTTA	TTATTTATCA	AGTTCTTGAA	GGAGGCAGAA	2580
AGAGGGACTC	CTCTCTCCCT	CCGTGTATAG	CTCTATAGTT	TGTGCTAGTT	TTTCTTTTTT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAACACGTT	2700
AGGTGTTGTT	TGGCAAGAAA	CCACACTGAC	TGATGAGGGG	TAAATGGA	CCAGGTAGAG	2760
CCACTCCGGG	CAGCTGTGAC	CCATTTCAGAA	CTTCTTTCCG	CAGCTGAAGA	AATGTTTCAGT	2820

AACCTGTTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAAG TGGCATTGAG 2880
 TGATCCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACAA ATCCAAAGGA TGTTACAGAA 2940
 AAGCTAGCCA CTGTGATTTT GTTTTGTTTA AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAGAA CTTTGTAGTA CAGCCAGAAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CTGTGAGTC AGAAGGGCTT TATTTCTCCC TTGATGGGG CCCCTTCTTC 3180
 TTTCTGTGTC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAA TGGTTTTAGT 3300
 AGATAAGGGA TGCCTACTAA TGCTTTTTTA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTTT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCA 3540
 AAAATAGTCT CATCTCTTTT TTCTCAAAAT GAGATCCGTG TTTTATTTTA GCATTAAATT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATTGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTAAATA GTGTGTGACG CTCAAAGTTA ATGTAACACTG 3720
 GAAAGGTGT GTGCTGTTG TTTTGTGTT TTGGTTAGCG TTGGTTTGT TTTTAAATT 3780
 TTATACTTTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAWG GWMCTAMARM 3840
 AAMMAAAAC AWYWTGGGG GGGCTTGGC CTGGAAAAA GTTTTAAACA CCACTTCGGG 3900
 TGGGCGCGG GGGCCACGT AGGTACGGCG ACCACCGGG CCCAACCGG ACCCCAGAAG 3960
 GAAACCTCG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGG 4020
 GGAAACCGCA GAGTGTGCG TAAACCAAC CCGAAGAGAG AACTCAGAAG CACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGAACCC GATAGAGTAC G

A151 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MWLLGPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNSG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKRSK CGPTFFPCAS GIHCCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGNNQOD NSDEBSCSS QBPSSQVFPV TSENQLVYYP SITYAIIGSS 180
 VFEVLVALL ALVLLHQRKR NMLMTLPVHR LQHPVLLSRL VVLDHPHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVGSPPSYS EALLDQRPBW YDLPPPPYSS DTESLNQADL PPYRSRSGSA 300
 NSASSQAASS LLSVEDTSHS PGQPGPQEGT AEPRDSEPSQ GTREV

A152 DNA SEQUENCE
 Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Nucleic Acid Accession #: NM_005656.1
 Coding sequence: 57-1535 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTGTATAAC AGCAAGATGG 60
 CTTTGAACCT AGGGTCAACA CCAGCTATTG GACCTTACTA TGAAAACCAT GGATAACCAAC 120
 CGGAAAACCC CTATCCCGCA CAGCCCACTG TGGTCCCCAC TGTCTACGAG GTGCATCCGG 180
 CTCAGTACTA CCGCTCCCCC GTGCCCCAGT ACGCCCCGAG GGTCTGACG CAGGCTTCCA 240
 ACCCGTCTGT CTGCACGAG CCCAAATCCC CATCCGGGAC AGTGTGCACC TCAAAGACTA 300
 AGAAAGCACT GTGCATCAAC TTGACCTTGG GGACCTTCTT CGTGGGAGCT GCGCTGGCCG 360
 CTGGCCTACT CTGGAAGTTC ATGGGCAGCA AGTGTCTCAA CTCTGGGATA GAGTGGGACT 420
 CCTCAGGTAC CTGCATCAAC CCTCTAACT GGTGTGATGG CGTGTACAC TGCCCCGGCG 480
 GGGAGGACGA GAATCGGTGT GTTCGCCTCT ACGGACCAAA CTTCATCCTT CAGATGTACT 540
 CATCTCAGAG GAAGTCTGTG CACCCTGTGT GCCAAGACGA CTGGAACGAG AACTACGGGC 600
 GGGCGGCTG CAGGACATG GGCCTATAAG ATAAATTTTA CTCTAGCCAA GGAATAGTGG 660
 ATGACACGCG ATCCACCAGC TTTATGAAAC TGAACACAAG TGCCGGCAAT GTGATATCT 720
 ATAAAAAACT GTACCACAGT GATGCCTGTT CTTCAAAAGC AGTGGTTTCT TTACGCTGTT 780
 TAGCCTGCGG GGTCAACTTG AACTCAAGCC GCCAGAGCAG GATCGTGGC GGTGAGAGCG 840
 CGCTCCCGG GGCCTGGCCC TGGCAGSTCA GCCTGCACGT CCAGAACGTC CACGTGTGCG 900
 GAGGCTCCAT CATCACCCCC GAGTGGATCG TGACAGCCGC CCACTGCGTG GAAAAACCTC 960
 TTAACAATCC ATGGCATTGG ACGGCATTTG CGGGGATTTT GAGACAACTT TTCTATTTCT 1020
 ATGGAGCCGG ATACCAAGTA CAAAAGTGA TTTCTCATCC AAATTATGAC TCCAAGACCA 1080
 AGAACAATGA CATTCGCTG ATGAAGCTGC AGAAGCTCT GACTTTCAAC GACCTAGTGA 1140
 AACCAAGTGT TCTGCCAAC CCAGGCATGA TGCTGCACGC AGAACAGCTC TGCTGGATTT 1200
 CCGGGTGGG GGGCACCGAG GAGAAAGGGA AGAOCCTCAG AGTGTGAAC GCTGCCAAGG 1260
 TGCTTCTCAT TGAGACACAG AGATGCAACA GCAGATATGT CTATGACAAC CTGATCACAC 1320
 CAGCCATGAT CTGTGCCGCG TTCTGTCAGG GAAACGTCGA TTCTTGCCAG GGTGACATG 1380
 GAGGGCCTCT GGTCACTTGG AACACAATA TCTGGTGGCT GATAGGGGAT ACAAGCTGGG 1440
 GTTCTGGCTG TGCCAAAGCT TACAGACCAG GAGTGTACGG GAATGTGATG GTATTCAACG 1500
 ACTGGATTTA TCACAAATG AAGGCAAAAC GCTAATCCAC ATGCTCTTGC TCCTTGACGT 1560
 CGTTTTACAA GAAACAATG GGGCTGGTTT TGCTTCCCGG TGCTATGATT ACTCTTAGAG 1620
 ATGATTCAGA GGTCACTTCA TTTTATTAA ACAGTGAAC TGTCTGGCTT TGGCACTCTC 1680
 TGCCATACTG TGCAGGCTGC AGTGGCTCCC CTGCCAGCC TGCTCTCCCT AACCCCTTGT 1740

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CCGCAAGGGG TGATGGCCGG CTGGTTGTGG GCACTGGCGG TCAATTGTGG AAGGAAGAGG 1800
GTTGGAGGCT GCCCCCATTT AGATCTTCCT GCTGAGTCCT TTCCAGGGGC CAATTTTGA 1860
TGAGCATGGA GCTGTCACTT CTCAGCTGCT GGATGACTTG AGATGAAAAA GGAGAGACAT 1920
GGAAAGGGAG ACAGCCAGGT GGCACCTGCA GCGGCTGCCC TCTGGGGCCA CTGGTAGTGG 1980
TCCCGAGCCT ACTTCACAAG GGGATTTTGC TGATGGGTTT TTAGAGCCTT AGCAGCCCTG 2040
GATGGTGGCC AGAAATAAAG GGACCAGCCC TTCTATGGGTG GTGACGTGGT AGTCACTTGT 2100
AAGGGGAACA GAAACATTTT TGTCTTATG GGGTGAGAAT ATAGACAGTG CCTTGGTGC 2160
GAGGGAAGCA ATTGAAAGG AACTTGCCTT GAGCACTCCT GGTGCAGGTC TCCACCTGCA 2220
CATTGGTGGG GGCTCCTGGG AGGGAGACTC AGCCTTCCTC CTCATCCTCC CTGACCTGTC 2280
TCCTAGCACC CTGAGAGAGT AATGCCCTT GGTCCCTGGC AGGGCGCCAA GTTTGGCACC 2340
ATGTCGGCCT CTTCAGGCCT GATAGTCATT GGAAATTGAG GTCCATGGGG GAAATCAAGG 2400
ATGCTCAGTT TAAGGTACAC TGTTTCCATG TTATGTTTCT ACACATTGAT GGTGGTGACC 2460
CTGAGTTCAG AGCCATCTT

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A153 Protein sequence:

Gene name: Transmembrane protease, serine 2 (TMPRSS2)
 Unigene number: Hs.105807
 Probeset Accession #: T48536
 Protein Accession #: NP_005647.1
 Signal sequence: none found
 Transmembrane domains: 85-107
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MALNSGSPPA IGPYYENHGY QPENPYPAQP TVVPTVYEVH PAQYYPSPVP QYAPRVLTQA 60
 SNPVVCTQPK SPSGTVCTSK TRKALCITLT LGTFLVGAAL AAGLLWKFMG SKCSNSGIEC 120
 DSSGTCINPS NWCDSVSHCP GGEDENRCVR LYGPFPILQM YSSQRKSWHP VCQDDWNENY 180
 GRAACRDMGY KKNFYSSQGI VDDSGSTFSM KLNTSAGNVD IYKKLYHSDA CSSKAVVSLR 240
 CLACGVNLNS SRQSRIVGGE SALPGAWPWQ VSLHVQNVHV CGSGIITPEW IVTAAHCVEK 300
 PLNNFWHTA FAGILRQSFH FYGAGYQVQK VISHPMYDSK TKNDIALMK LQKPLTFNDL 360
 VKPVLCPNPG MMLQPEQLCW ISGWGATEEK GRTSEVLNAA KVLLIETQRC NSRYVVDNLI 420
 TPAMICAGFL QGNVDSQGD SGGPLVTSNN NIWWLIGDTS WSGGCAKAYR PGVYGVNVMVF 480
 TDWIYRQMK NG

A154 DNA SEQUENCE

Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
 Unigene number: Hs.129179
 Probeset Accession #: AI694767
 Nucleic Acid Accession #: AI694767
 Coding sequence: 130-1086 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CAGAGAGGCT GTATTTTCAGT GCAGCCTGCC AGACCTCTTC TGGAGGAAGA CTGGACAAAG 60
GGGGTCACAC ATTTCCTTCA TACGGTTGAG CCTCTACCTG CCTGGTGCTG GTCACAGTTC 120
AGCTTCTTCA TGATGGTGGG TCCCAATGSC AATGAATCCA GTGCTACATA CTTTCATCCTA 180
ATAGGCTTCC CTGGTTTAGA AGAGGCTCAG TTCTGGTTGG CCTTCCCATT GTGCTCCCTC 240
TACCTTATTG CTGTGCTAGG TAACCTGACA ATCATCTACA TTGTGGGAC TGAGCACAGC 300
CTGCATGAGC CCATGTATAT ATTCTTTTGC ATGCTTTTCA GCATTGACAT CCTCATCTCC 360
ACCTCATCCA TGCCCAAAAT GCTGGCCATC TTCTGGTTCA ATTCCACTAC CATCCAGTTT 420
GATGCTGTTC TGCTACAGAT GTTTGCCATC CACTCCTTAT CTGGCATGGA ATCCACAGTG 480
CTGCTGGCCA TGCTTTTGA CCGCTATGTG GCCATCTGTC ACCCACTGGC CCATGCCACA 540
GTACTTAAGT TGCTCTGCTG CACCAAAATT GGTGTGGCTG CTGTGGTGCG GGGGGCTGCA 600
CTGATGGCAC CCCTTCTGTG CTTCATCAAG CAGCTGCCCT TCTGCCGCTC CAATATCCTT 660
TCCATTTCTT ACTGCCCTACA CCAAGATGTC ATGAAGCTGG CCTGTGATGA TATCCGGGTC 720
AATGTCGTTT ATGGCCTTAT CGTCATCATC TCCGCCATTG GCCTGGACTC ACTTCTCATC 780
TCCTTCTCAT ATCTGCTTAT TCCTAAGACT GTGTGGGCTG TGACACGTGA AGCCAGGCC 840
AAGGCATTG GCATCTGCTG CTCTCATGTG TGTGCTGTGT TCATATTCTA TGTACCTTTC 900
ATTGGATTGT CCATGGTGCA TCGCTTTAGC AAGCGGCGTG ACTCTCCACT GCCCGTCATC 960
TTGGCCAAATA TCTATCTGCT GGTTCCTCTT GTGCTCAACC CAATTGTCTA TGGAGTGAAG 1020
ACAAAGGAGA TCGACAGCG CATCCTTCGA CTTTCCATG TGGCCACACA CGCTTCAGAG 1080
CCCTAGGTGT CAGTGATCAA ACTTCTTTTC CATTAGAGT CCTCTGATC AGATTTTAAAT 1140
GTTAATCATTT TGGAGACAG TATTAGAAA AAAAATTTC TTAATAAAAA TACAATCAG 1200
ATCCTTCAA TATGAAACTG GTTGGGAAT CTCCATTTTT TCAATATTAT TTTCTTCTTT 1260
GTTTCTTTCG TACATATAAT TATTAATACC CTGACTAGGT TGTGGTTGGA GGGTTATTAC 1320
TTTTCAATTT ACCATGCAGT CCAAACTCAA ACTGCTTCTA CTGATGGTTT ACAGCATTCT 1380
GAGATAAGAA TGTATACATC AGAGAACATT TGCCAAAGGC CTAAGCACAG CAAGGAAAAA 1440
TAAACACAGA ATATAATAA ATGAGATAAT CTAGCTTAAA ACTATAACTT CCTCTTCAGA 1500
ACTCCCAACC ACATTGGATC TCAGAAAAAT ACTGTCTTCA AAATGACTTC TACAGAGAAG 1560
AAATAATTTT TCCTCTGGAC ACTAGCACTT AAGGGGAAGA TTGGAAGTAA AGCCTTGAAA 1620
AGAGTACATT TACCTACGTT AATGAAAGTT GACACACTGT TCTGAGAGTT TTCACAGACT 1680
ATGGACCCCTG TTTTCTCTAT TTAATTTTCT TATCAACCCCT TTAATTAGGC AAAGATATTA 1740
TTAGTACCTT CATGTAGCC ATGGGAAAAAT TGATGTTTCA TGGGGATCAG TGAATTTAAAT 1800
GGGGTCATAC AAGTATAAAA ATTAATAAAA AAAGACTTCA TGCCCAATCT CATATGATGT 1860
GGAAGAACTG TTAAGAGAGC CAACAGGGTA GTGGGTTAGA GATTTCAGAG GTCTTACATT 1920
TTCTARAGGA GGTATTTAAT TTCTTCTCAC TCATCCAGTG TTGATTATAG GAATTTCTTG 1980
GCAACAGAAC TCAATGCTTT AATCCCACTA GCTATTGCTT ATTGTCTTGG TCCAATTGCC 2040
AATTAAGCTG GTCTTGAAG AAGTGAATTC TAGGTTCACC ATTATGGAAG ATTCTTATTC 2100
AGAAAGTCTG CATAGGGCCT ATAGCAAGTT ATTTATTTTT AAAAGTTCCA TAGGTGTTTC 2160
TGATAGGCAG TGAGGTTAGG GAGCCACCAG TTATGATGGG AAGTATGGAA TGGCAGGTGT 2220
TGAAGATAAC ATTGGCCTTT TGAGTGTGAC TCGTAGCTGG AAAGTGAGG AATCTTCAGG 2280

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ACCATGCTTT ATTTGGGGCT TTGTGCAGTA TGAACAGGG ACTTTGAGAC CGGGAAGCA 2340
ATCTGACTTA GGCATGGGAA TCAGGCATTT TTGCTTCTGA GGGGCTATTA CCAAGGGTTA 2400
ATAGGTTTCA TCTTCAACAG GATATGACAA CAGTCTTAAC CAAGAACTC AAATTACATA 2460
TACTAAAACA TGTGATCATA TATGTGGTAA GTTTCATTTT CTTTTCATTA CCTCAGGTTT 2520
CCTGATATGG ATTCCTATNA CATGCTTTCA TCCCTTTTGG TAATGGATAT CATATTTGGA 2580
AATGCCTATT TAATACTTGT ATTTGCTGCT GGACTGTAAG CCCATGAGGG CACTGTTTAT 2640
TATTGAATGT CATCTCTGTT CATCATTGAC TGCTCTTGC TCATCATTGA ATCCCCCAGC 2700
AAAGTGCCTA GAACATAATA GTGCTTATGC TTGACACCGG TTATTTTTC TCAAACTTGA 2760
TTCCCTCTGT GCTGAACACA TAGCCAGGCA ATTTCCAGC CTCTTTGAG TTGGGTATTA 2820
TTAAATTTTA GCCATTACTT CCAATGTGAG TGAAGTGAC ATGTGCAATT TTATACCTG 2880
GCTCATAAAA CCTTCCCATG TGCAGCCTTT CATGTTGACA TTAATGTGA CTGGGAAGC 2940
TATGTGTAC ACAGAGTTAA TTAACNGAA AGCCTGGNA ATTTTGTGN ANNAACCTG 3000
TGGCCNAGG GCCCNCAACC CTTTNNNA ATTTGGCAAN NTCCCACTTT GTANTTTGGT 3060
AAGGAGGCCA GTTGGATAAG TGAAAAATA AGTACTATTG TGTC

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A155 PROTEIN SEQUENCE

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Gene name: Homo sapiens cDNA FLJ13581 fis, clone PLACE1009039
Unigene number: Hs.129179
Protein Accession #: not available
Signal sequence: none found
Pfam domain: 7tm_1 [43-293]
Transmembrane domains: 29-51, 57-79, 82-104, 203-225, 239-261, 273-295
Cellular Localization: not determined

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1 11 21 31 41 51
MVDPNNGESS ATYFILIGLP GLEEAQFWLA FPLCSLYLIA VLGNLTIIYI VRTEHSLHEP 60
MYIFLCMLSG IDILISTSSM PKMLAIFWFN STTIQFDACL LQMFALHSLS GMESTVLLAM 120
AFDRYVAICH PLRHATVLT PLRVKIGVAA VVRGAALMAP LPVFIKQLFF CRSNILSHSY 180
CLHQDVVKMLA CDIRVNVVY GLIVIIISAIG LDSLLI9PSY LLLIKTVLGL TREAQAKAFG 240
TCVSHVCAVF IFYVPFIFGLS MVHRFSKRRD SPLPVLANI YLLVPPVLNP IVYGVKTKEI 300
RQRILRLFHV ATHASEP

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A156 DNA SEQUENCE

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Gene name: vasoactive intestinal peptide receptor 1
Unigene number: Hs.198726
Probeset Accession #: X77777
Nucleic Acid Accession #: NM_004624.1
Coding sequence: 57-1544 (underlined sequences correspond to start and stop codons)

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TCGGAGCCTG CCGAGGGTGG TGGTGGTGGT GGTGGTGGCC CTCGCCCGCC TCACTCATGC 60
CTCTCTCTCC TCTGCTCTCG CTCAGGCGCC TCGGTGGCGG TTGGTCGGCG GTTACGCGGC 120
TGGTGGTTCG GCGGCGCGGG GCTCGCTCTC GGGGAGGCGG GGGCGGATCT CGCGGCGCAG 180
GCGGCGCGCG CCGAGGTGGG GTCCGCGCGC GGAGGCGGCT CGAGCTTCGT GCTGCGCGCT 240
CGCTCTTGGG CTCTCTCGTG CAGGAGGAGT GTGACTATGT GCAGATGATC GAGGTGCAGC 300
ACAAGCAGTG CTCGAGGAGG GCCCAGCTGG AGAATGAGAC AATAGGCTGC AGCAAGATGT 360
GGGCAACCTT CACTGTCTGG CCAGCCACCC CTCGGGCGCA GGTAGTTGTC TTGGCCTGTC 420
CCCTCATCTT CAAGCTCTTC TCCTCCATTC AAGGCGCA TGTAGCGCG AGCTGCACCG 480
ACGAAGGCTG GACGCACCTG GAGCCTGGCC CGTACCCCAT TGCCTGTGGT TTGGATGACA 540
AGGCAGCGAG TTTGGATGAG CAGCAGACCA TGTCTTACGG TTCTGTGAAG ACGGCTGACA 600
CCATTGGCTA CCGCTGTGCC CTCGCCACCC TTCTGTGTGC CACAGCTATC CTGAGCCTGT 660
TCAGGAAGCT CCACTGACAG CGGAATACA TCACATGCA CCTCTTCATA TCCTTCATCC 720
TGAGGGCTGC CGCTGTCTTC ATCAAGACT TGGCCTCTT CGACAGCGG GAGTGGGACC 780
AGTGCTCCGA GGGCTCGGTG GGCTGTAAAG CAGCCATGGT CTTTTTCAA TATTGTGTCA 840
TGGCTAACTT CTCTGCTGCT CTGGTGGAGG GCCTCTACCT GTACACCTTG CTGCGCTGCT 900
CCTCTCTCTC TGAGCGGAAG TACTTCTGGG GGTACATACT CATCGGCTGG GGGGTACCCA 960
GCACATTAC CATGTGTGG ACCATGCCA GGATCCATT TGAGGATTAT GGTCTGCTCA 1020
GGTGTGGGA CACCATCAAC TCCTCACTGT GGTGGATCAT AAAGGGCCCC ATCTCACTC 1080
CCATCTTGGT AAACCTTATC CTGTTTATTT GCATCATCCG AATCCTGCTT CAGAACTGC 1140
GGCCCCCAGA TATCAGGAAG AGTGACAGCA GTCCATACCT AAGGCTAGCC AGGTCCACAC 1200
TCCTGCTGTA CCCCCTGTTT GGAGTACACT ACATCATGTT CGCCTTCTTT CCGGACAATT 1260
TTAAGCCTGA AGTGAAGATG GTCTTTGAGC TCGTCTGGGG GTCTTTCCAG GGTTTTGTGG 1320
TGGCTATCCT CTACTGCTTC CTCAATGGTG AGGTGCAGGC GGAGCTGAGG CGGAAGTGGC 1380
GGCGCTGGCA CTTGCAGGGC GTCTTGGGCT GGAACCCCAA ATACCGGCAC CGTCCGGGAG 1440
GCAGCAACGG CCGCAGCTGC AGCACGCGAG TTTCCATGCT GACCCGCGTC AGCCAGGTTG 1500
CCCGCCGCTC CTCAGCTTC CAAGCGAAG TCTCCCTGGT CTGACCAACA GGATCCGAGC 1560
CCAAGCGGCC CCTCCGCGCC CTTCCTCACT GCAGCAGAGC CCGGGGACAG AGGCCTGCCC 1620
GGCGCGGCCA GCGCGCGCCC TGGCTCGGA GGTGCCCCC GCGCCCTGTT TCTCTGTTCC 1680
GGACACTCCT AGAAGACGCA GCCCTAGAGC CTGCTGGAG CGTTTCTAGC AAGTGAGAGA 1740
GATGGGAGCT CCTCTCTGG AGGATGACAG TGGAACTCAG TCATTAGACT CCTCTCCAA 1800
AGGCCCCCTA CGCCATCAAA GGGCAAAAAG TCTACATACT TTCACTCTGA CTCTGCCCCC 1860
TGCTGGCTCT TCTGCCAATG TGGAGGAAAG CAACCGGTGG ATCTCTCAA AACACTGGTG 1920
TGACTGAGG GCAGAAAGGT TCTGCCCGGG AAGGTCAACA GCACCAACAC CACGGTAGTG 1980
CCTGAAATTT CACCATTGCT GTCAAGTTCC TTTGGGTTAA GCATTACAC TCAGGCATTT 2040
GACTGAAGAT GCAGCTCACT ACCCTATTCT CTCTTTACGC TTAGTTATCA GCTTTTAAA 2100
GTGGGTATT CTGGAGTTT TGTTTGGAGA GCACACCTAT CTTAGTGGTT CCCCACGAA 2160
GTGGAAGTGC CCTTGGGTCA GTCTGGTGGG AGGACGGTGC AACCACAGGA CTGAGGGACT 2220
CTGAAGCCTC TGGGAAATGA GAAGGCAGCC ACCAGCAAT GCTAGGTCTC GGACTAGGCC 2280
TACCTGCTCT CCAAGTCTCA GTGGCTTCAT CTGTCAAGTG GACTCTGTCT ACACCAGCCA 2340
TTCTTATCTC TCTGTGCTGT GGAAGCAACA GGAATCAAGA GACTGCCCTC CTGTCCACC 2400
CACCTATGTG CCAACTGTTG TAACCTAGGCT CAGAGATGTG CACCCATGGG CTCTGACAGA 2460

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AAGCAGATCC TCACCCCTGCT ACACATACAG GATTTGAAGT CAGATCTGTC TGATAGGAAT 2520
GTGAAAGCAC GGACTCTTAC TGCTAACTTT TGTGTATCGT AACCAGCCAG ATCCTCTTGG 2580
TTATTTGTTT ACCACTTGTG TTAITTAATGC CATTATCCCT GAATTCOCCT TGCCACCCCA 2640
CCCTCCCTGG AGTGTGGCTG AGGAGGCCTC CATCTCATGT ATCATCTGGA TAGGAGCCTG 2700
CTGGTCACAG CTCTCTCTGT CTGCCCTTCA CCCCAGTGGC CACTCAGCTT CCTACCCACA 2760
CCTCTGCCAG AAGATCCCTT CAGGACTGCA ACAGGCTTGT GCAACAATAA ATGTTGGCTT 2820
GGAAAAAAA AAAA

10 A157 Protein sequence:
Gene name: vasoactive intestinal peptide receptor 1
Unigene number: Hs.198726
Probeset Accession #: X77777
Protein Accession #: JC2195
Signal sequence: none found
15 Transmembrane domains: 181-202, 214-236, 255-277, 290-311, 332-354, 377-399, 408-430
Cellular Localization: plasma membrane

20
1 11 21 31 41 51
| | | | | |
MPPPPLLSLR RLGGGWSAVT RLVVAAAGAR SRGGRGSGRG AGGGRGGGVA RRRRLRLRAA 60
RSLLGSSLQE BCDYVQMIEV QHKQCLEEAQ LENETIGCSK MWDNLTCHPA TPRQVVLVA 120
CPLIFKLFSS IQGRNVSRSC TDEGWHLEP GPYPIACGLD DKAASLDEQQ TMFYGSVKTG 180
25 YTIYGLSLA TLLVATATLS LFRKLHCTRN YIHMHLFISF ILRAAAVPIK DLALFDSGES 240
DQCSGSGVGC KAAWVFQYQC VMANFFWLLV EGLYLYTLA VSFFSERKYF WGYILIGWGV 300
PSTFTMVWTI ARIHFEDYGL LRCWDTINSS LWNIIKGPIL TSILVNFILF ICIRILLQK 360
LRPPDIRKSD SSPYSRLARS TLLLIPLFGV HYIMFAFPFD NFKPEVKMVF ELVVGSGFQGF 420
VVAILYCLFN GEVQAELERRK WRRWHLQGV L GWNPKYRHP S GSGNGATCST QVSMLTRVSP 480
GARRSSSFQA EVSLV

30 A158 DNA SEQUENCE
Gene name: ESTs
Unigene number: Hs.29383
Probeset Accession #: AW207206
35 Nucleic Acid Accession #: AL133619
Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | | |
ATGAGCGGTG CGGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCGGAC CCGGGGCTCT 60
CGGCGCGCGC GCCAGCGCCC CTCTGTGGGC GTCCAGTCTT TGAGGCGCGA GAGCCCGCAG 120
CTCAGGCAGA GCGACCCGCA GAAACGGAAC CTGGACCTGG AGAAAGCCCT GCAGTTCCTG 180
CAGCAGCAGC ACTCGGAGAT GCTGGCCAAG CTCCATGAGG AGATCGAGCA TCTGAAGCGG 240
45 GAAACAAAGG GTGAGCGGCG GCGGGGCCCT AGGCGGCGCC TGCCCTCCCA GGCACACTCA 300
ACACTGCCGC TCOCGCAGCA CAGAAACACA GCCATCAACT CCAGCACACG CCTGGGCTCA 360
GGGGGAACAC AGGACGGGGA GCCCTCCAG ACTGTCTTGG CCCACCTGGC TGCACTGGCC 420
CCTGTATGCC AACCCAGTGG GTACAGGTTT TGGGGGACCT GGCAGATGC CGCTACCTCT 480
AGCGGTGGCT GGACGATGTT ATGCAGCCAA GCACAGCAGG TGCTGCTCTC GGGGAAGCCCA 540
GGGCGTGAAG TCATTGCAAG GCGGCAGGTG GCCACAGGGT GCTCCCCAGA CCTCCCTCTC 600
50 CCAAGTGAAG CTGAATGGG AAGGAACCCC TGGGACAGCC CCTGCCCTGC TAGATCTTTG 660
CCTCAGATTG CTGCTGTGGC CAGGCCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
GCAGCAACCA TGGGAGCAAA GGGAGGAAGC AGAGTCTTGT TTCCTTGCCA CTTGTCCAAG 840
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55 GCTCACTTCC CATTTATCTT GGGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGGA 960
TGGAGCCAGC CTGGGAACAT GCGAGCTGGG GCGAGTGCTA GGGCTCTCCC TTCCAGGGA 1020
GACATGGAGA AGGGGGTTGA GGGAGGGGCC TTCCTAGACC GCTGTGGCAA CTCAGTGAG 1080
CTGTTCTGGG CAAAGTGTGG CCCAAGTCGG CAGCCCCAGC CCTGCACTGC TGGGAGCGCT 1140
GACAGGACAC GGAAGAGAGC CATGCTTTCC CTCGGGACCT GCTGTTCAT GTGTCCCAAG 1200
60 CCTCTCTGCT TTCCAGATGG CCCCTCAGGA AACCACCTTT CCAGGGCCTC TGCTCCCTTG 1260
GGCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CGGGAGGACC CAGCCCTGCG 1320
AGGCTGAAGG AGGCTCTCTC ACGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGG 1380
GGCGGTAGCG CCGACACTGT GCGCTCTCTC GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
TCTGTCAAGT CCATCTCTAA TTCAGCCAAC TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
65 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCGAGA AGGCGGACCT GGAAGAGGAG 1560
CCCTTACTTC AACAAGCAA GCTGGACAAA GTTCTCTGGG TACAAGGGCA GGCCAGAAAG 1620
GAGAAAGCAG AGGCTCTTAA TGCAAGAGCT GCCTGTATGG GGAACAGCCA GCACAGGGC 1680
AGGCAGATGG GGGCGGGGGC ACACCCCCCA ATGATCTCTG CCCTTCCCTT GCGAAAGCCC 1740
ACCACACTTA GGCAGTGCGA AGTGCTCATC CCGAGCTGT GGAATACCAA CCTCTGCAAG 1800
70 ACCCAAGAGC TGCGGCACTC CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGAGGCC 1860
CCGAGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCACGC ATTTCCCAA GGTCTCCACC 1920
AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGCGCG AGCGTGCCAT CCTGCCGCA 1980
CTGAAGCAGA CCCGGAAGAA CAACCTTGGC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
AAACGGCGCC TGCATCGCTC AGTGCTTGA

75 A159 Protein sequence:
Gene name: ESTs
Unigene number: Hs.29383
80 Probeset Accession #: AW207206
Protein Accession #: T43457
Signal sequence: none found
Transmembrane domains: 303-322
Cellular Localization: not determined

	1	11	21	31	41	51	
5	MSGAGVAAAT	RPPSSPTPGS	RRRRQRPSVG	VQSLRPQSPQ	LRQSDPQKRN	LDLEKSLQFL	60
	QQQHSEMLAK	LHEEIEHLKR	ENKGEPARGP	RPALPPQAH	TLPLPQHRNT	AINSSTRLGS	120
	GGTQDGEPLQ	TVLAHLAALA	PVCQPSGYRF	WGTWTDAA	SRGWMLCSQ	AQHVLLSGSP	180
	GPEVIAGRQV	ATGCSFDLPP	PSRAEMGRNP	WDSFPCPARSL	PQIAAVARPR	ISSPMLALSPH	240
10	MLGAQGIWTH	SIQGSPLPAIW	AATMGTKGG	RVLFPCHLSK	ALPHPDSPGH	PAQDPGLMSQ	300
	AHFPLSLGLG	LTSGGHLTGG	WSQPGNIAAG	AVPRALPSQG	DMEKGVVEGPH	FPSRCGNSSE	360
	LFWAKCGPSR	QPQPCSGADA	DRTREAML	LGTCCSMCPK	PSCFPDGP	NHLSTRASAPL	420
	GARMVCINGV	WVEPGGSPSA	RLKEGSSRTH	RPQKGRRLA	GGSDATVRSR	ADSLSMSFQ	480
	SVKSISSNSAN	SQGKARPQPG	SFNKQDSKAD	VSQKADLEEE	PLLHNSKLDK	VPGVQGGARK	540
15	EKAESNAGA	ACMNSQHQG	RQMGAGAHPP	MILPLPLRKP	TTLRQCEVLI	RELWNTNLLQ	600
	TQELRHLKSL	LEGSQRPAQA	PEEASFPRDL	EATHFPKYST	KSLSKKCLSP	PVAERAILPA	660
	LKQTPKNFNA	ERQKRLQAMQ	KRRLHRSVL				

20 A160 DNA SEQUENCE
 Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Probeset Accession #: U41060
 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
30	CTCGTCCGCA	ATTCCGACAG	AGACCCGCGT	TTCCGCGCTG	GTAGAGATT	CTCGAAGACA	60
	CCAGTGGGCC	CGTGTGGAA	CAAACTCGCG	CGCGTGGCCG	GGCCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGCGCGCAAT	GCGAGGAAGT	TATCTGTAA	CTTGATCCTG	ACCTTTGCC	180
	TCTCTGTAC	AAATCCCTTT	CATGAACATA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATTGGGAA	TCTGGCATT	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAAATAA	TTCTTTGTCA	GTTGAAGG	360
35	TCAGAAATTT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AAGAAATCCAT	ATACACCATG	420
	ACCAACGACA	TCACTCAGAC	CAACGAGCAT	ACTCAGACCA	TGAGCGTCA	TCAGACCATG	480
	AGCATCACTC	AGACCAAGAG	CATCACTCTG	ACCATGATCA	TCACTCTCAC	CATAATCATG	540
	CTGCTTCTGG	TAAAAATAAG	CGAAAAGCTC	TTTGCCCGAG	CCATGACTCA	GATAGTTCAG	600
	GTAAGAGATCC	TAGAAACAGC	CAGGGGAAAG	GAGCTCACCG	ACCAGAACAT	GCCAGTGGTA	660
40	GAAGGAATGT	CAAGGACAGT	GTTAGTGCTA	GTGAAGTGAC	CTCAACTGTG	TACAACACTG	720
	TCTCTGAAGG	AACCTCAGTT	CTAGAGACAA	TAGAGACTCC	AAGACCTGGA	AAACTCTTCC	780
	CCAAAGATGT	AAGCAGCTCC	ACTCCACCCA	GTGTACATC	AAAGAGCCGG	GTGAGCCGGC	840
	TGGCTGGTGA	GAACACAAAT	GAATCTGTGA	GTGAGCCCGG	AAAAGGCTTT	ATGTATTCCA	900
	GAACACACAA	TGAAATTCCT	CAGGAGTGTT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
45	GCATGGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
	TCACCAAAAT	TGATGTCTAGA	TCTTGTCTGA	TTCATACAAG	TGAAAAGAAG	GCTGAAATCC	1080
	CTCCAAAGAC	CTATTCTATTA	CAAATAGCCT	GGGTTGGTGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTCTCT	GTCTCTGTCT	GGGGTTATCT	TAGTGCTCT	CATGAATCGG	GTGTTTTTCA	1200
	AAATTCTCTCT	GAGTTTCTCT	GTGGCACTGG	COGTTGGGAG	TTTGAGTGGT	GATGCTTTTT	1260
50	TACACCTTCT	TCCACATTTCT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
	CAATGGAAT	GAAGAAGAGGA	CCACTTTTCA	GTCTCTGTCT	TTCTCAAAAC	ATAGAAGAAA	1380
	GTGCTTATTT	TGATTCCACG	TGGAAGGGTC	TAACAGCTCT	AGGAGGCCCTG	TATTTTCATG	1440
	TTCTTGTTGA	ACATGTCTCT	ACATTGATCA	AACAAATTAA	AGATAAGAAG	AAAAAGAAAT	1500
	AGAAGAAACC	TGAAAATGAT	GATGATGTGG	AGATTAAAG	GCAGTTGTCC	AAGTATGAAT	1560
55	CTCAACTTTT	AACAAATGAG	GAGAAAGTAG	ATACAGATGA	TCGAACGTAA	GGCTATTTC	1620
	GAGCAGACTC	ACAAGAGCCC	TCCCACTTTG	ATTCTCAGCA	GCCTGCAGTC	TTGGAAGAAG	1680
	AAGAGGTCAT	GATAGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GTACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTACACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCACCAA	AACCACCATC	1860
60	CTCACAGTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTGCCCACTT	1920
	TGGCCTGGAT	GGTGATAATG	GGTGATGGCC	TGCACAATTT	CAGCGATGGC	CTAGCAATTG	1980
	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTGCT	GTGTTCTGTC	2040
	ATGAGTTGCC	TCATGAATTA	GGTGACTTTG	CTGTCTTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CCTTTATAAT	GCATTGTACG	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
65	GAATTTTCAT	TGGTCATTAT	GCTGAAAATG	TTTCTATGTG	GATATTTGCA	CTTACTGCTG	2220
	GCTTATTCAT	GTATGTTGCT	CTGGTTGATA	TGGTACCTGA	AATGCTGCAC	AATGATGCTA	2280
	GTGACCATGG	ATGTAGCCGC	TGGGGGTATT	TCCTTTTACA	GAATGCTGGG	ATGCTTTTGG	2340
	GTTTGGGAAT	TATGTTACTT	ATTTCCATAT	TTGAACATAA	AATCGTGTTT	CGTATAAATT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGAGTAGCT	TAAAAAGTTG	TCATAGTTTC	AGTAGGTCAT	2460
70	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
	TTGATTGAA	TATTGCTGTC	TGTTACAAAG	TCAGTTAAAG	GTACGTTTTA	ATATTAAAGT	2580
	TATTCTATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCAAC	GGTATTACCA	GTTTATTATG	2640
	TAAACAAGAG	ATTTGGCATG	ACATGTTCTG	TATGTTTCAG	GGAAAAATGT	CTTTAATGCT	2700
	TTTCAAGAA	CTAACACAGT	TATTCTATTA	CTGGATTTTA	GGTCTCTGAA	GAACTGCTGG	2760
75	TGTTTAGGAA	TAAGAATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACTGAATTAT	2820
	AGCAAGGAAA	TAAAGGAGAA	AAGAGAAGAA	TCTGAGAATT	GGGGAGGCAT	AGATTCTTAT	2880
	AAAAATCACA	AAATTTGTGT	TAAATTAGAG	GGGAGAAATT	TAGAAATTAG	TATAAAAAGG	2940
	CAGAAATTAGT	ATAGAGTACA	TTCAATTAAAC	ATTTTGTGCA	GGATTATTTC	CCGTAATAAC	3000
	GTAGTGAGCA	CTCTCATATA	CTAATTAGTG	TACATTTAAC	TTTGTATAAT	ACAGAAATCT	3060
80	AAATATATTT	AATGAATTTA	AGCAATATAC	ACTTGACCAA	GAAATTGGAA	TTTCAAAATG	3120
	TTCTGTGGGG	TTATATACCA	GATGAGTACA	GTGAGTAGTT	TATGTATCAC	CAGACTGGGT	3180
	TATTGCCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGTTT	ACCTGGTTTA	3240
	CAAAATTATC	AGAGTAGTAA	AACTTTGATA	TATATGAGGA	TATTAATACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTACAGAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTGT	3360

GAGCAATTGT CTTTATATAC GGTACTGTAG CCATACTAGG CCTGTCTGTG GCATTCTCTA 3420
GATGTTTCTT TTTTACACAA TAAATTCCTT ATATCAGCTT G

5

A161 PROTEIN SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
Unigene number: Hs.79136
Protein Accession #: NP_036451
Signal sequence: 1-21
Pfam domain: Zip[591-743]
Transmembrane domains: 330-346, 352-368, 427-444, 663-679, 688-703, 730-745
Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MARKLSVILI LTFALSVTNP LHELKAAAFP QTTEKISPNW ESGINVDLAI STRQYHLQQL 60
FFRYGENNSL SVEGFRKLLQ NIGIDKIKRI HIHHDHHDHS DHEHSDHER HSDHEHSDH 120
EHHSDDHDS HNHHAASGKN KRKALCPDHD SDSSGKDPKN SQKGGAHRPE HASGRNRVND 180
SVSASEVST VYNTVSEGT FLETIETPRP GLFPPKDVSS STPPSVTSKS RVSRLAGRKT 240
NESVSEPRKG FMYSRNTNEN PQECFNASKL LSHGMGIQV PLNATEFNVL CPAIINQIDA 300
RSCLHTSEK KAEIPPKTYS LQIAWVGFI AISIISPLSL LGVILVPLMN RVFPKFLLSF 360
LVALAVGTLS GDAPFLHLLPH SHASHHSHS HEEPAMEMKR GPLFSLHSSQ NIEESAYPDS 420
TNKGLTALGG LYFMFLVEHV LTLIKQFKDK KKNQKKPEN DDDVEIKQL SKYESQLSTN 480
ESKVDTDRT EGYLRADSOE FSHFDSQOPK VLEEEVSMIA HAHPEQVYNE YVPRGCKNKC 540
HSHFDTLGG SDDLHHDHHD YHHILHHDH QNHHPHSHSQ RYSREELKDA GVATLAWMI 600
MGDGLHNFSD GLAIGAAFT GLSSGLSTSV AVFCHPELPE LGDFAVLLKA GMTVKQAVLY 660
NALSAMLAYL GMATGIFIGH YAENVSMWIF ALTAGLFMYV ALVDMVPEML HNDASDHGCS 720
RWGYFFLQNA GMLLGFGLML LISIFEKIV PRINF

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A162 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
CGCGGGGCGG GGAGTCGGCG GGGCCTCGCG GGACGCGGGC AGTCGCGAGA CCGCGGCGCT 60
GAGGACGCGG GAGCGGGGAG CGCACGCGCG GGTGGAGTT CAGCCTACTC TTTCTTAGAT 120
GTGAAGAGAA AGGAAGATCA TTTTCATGCT TGTGTATAAA GGTTCAGACT TCTGCTGATT 180
CATAACCATT TGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
TGCCATAAGT GAGAAGCAAA CTTCTTGAT AACATGCTTT TCGCAAGTGC AGGAAAAATTA 300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGG TCCAAAGGTC 360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCCTGTG GGTCACTTCT 480
GGTTGCTTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG AACTCCTCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCCTACA 600
CTGCCCTCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACCACAG GGCCTTACTT 660
ATATCTGTGA CTGCTGTGAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG 720
TATAAAGAGC AAGAAACCAAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAAACTTAC 780
ATTCTCTCTG GAGAAATCCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCCCTC CTCTGCTGCT CCAAGGACTC ATAGCTAAGC AGATTGAGT GGTGAAACAG 900
ATTGGAAGAG GTGCTATGAG GGAAGTTTGG ATGGGAAAGT GGCCTGGCGA AAAGTAGTCT 960
GTGAAGTGT TCTTCAACCA AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGGACA 1080
GGGTCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
TATCTGAAGT CCACCAACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCCTCTGTC 1200
AGTGGCTTAT GTCAATTACA CACAGAAATC TTTAGTACTC AAGGCAACCC AGCAATTGCC 1260
CATCGAGATC TGAAAGATGA AAACATTCTG GTGAAGAAAA ATGGAACCTG CTGTATTGCT 1320
GACCTGGGCC TGCGTGTATA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
ACTCGAGTTG GCACCAACAG CTATATGCCT CCAGAAGTGT TGGACGAGAG CTTGAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CCTTTGGGAG 1500
GTTGCTAGGA GATGTGTATC AGGAGGTATA GTGGAAGAAT ACCAGCTTCC TTATCATGAC 1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAG ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620
CGCCCTCAT TCCCAAAACG GTGGAGCAGT GATGAGTGTG TAAGGCAGAT GGGAAAACTC 1680
ATGACAGAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTTAAGAAA 1740
ACACTTGCCA AAATGTCAGA GTCCCAGGAC ATTAACTCTG GATAGGAGAG GAAAAGTAAG 1800
CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAAA 1860
TAAGCATCCA CAGTACAAGC CTTGAACATC GTCTGCTTC CAGTGGGTG CAGACCTCAC 1920
CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
TCTGTTTGA GCGGAGAGAA CCGTTGGGTA ACTGTTTCAA GATATGATGC AT

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A163 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.72472 / Hs.87223
Probeset Accession #: AA250737 / U89326
Protein Accession #: NP_001194
Signal sequence: 1-13
Transmembrane domains: 128-144
PFAM domains: activin_receptor [30-111], protein kinase [204-491]
Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
5  MLLRSAGKLN VGTKKEDGES TAPTTPRPVKL RCKCHHHCE DSVNNICSTD GYCFTMIEED 60
   DSGLEPVVTS GLGLEGSDFQ CRDTPIPHQR RSIECCTERN ECKNDLHPTL PPLKNRDFVD 120
   GPIHHRALLI SVTVCSLLLV LIILFCYFRY KRQETRPYS IGLEQDETYI PPGESLRDLI 180
   EQSQSSGSGS GLPLLQRTI AKQIQMVQKI GKGRYGEVWM GKWRGEKVAV KVFFTEEAS 240
   WFRETEIYQT VLMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTTLDAKS 300
10  MLKLAYSSVS GLCHLHTEIF STQKPAIAH RDLKSKNIV KKNGTCCIAI LGLAVKFISD 360
   TNEVDIPNPT RVGTIKYMPP EVLDESLNRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
   EYQLPYIDIL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480
   RLTAIRVKKT LAQMSQDI KL

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A164 DNA sequence

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15  Gene name: ESTs
   Unigene number: Hs.157601
   Probeset Accession #: W07459
   Nucleic Acid Accession #: AC005383
   Coding Sequence: 328-2751 (underlined sequences correspond to start and stop codons)
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1      11      21      31      41      51
|      |      |      |      |      |
25  GACAGTGTTC GCGGCTGCAC CGCTCGGAGG CTGGGTGACC GCGGTAGAAG TGAAGTACTT 60
   TTTTATTGTC AGACCTGGGC CGATGCCGCT TTAATAAACG CGAGGGGCTC TATGCACCTC 120
   CCTGGCGGTA GTTCTCCCGA CCTCAGCCGG GTCCGGTCTGT GCCGCCCTCT CCCAGGAGAG 180
   ACAAAACAGGT GTCCCACTGG GCAGCCGCGC CCCGGGGCGC CCTCCTGTGA TCCCGTAGCG 240
   CCCCCCTGCC CGAGCCGCGC CCGGGTCTGT GAGTAGAGCC GCCCGGGCAC CGAGCGCTGG 300
   TCGCCGCTCT CCTTCGGTTA TATCAACATG CCCCCTTTCC TGTGTCTGGA GCGCGTCTGT 360
30  GTTTTCCTGT TTTCCAGAGT GCCCCATCT CTCCCTCTCC AGGAAGTCCA TGTAAGCAA 420
   GAAACCATCG GGAAGATTTC AGCTGCCAGC AAAATGATGT GGTGCTCGCC TGCAGTGGAC 480
   ATCATGTTTC TGTAGATGG GTCTAACAGC GTCCGGAAAG GGAGCTTTGA AAGGTCCAAG 540
   CACTTTGCCA TCACAGTCTG TGACGGTCTG GACATCAGCC CGAGAGGGGT CAGAGTGGGA 600
   GCATTCCAGT TCAGTTCCAC TCCTCATCTG GAATTCCTCT TGAATTCATT TTCAACCCAA 660
35  CAGGAAGTGA AGGCAAGAAT CAAGAGGATG GTTTTCAAAG GAGGGCGCAC GGAGACGGAA 720
   CTGTCTCTGA AATACCTTCT GCACAGAGGG TTGCTGGAG GCAGAAATGC TTCTGTGCC 780
   CAGATCTCTA TCATCTGTAC TGATGGGAAG TCCAGGGGG ATGTGGCACT GCCATCCAAG 840
   CAGCTGAAGG AAAGGGGTGT CACTGTGTTT GCTGTGGGG TCAGGTCTCC CAGGTGGGAG 900
   GAGCTGCATG CACTGGCCAG CGAGCCTAGA GGGCAGCACG TGCTGTGGC TGAGCAGGTG 960
40  GAGGATGCCA CCAACGCCCT CTTACGACCC CTCAGCAGCT CGGCCATCTG CTCAGCGCC 1020
   ACGCCAGACT GCAGGGTCCA GGCTCACCCC TGTGAGCACA GACGCTGGA GATGTCGG 1080
   GAGTTGCTG GCAATGCGCG ATGCTGGAGA GGATCGGGC GGACCTTGC GTGTGCTGG 1140
   GCACACTGTC CCTTCTACAG CTGGAAGAGA GTGTTCTCAA CCCACCTGTC CACTGCTAC 1200
   AGGACCCAG CTCTGTGGG CAGCCCTGOC CAGCCCTGOC AGAATGGAGG CACATGTGTT 1260
45  CCAGAAGGAC TGGACGGCTA CCAGTGCCTC TGCCCGCTGG CCTTGGAGG GGAGGCTAAC 1320
   TGTGCCCTGA AGCTGAGCCT GGAATGCAGG GTCCAGCTCC TCTTCTGCTT GGACAGCTCT 1380
   GCGGGCACCA CTCTGGAAGG CTTCTGCGG GCCAAAGTCT TGTGAGAGCG GTTGTGCGG 1440
   GCGGTGCTGA GCGAGGACTC TCGGGCCCGA GTGGGTGTGG CCACATACAG CAGGGAGCTG 1500
   CTGTTGCGCG TCGCTGTGGG GAGTACCAG GATGTGCTG ACCTGTGCTG GAGCCTCGAT 1560
50  GGCAATTCCT TCCGTGTGG CCCCACCTG ACGGGCACTG CCTTGGGCA GCGGCGAGAG 1620
   CGTGGCTTGC GGAGGCCAC CAGGACAGGC CAGGACCGGC CACGTAGAGT GGTGTTTGT 1680
   CTCACTAGAT CACTCTCGA GGATGAGGTT GCGGGCCAG CGCGTACGC AAGGGCGCGA 1740
   GAGCTGCTCC TGCTGGGTGT ABGCACTGAG GCGGTGCGG CAGAGCTGGA GGAGATCACA 1800
   GGCAAGCCAA AGCATGTGAT GGTCTACTCG GATCCTCAGG ATCTGTTCAA CCAAATCCCT 1860
55  GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG CGGCCAGGCT GCGGACACA AGCCCTGGAC 1920
   CTCGTCTTCA TGTGAGACAC CTCTGCCCTA GTAGGGCCCG AGAATTTTGC TCAGATGCAG 1980
   AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT GAGGTGAACC CTGACGTGAC ACAGGTCCGC 2040
   CTGTGTGTGT ATGCGAGCCA GGTGCAGACT GCTTCCGGGC TGACACCAA ACCCACCGG 2100
   GCTGCGATGC TGCGGGCCAT TAGCCAGGCC CACTACCTAG GTGGGTGGG CTCAGCCGGC 2160
60  ACCGCCCTGC TGACATCTA TGACAAAGTG ATGACCGTCC AGAGGGGTGC CCGGCTGGT 2220
   GTCCCCAAG CTGTGGTGGT GCTCACAGGC GGGAGAGGCG CAGAGGATGC AGCCGTTCT 2280
   GCCCAGAAGC TGAGGAACAA TGGCATCTCT GTCTGGTGG TGGCGTGGG GCTGTCTTA 2340
   AGTGAGGCTC TGCGGAGGCT TGACAGTCCC CGGATTTCCC TGATCCAGT GGCAGCTTAC 2400
   GCGAGCCTGC GGTACACCA GGAAGTGTCT ATGAGTGGC TGTGTGAGA AGCCAGCAG 2460
65  CCAGTCAACC TCTCAAACC CAGCCCGTGC ATGAATGAGG GCAGCTGCGT CTGACAGAAT 2520
   GGGAGCTACC GCTCAAGTG TCGGATGCG TGGGAGGGCC CCCACTGCGA GAACCGTGAG 2580
   TGGAGCTCTT GCTCTGTATG TGTGAGCCAG GGATGGATT TTAGAGCGCC CTGAGGCAC 2640
   ATGCTCCCG TGCGAGGGG CAGCAGCGT ACCCTCCCA GCAACTACAG AGAAGGCCCTG 2700
   GGCACTGAAA TGGTGCTTAC CTTCTGGAAT GTCTGTGCC CAGGTCTCTA GAATGTCTG 2760
70  TTCCCGCGCT GGCCAGGACC ACTATTCTCA CTGAGGAGG AGGATGTCCC AACTGCAGCC 2820
   ATGCTGCTTA GAGACAAGAA AGCAGCTGAT GTCAACACA AACGATGTTG TTGAAAAGTT 2880
   TTGATGTGTA AGTAAATACC CACTTTCTGT ACCTGCTGTG CCTTGTGAG GCTATGTAT 2940
   CTGCCACCTT TCCCTTGAGG ATAAACAAGG GGTCTCTAAG ACTTAAATTT AGCGGCTGTA 3000
   CGTTCCTTT TAGAGCATCC TTTGGACGGC GAAGGCCACG GCCTTTCAAG ATGGAAGCA 3060
75  AGGCCTTTAC CACTTCCCCA GAGACATTCT GGATGCATT GCATTGAGTC TGAAGGGGG 3120
   GCAAGTTCCT CACTTCCCCA GAGACATTCT GGATGCATT GCATTGAGTC TGAAGGGGG 3180
   CTGAGGGGAC GTTGTGACT TCTTGGCGAC TGCTTTTGT GTGTGGAAGA GACTTGGAAA 3240
   GGTCTCAGAC TGAATGTGAC CAATTAAACA GCTTGTGTA TGATGGGGGA GGGGCTGAGT 3300
80  TGTGCATGG CCCAGGCTG GAGGCCACG TAAATCGTT CTGAGTCTGT AGCAGTGTCC 3360
   ACCTTGAAGG TCTTC

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A165 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
MPPFLLEAV CVFLFSRVPP SLPLQEVHVS KETIGKISAA SKMMWCSAAV DIMFLLDGSN 60
SVGKGSFERS KHFAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRRET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERGVTV 180
FAVGVRFFRW EELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCPFYSWK RVFLTHPATC YRTTCGPGCD 300
SQPCQNGGTC VPEGLDGYQK LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDGFL 360
RAKVVFVRKFV RAVLESDSRA RVGVATYSRE LLVAVPVGEY QDVPDLVWSL DGIPFRGGPT 420
LTGSALRQAA ERGFGSATRT QQDRPRRVVV LLTSHSEDE VAGPARHARA RELLLLGVS 480
EAVRAELEBI TGSPKXVMVY SDPQDLFNQI PBLQGLKCSR QRPQCRTQAL DLVFMLD TSA 540
SVGPENFAQM QSFVRSCALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
APYLGSGVGA QSLALHIYDK VMTVQRGARP GVPKAVVVLV GGRGAEDAAV PAQKLRRNGI 660
SVLVVGVGPV LSEGLRLLAG PRDSLHVAA YADLRVHQDV LIEWLCGEAK QFVNLCCKPSP 720
CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
RTPPSNYREG LGTEMVPTFW NVCAPGP

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A166 DNA sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Probeset Accession #: AA011176
 Nucleic Acid Accession #: AF272890
 Coding Sequence: 87-1520 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
TGCTACCCGC GCCCGGGCTT CTGGGGTGTG CCCCAACCAC GCGCCAGCCC TGCCACACCC 60
CCCGCCCCCG GCCTCCGCAG CTCGGCATGG GCGGGGGGGT GCTCGTCTTG GCGCCTCCG 120
AGCCCGGTAA CCTGTGTCGC GCCGCACCGC TCCCGACGCG CGCGGCCACC GCGCGCGGCG 180
TGCTGTGTCG CGCGTGCGCG CCCGCTCTGT TGCTGCTCCG CGCCAGCGAA AGCCCCGAGC 240
CGCTGTCTCA CCACTGGACA GCGGGCATGG GTCTGCTGAT GGCGCTCATC GTGCTGCTCA 300
TCGTGGCGGG CAATGTGCTG GTGATCGTGG CCATCGCCAA GACGCGCGCG CTGCAGACGC 360
TCACCAACCT CTTTCATCATG TCCCTGGCCA GCGCGACCTT GGTCTATGGG CTGCTGCTGG 420
TGCCGTTCGG GGCACCATC GTGCTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGCG 480
AGCTGTGGAC CTCAGTGGAC GTGCTGTGGG TGAAGGCGAC CATGAGACCT CTGTGTGTCA 540
TTGCCCTGGA CCGCTACCTC GCCATCACCT CGCCCTTCGG CTACAGAGC CTGCTGACGC 600
GCGCGCGGCG GCGGGGCTCT GTGTGCAACG TGTGGGCGAT CTGCGCCCTG GTGTCTCTCC 660
TGCCCATCCT CATGCACTGG TGGCGGGGCG AGAGCGACGA GCGCGCGCGG TGCTACACG 720
ACCCCAAGTG CTGCGACTTC GTCAACCACT GCGCCTACGC CATCGCCTCG TCCGTAGTCT 780
CCTTCTACGT GCCCTGTGTC ATCATGGCCT TCGTGTACTT GCGGGTGTTC CCGAGGCGCC 840
AGAAGCAGT GAAGAAGATC GACAGCTGCG AGCGCGGTTT CCTCGCGCGC CCAGCGCGGC 900
CGCCCTCGCC CTCGCTCTCG CCCGTCCCGG CGCCCGCGCC GCGCGCGCGC CCGCGCGGCC 960
CGCGCGCGCG CGCGCGCTCG GCGCGGCTCG CCAACGGGCG TGCGGTAAAG CGGCGGCGCT 1020
CGCGCTCTGT GGCCTACGCG GAGCAGAAGG CGCTCAAGAC GCTGGGCATC ATCATGGGCG 1080
TCTTACAGCT CTGCTGGCTG CCTTCTCTCC TGGCCAAAGT GGTGAAGGCC TTCCACGCGC 1140
AGCTGTGTCC CGACCGGCTC TTCTCTCTCT TCAACTGGCT GGGCTACGCC AACTCGGCTC 1200
TCAACCCCAT CATCTACTGC CGCAGCCCGG ACTTCGCGAA GGCCTTCCAG GGAAGTCTCT 1260
GCTGCGCGCG CAGGGCTGCC CGCGCGCGCC AGCGGACCCA CGGAGACCGG CCGCGCGCCT 1320
CGGCTGTCTT GCGCGGCGCC GACCGCCCGC CATCGCCCGG GCGCGCTCG GACGACGACG 1380
ACGACGATGT CGTGGGGGCC ACGCGCGCCG CGCGCGCTGT GAGCGCTTGG GCGCGCTGCA 1440
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CCTCGGAATC CAAGGTGTAG GCGCGCGCGC GGGCGCGGGA CTCCGGGCAC GGCTTCCGAG 1560
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CCTGTCTGTA ATCATCGGAG GCAAGAGAA AAGCCACGGA CCGTGCACA AAAAGGAAAG 1680
TTTGGGAAGG GATGGGAGAG TGGCTGTCTG ATGTTCCTTG TGG

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A167 Protein sequence

Gene name: Homo sapiens beta-1 adrenergic receptor mRNA, 3' UTR
 Unigene number: Hs.37744
 Protein Accession #: AA011176
 Signal sequence: none found
 Transmembrane domains: 62-84, 95-117, 135-157, 177-198, 226-248
 Pfam domain: 7tm_1 [75-377]
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MGAGVLVIGA SEPGNLSSAA FLPGDAATAA RLLVPASPPA SLLPPASESP EPLSQWTAG 60
MGLLMALIVL LIVAGNVLVI VAIKTPRLQ TLTNLFIMSL ASADLVMLGL VVFPFGATIV 120

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5 WGRWEYGSFF CELWTSVDVL CVTASIELTC VIALDRYLAI TSPFRYQSLT TRARARGLVC 180
 TWVAISALVS FLPIIMHWHWR AESDEARRCY NDPKCCDFVT NRAYAIASSV VSFYVPLCIM 240
 AFVYLRLVRE AQKQVKKIDS CERRFLGGPA RPPSPSPSPV PAPAPPPGPF RPAAAAATAP 300
 LANGRAGRRR PSRLVALREQ KALKTLGIIM GVFTLCWLPF FLANVVKAFH RELVPDRLFV 360
 FFWNLGYANS AFNPFIYCRS PDPRKAPQGL LCCARRAARR RHATHGDRPR ASGCLARPGV 420
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10 A168 DNA sequence
 Gene name: CEGP1
 Unigene number: Hs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 15 Coding sequence: 81-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 30 GCAGCGTCGC CTGTGAGTGC AGGCTGTGTT TTGAGCTGGC CAAGAACCAG AGAGACTGCA 720
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 75 TTGGTCAGCC TAGGTGAGAC TCACCTGTCC TTCTGGGGTC TTAATCTCTC TCAAGGAGTC 3420
 TGTAGTGGAA AGGAGGCCAC AGAATAAGCT GCTTATTCTG AAACCTCAGC TTCTCTTAGC 3480
 CCGGCCCTCT CTAAGGGAGC CCTCTGCAC CTGTGTCAGG CTCTGACCA GAGAAACAGG 3540
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 AGCACTTCTG GAGACAT

A169 Protein sequence
 Gene name: CEGP1
 Unigene number: Hs.222399

Probeset Accession #: AA256485
 Protein Accession #: CAB92285
 Signal sequence: 1-31
 Transmembrane domains: none
 5 PFAM domains: EGF-like_domains [49-84,132-167,177-213,286-321,407-442] CUB_domain [809-918]
 Cellular Localization: may be secreted

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 MGVAGRNRP AANAVLLLLL LLPPLLLLAG AVPPGRGAA GPQEDVDECA QGLDDCHADA 60
 LCQNTPTSYK CSCKPGYQGE GRQCEDIDEC GNEELNGGCVH DCLNIPGNYR CTCFDGFMIA 120
 HDGHNCLDVD ECLENNNGGCG HTCVNVMSY ECCCKEGFPL SDNQHTCIHR SEEGLSOMNK 180
 15 DHGCSHICKE APRGSVACEC RPFGLAKNQ RDCILTCNHG NGGCQHSDD TADGPECSCH 240
 PQYKMTDGR SCLEREDTVL EVTESNTTSV VDGDKRVKRR LLMETCAVNN GGCDRTCKDT 300
 STGVHSCFPV GFTLQLDGRK CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFLLTDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLYGFTH CGDTNECSIN NGGCQVCVN 420
 TVGSYECQCH PGYKLHWNKK DCVEVKGLLP TSVSPRVSLH CGKSGGSDGC FLRCHSGIHL 480
 20 SSDVTITRTS VTFKLNKGK SLKNAELFPE GLRPALPEKH SSVKESFRYV NLTCSSGKQV 540
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 FHQLQSGMNL DVAKPPPTS ERQAESCQGV QGHAENQCVS CRAGTYDGA RERCILCPNG 660
 TTFQNEGQMT CEPCCRPNGS GALKTPEAWN MSECGLCQP GEYSADGFAP CQLCALGTFQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSGPHFY NTHTHRCIRC PVGTYYQPEFG 780
 25 KNNCVSCPGN ITQCKNRRCG IELGDFITGYI ESPNYPGNYV ANTECTWTIN 840
 PPFKRRLIV VPEIFLPIED DQGDYLVMRK TSSSNVTTY ETCQTYERPI AFTSRSKKLW 900
 IQFKSNENGS ARGFQVPYVT YDEDYQELIE DIVRDGRLYA SENHQEILKD KKLKALFDV 960
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30 A170 DNA sequence
 Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Nucleic Acid Accession #: AF007170
 35 Coding sequence: 1-1725 (underlined sequences correspond to stop codon)

1 11 21 31 41 51
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 AAGGAGGCGG CCTCCGGGAA AAGCGACCGC AGGACTCCTG AGAGCAGCCT CCATGAGGCC 60
 CTGGACCACT GCATGACCGC CCTGGACCTC TTCCTCACCA ACCAGTTCTC AGAAGCACTC 120
 40 AGCTACCTCA AGCCAGAAC CAAGGAAAGC ATGTACCACT CACTGACATA TGCCACCATC 180
 CTGGAGATGC AGCCCATGAT GACCTTTGAC CCTCAGGACA TCCTGCTTGC CGGCAACATG 240
 ATGAAGGAGG CACAGATGCT GTGTGAGAGG CACCGGAGGA AGTCTTCTGT AACAGATTCC 300
 TTCAGCAGCG TGGTGAACCG CCCCACTGCT GGCCAAATTC CTGAAGAAGA AATCCACGCT 360
 45 GAGGTCTGCT ATGCAGAGTG CCTGTGCGAG CGAGCAGCCC TGACCTTCTC GCAGGACGAG 420
 AACATGGTGA GCTTCATCAA AGGCGGCATC AAGTTGGA ACAGCTACCA GACCTACAAG 480
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 80 AAATTTGGGG GGCAGGAGGA GGTTCCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
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 AA

A171 Protein sequence

Gene name: DEME-6 protein (KIAA0452)
 Unigene number: Hs.125783
 Probeset Accession #: AL039402
 Protein Accession #: AAC39582
 Signal sequence: none
 Transmembrane domains: 210-226
 Cellular Localization: plasma membrane

10 1 11 21 31 41 51
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 MTLALDLFLTN QFSEALSYLK PRTKESMYHS LTYATILEMQ AMMTFDPQDI LLAGNMMKEA 60
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 FIKGGIKVRN SYQTYKELDS LVQSSQYCKG ENHPHFEGGV KLGVGAFNLT LSLMPLTRILR 180
 15 LLEFVFGSGN KDYGLLQLEE GASGHSFRSV LCVMLLLCYH TFLTFLVLGTG NVNIEEAEKL 240
 LKPYLNRYPK GAIFLFFAGR IEVIKGNIDA AIRRFEECE AQQHWKQPHH MCYWELMWCF 300
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 KLIKAGKSLP TEKFAIRKSR RYFSSNPISL PVPALEMYI WNGYAVIGKQ PKLTDGILBI 420
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 20 LIPNALLLELA LLLMEQDRNE EAIKLLSAK QNYKNYSMES RTHFRQAAT LQAKSSLENS 540
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A172 DNA sequence

Gene name: EST
 Unigene number: Hs.200102
 Probeset Accession #: AL117406
 Nucleic Acid Accession #: none found
 Coding sequence: 1-4044 (underlined sequences correspond to start and stop codons)

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 70 AGTCAGGCTC TGGCCACCTC CCTGGAAGAG TCTCTCAACG GAAATGCTGT GCGGAGCAT 2220
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 75 AATCTCAAC TCTCCTTCTA CCAGCTGGTG TAAGGGCTCA ACGCCCTGCT CCTCATCTGT 2520
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	CCACAGCATG GGGAAATCAT ATTTACAGGAT TATCACATGA AATACAGAGA CAACACACCC 3360
	ACCGTGTCTC ACGGCATCAA CCTGACCATC CGCGGCCACG AAGTGGTGGG CATCGTGGGA 3420
	AGGACGGGCT CTGGGAAGTC CTCCTTGGGC ATGGCTCTCT TCGGCCTGGT GGAGCCCATG 3480
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	TCCAAGCTCT CAGTGATCCC TCAAGATCCA GTGCTGCTCT CAGGAACCAT CAGATTCAAC 3600
10	CTAGATCCCT TTGACCGTCA CACTGACCAG CAGATCTGGG ATGCCTTGGG GAGGACATTG 3660
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	GGAAACTTCT CTGTGGGGGA GAGGCAGCTG CTCTGCATTG CCAGGGCTGT GCTTCGCAAC 3780
	TCCAAGATCA TCCTTATCGA TGAAGCCACA GCCTCCATTG ACATGGAGAC AGACACCTTG 3840
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	ACAGCCACTT ATGCTGAGAG ATAAGGAGAT GTGGAGACTT CATGGAGGCT GGCAGCTGAG 4080
	CTCAGAGGTT CACACAGGTG CAGCTTCGAG GCCACAGATC TGCGACCTTC TTGTTGGGAG 4140
	ATGAGAAGCT CTCCTGGAAG CAGGGGTAAA TGTAGGGGGG GTGGGGATTG CTGGATGGAA 4200
20	ACCTTGGAAAT AGGCTACTTG ATGGCTCTCA AGACCTTAGA ACCCCAGAAC CATCTAAGAC 4260
	ATGGGATTCA GTGATCATGT GGTTCCTCTT TTAACCTACA TGCTGAATAA TTTTATAATA 4320
	AGGTAAAGC TTATAGTATT CTGATCTGTG TTAGAAGTGY TGCAATGCT GTACTGACTT 4380
	TGTAATAATAT AAAACTAAGG AAAACTCAAA AAAAAAAAAA AAAAAA
25	<u>A173 Protein sequence</u>
	Gene name: EST
	Unigene number: Hs.200102
	Probeset Accession #: AL117406
	Protein Accession #: none found
30	Signal sequence: none found
	Transmembrane domains: 169-185, 199-215, 275-291, 304-320, 387-403, 770-786, 829-845, 907-923, 927-943, 1018-1034
	PFAM domains: ABC_transporter [502-673], ABC_membrane_region [163-432, 771-1060]
	ATP-binding_domains [508-516, 1139-1147]
35	Cellular Localization: plasma membrane
40	1 11 21 31 41 51
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	WGKYDAALRT MIPFRPKPRF PAPQPLDNAG LFSYLTVSWL TPLMIQSLRS RLIDENTIPPL 120
	SVHDSADKNV QRLHRLWEEV VSRRGIEKAS VLLVMLRFQR TRLIFDALIG ICFCIASVLG 180
	PILITPKILE YSEEQLEGNV HGVLCLFALF LSECVKSLSF SSSWIINQRT AIRFRAAVSS 240
	FAFEKLIQFK SVIHITSGEA ISFFTGDVNY LFEGVCYGPL VLITCASLVI CSISSYFIIG 300
	YTAFIAILCY LLVFPLAVFM TRMAVKAQHH TSEVSDQIR VISEVLTCIK LIKMYTWEKP 360
45	PAKIEGMES LTPCSXPQGG MAPSMLASLN LLRLSVFFVP IAVKGLTNSR SAVMRFKKFP 420
	LQESPVFVYQ LQDDPSKALV FEEATLSWQQ TCPGIVNGAL ELERNGHASE GMTRPRDALG 480
	PEEENSLGP ELHKINLVVS KGMMLGVCNG TGSGKSSLLS AILEEMHLE GSVGVQGSLLA 540
	YVPOQAWIVS GNIRENIMLG GAYDKARYLQ VLHCCSLNRD LELLFPDGMT EIGERGLNLS 600
	GGQKQRISLA RAVYSRQIY LLDDPLSAVD AHVGKHIFEE CIKTLRGT VVLVTHQLQY 660
50	LEFCQIILL ENGKICENTG HSELMQKKGK YAQLIQMKHK EATSDMLQDT AKIAEKPKVE 720
	SQALATSLKE SLGNNAVPEH QLTQEEMEE GSLSWRVYHH YIQAGGYMV SCIIFFPVVL 780
	IVFLTTFSWF WLSYNLEQGS GTNSRESNNG TMADLGNLAD NPQLSFYQLV YGLNALLLIC 840
	VGVCCSGIFT KVTAKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP 900
	IFSEQPLVLS LMVIAVLLIV SVLSPYILLM GAIIMVICPI YMMFKKAIG VFKRLENYSR 960
55	SPLPSHILNS LQGLSSIHVY GKTEDFISQF KRLTDAQNNY LLLFLSSTRW MALRLEIMTN 1020
	LVTLAVALFV AFGISSTPYG FKVMANIVL QLASSPQATA RIGLETAQF TAVERILQYM 1080
	KMCVSEAPLH MEGTSCPOGW PQHGEIIFQD YHMKYRDNTF TVLHGINTLI RGHEVVGIVG 1140
	RTGSGKSLG MALFRIVBPM AGRILIDVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRPN 1200
60	LDPFRDHTDQ QIWDALERTF LTKAISKFPK KLHTDVVENG GNFSVGERQL LCIAARAVLRN 1260
	SKILIDEAT ASIDMETDTL IQRTIREAFQ GCTVLVIAHR VTTVLNCDHI LVMGNKGKVE 1320
	FDRPEVLRKK PGSLPAALMA TATSSLR
65	<u>A174 DNA sequence</u>
	Gene name: ESTs
	Unigene number: Hs.128899
	Probeset Accession #: AA983251
	Nucleic Acid Accession #: AA983251
	Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)
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	ATGCTGTCTG GCTTCTTGAT GAGTCCAGT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
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75	GACCGGAGGA GGGAGAGCCG GCCGGAGGCT GCGCGGCTCC TGTGGGACCG CGCTGCAGCC 180
	GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240
	CCGCGGCGCG CGCAGCTGG CAGAGCTCCC GGGACTGCGG CTGGGGGCGC GCAGGACCTC 300
	CGCTCGGCTC CTGACGCTTC CCGGGGGAGG GTCCGGTTGC CAGTGAACCC TCCAGAGGCT 360
	TCCGGACGAC AGCCCCGGGG GCCTTCTGAC TGATCCCGGA GATTTCATC AGCGAGTGCA 420
80	ACTCATAAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
	GCTCCTGGAC CTAGGGCCCG GCCTCGTGGC CTCTCGGGCG TCGCGGAGA GGGGAGTGGC 540
	CGCGCGGAA AGCGCCGCGG GACAGTCAGT GACGAGGCCC GGGGGTGGCC GGGGCCACGA 600
	CTTCTCGGAG ACCGTCTCTG GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTGCCA 660
	TGTGGGGCGC TCGCGCTCTG TCCGCTCTCT CATCTCGGAA CGCGGCTTCG CTCTGCAGC 720
	TGCTGCTGGC TCGCTGCTG GCGGCGGGGG CGAGGGCCCA GCGCGAGTA CTGCCACGGC 780

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TTTTTAATA ACCAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAAATA AAAAAAATA AAAAAAATA
  
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A175 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

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 65
 70

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1      11      21      31      41      51
|      |      |      |      |      |
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GEAEKGNRGE PPWIRAOQQ PRPPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPPPEA 120
SGRQPRGPSD CIPRFPASAS THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAAEGSSG 180
PRGKRRGTVS DEARGSPGPR LLGDRPALSG DALSAPRVVP CGALAAAPSP HPGTPLRSCS 240
CCWLRCMRRG RGPSSGYCHG WLDAGQVWRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
ARLDQGGCDN DRQQAGGEPG RADKDGPRL GRASCLRGTQ GDGEGAPFPV RAWQRCSPFG 360
SPKGRQLLRA FPGLLPRARR RGFPSSPRGG PSPLQRPALP IYVPFLIVGS VFVAFILGS 420
LVAACCCRCI RPKQDPQQR APGNNRLMET IPMIPSASTS RGSSSRQSST AASSSSSANS 480
GARAPPTRSQ TNCCLPBETH NNVVNMPTN FSVLNCQAT QIVPHQGYL HPYVGYTVQ 540
HDSVPMTAVP PFMDGLQPGY RQIQSPFFHT NSEQRMYPV TV
  
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A176 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

80

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 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCCTCATGC TGAAGGAGCA GAACCGACTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAOCG AGCTGGAGCA GGAGAACTCG 480
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 30 CCGATGCGG GGTCACTGGG TGGGGGGCGC AGGGCCCCCT CGTGTCCAGG GCACCTTGTG 1800
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 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

A177 DNA SEQUENCE

55 Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

60 1 11 21 31 41 51
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 65 CCTCCGAGCC GTGCCGGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GGGGAGGGG 180
 CCGAGCAGGA GCGCGGCCAG GCGCTGGGGA AAGTATTCAT GGGCTGCCCT GGGCAAGAGC 240
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 70 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCCTGAAAAT GGCAAGGGTC 420
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A178 Protein sequence:

35 Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675
 40 Cellular localization: plasma membrane

45 1 11 21 31 41 51
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 KGPPFORLQ LKSNDRDQK IFYSITGPGA DSPPEGVFAV EKETGWLLN KPLDREEIAK 180
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 50 DEDDAIITYN GVVAYSISHS EPKDPHDLMP TIHRSTGTIS VISSGLDREK VPEYTLTIQA 300
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 PTSTATIVVH VEDVNEAPVF VPPSKVVEVQ EGIPTGEFVC VYTAEDPDKE NQKISYRILR 480
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 GAVLALLPLL LVLLLVRK RKIKEPLLLP EDDTRDNVFP YGEEGGGEED QDYDITQLHR 720
 GLEARPEVVL RNDVAPTII TPMYRPRPAN PDEIGNFIIE NLKAANTDPT APFYDTLLVF 780
 DYEAGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRPKILA DMYGGGEDD

A179 DNA SEQUENCE

60 Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7
 Unigene number: Hs.258583
 Probeset Accession #: NM_012152
 65 Nucleic Acid Accession #: NM_012152
 Coding sequence: 43-1104 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 CTTCCTTAAA TTTCTTTCTA GGATGTTTAC TTCTTCTCCA CAATGAATGA GTGTCACTAT 60
 GACAACACA TGAGACTTTT TTATAATAGG AGCAACACTG ATACTGTGCA TGACTGGACA 120
 GGAACAAGC TTGTGATTGT TTGTGTGTTT GGGACGTTT TCTGCCCTGT TATTTTTTTT 180
 TCTAATCTCT TGTCTATCGC GGCAGTGATC AAAAAACAGAA AATTTCATT CCCCTCTAC 240
 75 TACCTGTTGG CTAATTAGC TGCTGCGGAT TTCTTCGCTG GAATTGCCIA TGTATTCTCTG 300
 ATGTTTAAACA CAGGCCCACT TTCAAAAACT TTGACTGTCA ACCGCTGGTT TCTCCGTCAG 360
 GGGCTTCTGG ACAGTAGCTT GACTGCTTCC CTCACCAACT TGCTGGTTAT CGCCGTGGAG 420
 AGGCACATGT CAATCATGAG GATGCGGGTC CATAGCAACC TGACCAAAAA GAGGGTGACA 480
 CTGCTCATTT TGCTTGTCTG GGCCATCGCC ATTTTATAGG GGGCGGTCCC CACACTGGGC 540
 80 TGGAAATGCC TCTGCAACAT CTCTGCCCTG TCTTCCCTGG CCCCATTTA CAGCAGGAGT 600
 TACCTTGTCT TCTGGACAGT GTCCAACTCT ATGGCCTTCC TCATCATGGT TGTGGTGTAC 660
 CTGCGGATCT ACGTGTACGT CAAGAGGAAA ACCAAGCTCT TGTCTCCGCA TACAAGTGGG 720
 TCCATCAGCC GCGGAGGAC ACCCATGAAG CTAATGAAGA CGGTGATGAC TGTCTTAGGG 780

	GGCTTTGTGG	TATGCTGGAC	CCCGGGCCTG	GTGGTTCTGC	TCCTCGACGG	CCTGAACCTGC	840
	AGGCAGTGTG	GCCTGCAGCA	TGTGAAAAGG	TGTTTCCTGC	TGCTGGCGCT	GCTCAACTCC	900
	GTCGTGAACC	CCATCATCTA	CTCCTACAAG	GACGAGGACA	TGTATGGCAC	CATGAAGAAG	960
5	ATGATCTGCT	GCTTCTCTCA	GGAGAACC	GAGAGCGTC	CCTCTGGCAT	CCCCCTCACA	1020
	GTCCTCAGCA	GGAGTGACAC	AGGCAGCCAG	TACATAGAGG	ATAGTATTAG	CCAAGGTGCA	1080
	GTCTGCAATA	AAAGCACTTC	<u>CTAAACTCTG</u>	GATGCCTCTC	GGCCACCCA	GGTGATGACT	1140
	GTCTTAGG						
10	<u>A180 Protein sequence:</u>						
	Gene name: endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 7						
	Unigene number: Hs.258583						
	Probeset Accession #: NM_012152						
15	Protein Accession #: NP_036284						
	Signal sequence: none found						
	Transmembrane domains: 31-53, 66-88, 150-172, 190-211, 239-261, 277-295						
	Cellular Localization: plasma membrane						
20	1	11	21	31	41	51	
	MNECHYDKHM	DFYFNRSNTD	TVDDWTGTLK	VIVLCVGTFF	CLFIPFNSNL	VIAAVIKNRK	60
	FHEFFYYLLA	NLAADFFAG	IAYVFLMFNT	GFVSKTLTVN	RWPLRQGLLD	SSLTASLTNL	120
25	LVIAYERHMS	IMRMVRHNSL	TKKRVTLLIL	LVWAIAIFMG	AVPTLGNCL	CNISACSSLA	180
	PIYSRSLYLV	WTYSNLMAPL	IMVVVYLRIY	VYVKKRTNVL	SPHTSGSISR	RRTPMKLMKT	240
	VMTVLGAFVV	CWTPGLVLL	LDGLNCRQCG	VQHVKNRFL	LALLNSVNVN	IISYKDEDM	300
	YGTMMKIMIC	FSQENPERRP	SRIPSTVLSR	SDTGSQVIED	SISQGAVCNK	STS	
30	<u>A181 DNA SEQUENCE</u>						
	Gene name: ESTs						
	Unigene number: Hs.162859						
	Probeset Accession #: AA569531						
	Nucleic Acid Accession #: AA569531						
35	Coding sequence: 1-504 (underlined sequences correspond to start and stop codons)						
	1	11	21	31	41	51	
	<u>ATGACCTACA</u>	<u>GTTACTCATT</u>	<u>TTTCAGGCCT</u>	<u>GAGTTGATCG</u>	<u>TTAATCATCT</u>	<u>TAATTATGTT</u>	60
	CATTCTGAAG	CCAACAGGAG	AACCAAGACC	AAAACITTTAT	TGCTCTGCT	TTCATTTCTT	120
40	GATGAAACCT	CTGGACTAAG	CACACATCTT	CCTTGTGTTAT	CTCTCTCAAA	GGAGTGTGGA	180
	GTGCTTCATC	TGGACATCCA	CGGGAAGAAG	GAAGACATGA	GAATCACCCA	ACAGTCTTCC	240
	CAGCTATACC	TGTGGGACAT	GGTGTGTTT	ACAATATTTA	AGAACCTGTG	GATGAGCCTC	300
	ATACCCAGAG	GGAAACAAAC	CTCCCCAAA	AGAGTTACAG	AAACATCCT	GAGAGATTTT	360
45	AAGCAGAAGC	AAAGTTCAAA	GATCCAAGAG	GAGAGACGAA	GAGAGTCTGC	AGGACCAAAC	420
	CTCTCTTCAT	TCTGTTTGT	GGGGAATGCT	GGAAGAGGAG	ACAGGCCCCA	GATTTGGGCA	480
	GGAAGTAAAC	AGTTTTCAGG	CTGAGGCCAA	TCTGAGCAGG	AACATTCCAA	TATTTCITCA	540
	GCTACGTTGT	CCAGCAGCTT	CACTGGTTAA	CCTTTTATGT	CCACCATTGT	TGGATTTTCA	600
	AGCTACTTGT	CAATGGTGAA	TATTGATCAT	CATCATTTATC	TACTGAGCTG	CTACCATATC	660
50	CCAGCTACTC	CTGCAATGTT	GTTCAATTAT	TTCTCAACAC	TCAGCATATT	TGCAATATGT	720
	TATGTAATAT	CACAGACAAG	GAAACTGAAC	GCAGAAATGT	TTTATTTCTT	GCCAAACATC	780
	ACATGAGGAT	GAACAATGAA	ACCGATTGGA	AACCAAGGAT	GTCTGATTCC	AACATCTCTG	840
	GGTCCITTTT	CACTCTGATA	TGCTGCAATT	AAAAAGCCAT	TTCTAAGACT	GT	
55	<u>A182 Protein sequence:</u>						
	Gene name: ESTs						
	Unigene number: Hs.162859						
	Probeset Accession #: AA569531						
60	Protein Accession #: none found						
	Signal sequence: 1-46						
	Transmembrane domains: none found						
	Cellular Localization: not determined						
65	1	11	21	31	41	51	
	MTYSYSFFRP	ELIVNHLNVV	HSEANRRRTK	KTLLSLLSPL	DETSGLSTHL	PCLSLSKBEG	60
	VLHLDIHGKK	EDMRITQSS	QLYLWDMGGF	TIFQNLWMSL	IPRGNKRSKP	RVTETILRDP	120
70	KQKQSSKIQE	ERRRESAGPN	LSSFVFWGNA	GRGDRPQIWA	GSKQFSG		
75	<u>A183 DNA SEQUENCE</u>						
	Gene name: ESTs						
	Unigene number: Hs.179809						
	Probeset Accession #: N95796						
	Nucleic Acid Accession #: XM_050197						
	Coding sequence: 310-1971 (underlined sequences correspond to start and stop codons)						
80	1	11	21	31	41	51	
	TCACACGTGC	CAAGGGGCTG	GCTCAGCGGA	ACCAGCCTGC	ACGCGCTGGC	TCGGGGTGAC	60
	AGCCGCGCGC	CTCGGCCAGG	ATCTGAGTGA	TGAGACGTGT	CCCTACTGAG	GTGCCCCACA	120
	GCAGCAGGTG	TTGAGCATGG	GCTGAGAAGC	TGGACCGGCA	CCAAAGGGCT	GGCAGAAATG	180
	GGCGCCTGGC	TGATTCTTAG	GCAGTTGGCG	GCAGCAAGGA	GGAGAGGGCG	CAGCTTCTGG	240
	AGCAGAGCCG	AGACGAAGCA	GTTCTGGAGT	GCCTGAACGG	CCCCCTGAGC	CCTACCCGCC	300

5 TGGCCCACTA TGGTCCAGAG GCTGTGGGTG AGCCGCTGTC TGGGGCACCG GAAAGCCCAG 360
 CTCTGTGCTGG TCAACCTGCT AACCTTTGGC CTGGAGGTGT GTTTGGCCCG AGGCATCACC 420
 TATGTGCCCG CTCTGCTGCT GGAAGTGGGG GTAGAGGAGA AGTTTCATGAC CATGGTGTG 480
 GGCAATTGGTC CAGTGTCTGG CTTGTCTGT GTCCCGCTCC TAGGCTCAGC CAGTGACCAC 540
 10 TGGCGTGGAG GCTATGGCCG CCGCCGGCCC TTCATCTGGG CACTGTCTTT GGGCATCCTG 600
 CTGAGCCTCT TTCTCATCCC AAGGGCCGGC TGGCTAGCAG GGCTGTCTGT CCGGATCCC 660
 AGGCCCCTGG AGCTGGCACT GCTCATCTGT GGGTGGGGC TGTGGACTT CTGTGGCCAG 720
 GTGTGCTTCA TCCCACTGGA GGCCCTGCTC TCTGACCTCT TCCGGGACCC GGACCACTGT 780
 CGCCAGGCCT ACTCTGTCTA TGCCCTTCATG ATCAGTCTTG GGGCTGCCT GGGCTACCTC 840
 CTGCCTGCCA TTGACTGGGA CACCACTGCC CTGGCCCCCT ACCTGGGCAC CCAGGAGGAG 900
 TGCCCTTTTG GCGTGTCTAC CCTCATCTTC CTCACCTGCG TAGCAGCCAC ACTGCTGGTG 960
 GCTGAGGAGG CAGCGCTGGG CCCCACCGAG CCAGCAGAAG GGCTGTCCGC CCCCTCCTTG 1020
 TCGCCCCACT GCTGTCCATG CCGGGCCCGC TTGGCTTTCC GGAACCTGGG GCGCCTGCTT 1080
 15 CCCCCGGTGC ACCAGCTGTG CTGCCGCTATG CCCCACCGCC TGGCCCGGCT CTTCGTGGCT 1140
 GAGCTGTGCA GCTGGATGGC ACTCATGACC TTCACGCTGT TTTACACGGA TTTGCTGGGC 1200
 GAGGGGCTGT GCGTGTCTAC GCGCAGAGCT GAGCCGGGCA CCGAGGCCCG GAGACACTAT 1260
 GATGAAGGCG TTCCGATGGG CAGCCTGGGG CTGTCTCTGC AGTGCGCCAT CTCCCTGGTC 1320
 TTCTCTCTGG TACCTGACCG GCTGGTGCAG CGATTGCGCA CTCGACGAGT CTATTTGGCC 1380
 20 AGTGTGGCAG CTTTCCCTGT GGTGCGCGT GCCACATGCC TGTCCACAG TGTGGCCGTG 1440
 GTGACAGCTT CAGCGCCCTT CACCGGGTTC ACCTTCTCAG CCTTCAGAT CCTGCCCTAC 1500
 ACACCTGGCT CCTCTACCA CCGGGAGAG CAGGTGTTCC TGCCCAAATA CCGAGGGGAC 1560
 ACTGAGGTGT CTAGCAGTGA GGACAGCCTG ATGACCACTT TCCTGCCAGG CCCTAAGCCT 1620
 GGAGCTCCCT TCCCTAATGG ACACGTGGGT GCTGGAGGCA GTGGCCTGCT CCCACCTCCA 1680
 25 CCGCGCTCTT GCGGGGCTCT TGCCCTGTAT GTCTCGTAC GTGTGTGGT GGGTGGAGCC 1740
 ACGAGGCCA GGGTGGTTCC GGGCCGGGGC ATCTGCTGTG ACCTCGCCAT CCTGGATAGT 1800
 GCGCTCTGTC GTTCCAGGT GCGCCCATCC CTGTTTATGG GCTCCATTGT CCAGCTCAGC 1860
 CAGTCTGTCA CTGCTATATG GGTGTCTGCC GCAGGCTCGG GTCTGGTTCG CATTTACTTT 1920
 GCTACACAGG AGGCCAGAG CAAGAGCGAC TTGGCCAAAT ACTCAGCGTA GAAACCTTCC 1980
 30 AGCACATTTG GGTGGAGGGC CTGCTCTACT GGGTCCCAGC TCCCCGCTCC TGTTAGCCCC 2040
 ATGGGGCTGC CGGGCTGGCC GCCAGTTTCT GTTGTCTGCA AAGTAATGTG GCTCTCTGCT 2100
 GCCACCTGTG CTGCTGAGG TGCGTAGCTG CACAGCTGGG GGCTGGGGC TCCCTCTCCT 2160
 CTCTCCCCAG TCTCTAGGGC TGCTGACTG GAGGCCCTCC AAGGGGGTTT CAGTCTGGAC 2220
 TTATACAGGG AGGCCAGAG GGTCTCATGC ACTGGAATGC GGGGACTCTG CAGGTGGATT 2280
 35 ACCCAGGCTC AGGGTTAACA GCTAGCCTCC TAGTTAGAG ACACCTAGAG AAGGGTTTTT 2340
 GGGAGCTGAA TAAACTCAGT CACCTGGTTT CCATCTCTTA AGCCCCTTAA CCTGCAGCTT 2400
 CGTTTAATGT AGCTCTTGCA TGGGAGTTTC TAGGATGAAA CACTCCTCCA TGGGATTGTA 2460
 ACATATGAAA GTTATTGTGA GGGGAAGAGT CCTGAGGGGC AACACACAAG AACCAAGTCC 2520
 40 CCTCAGCCCC ACAGGCACTG GTCTTTTTTG CTNGANTCCA CCCCCCCCCT CTTTACCCTT 2580
 TT

A184 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.179809
 45 Probeset Accession #: N95796
 Protein Accession #: XP_050197
 Signal sequence: none
 Transmembrane domains: 21-43, 53-75, 90-112, 125-147, 160-182, 199-221, 323-345, 350-372, 379-401
 50 Cellular Localization: plasma membrane

1 11 21 31 41 51
 55 MVQRLWVSRL LRRKAQLLL VNLTPGLEV CLAAGITYYP FLILLEVGVE KFMTHVLGIG 60
 PVLGLVVCPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL FLIPRAGMLA GLLCPDPRPL 120
 ELALLILGVG LLDFOGQVCF TPLEALLSDL FRDPDHCRQA YSVYAFMISL GGCLGYLLPA 180
 IDWDTSALAP YLGTQEELF GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH 240
 CPCRARIAP RNLGALLPRL HQLCCRMPT LRLFLVAELC SWMALMTFTL FYTDFVGEGL 300
 60 YQGVPRABPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFG TRAVYLASVA 360
 APFVAAGATC LSHSVAVVTA SAALTGFTPS ALQILPYTLA SLVHREKQVF LPKYRGDTGG 420
 ASSEDSLMTS FLPGPKPGAP FPNGHVAGG SGLLPPPPAL CGASACDVSV RVVVGEPTFA 480
 RVVPGRGICL DLAILDSAPL LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ 540
 VVFDKSDLAK YSA

A185 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 70 Nucleic Acid Accession #: AK002126
 Coding sequence: 1-1593 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 75 ATGGTTCGCC GGGGGCTGCT TGCGTGGATT TCCCGGGTGG TGGTTTGTCT GSTGCTCCTC 60
 TGCTGTGCTA TCTCTGTCTT GTACATGTTG GCCTGCACCC CAAAAGGTGA CGAGGAGCAG 120
 CTGGCACTGC CCAGGGCCAA CAGCCCCAGG GGAAGGAGG GGTACCAAGC GGTCTCTCAG 180
 GAGTGGGAGG AGCAGCACCG CAACTACGTG AGCAGCCTGA AGCGGCAGAT CGCACAGCTC 240
 80 AAGGAGGAGC TGCAGGAGAG GAGTGAGCAG CTCAGGAATG GGCAGTACCA AGCCAGCGAT 300
 CTGTCTGGCC TGGGTCTGGA CAGGAGCCCC CCAGAGAAAA CCCAGGCCGA CCTCTGGGCC 360
 TTCTCTCACT CGCAGGTGGA CAAGGCAGAG GTGAATGCTG GCGTCAAGCT GGCCACAGAG 420
 TATCAGCAGC TGCCCTTCGA TAGCTTTACT CTACAGAAGG TGTACCAAGT GGAGACTGGC 480
 CTTACCCGCC ACCCCAGGGA GAAGCCTGTG AGGAAGGACA AGCCGGATGA GTTGGTGGAA 540
 GCCATTGAAT CAGCCTTGGA GACCCCTGAAC AATCTGCAG AGAACAGCCC CAATCACCCT 600

5 CCTTACACGG CCTCTGATT CATAGAAAGG ATCTACCGAA CAGAAAGGGA CAAAGGGACA 660
 TTGTATGAGC TCACCTTCAA AGGGGACCAC AAACACGAAT TCAACCGSCT CATCTTATTT 720
 CGACCATTCG GCCCATCAT GAAAGTGAAA AATGAAAAGC TCAACATGGC CAACACGCTT 780
 ATCAATGTTA TCGTGCTCT AGCAAAAAGG GTGGACAAGT TCCGCGAGTT CATGCAGAAT 840
 TTCAGGGAGA TGTGCATTGA GCAGGATGGG AGAGTCCATC TCACCTGTGT TTACTTTGGG 900
 AAAGAAGAAA TAAATGAAGT CAAAGGAATA CTTGAAAACA CTTCCAAGC TGCCCACTTC 960
 AGGAACCTTA CCTTCATCCA GCTGAATGGA GAATTTTCTC GGGGAAAGGG ACTTGATGTT 1020
 GGAGCCCGCT TCTGGAAGGG AAGCAACGTC CTTCTCTTTT TCTGTGATGT GGACATCTAC 1080
 TTCACATCTG AATTCCTCAA TACGTGTAGG CTGAATACAC AGCCAGGGAA GAAGGTATTT 1140
 10 TATCCAGTTG TTTTCAGTCA GTACAATCCT GGCATAATAT ACGGCCACCA TGATGCAGTC 1200
 CCTCCCTTGG AACAGCAGCT GGTCAATAAG AAGGAAACTG GATTTTGGAG AGACTTTGGA 1260
 TTTGGGATGA CGTGTCACTA TCGGTCAAGC TTATCAATA TAGGTGGGTT TGATCTGGAC 1320
 ATCAAAGGCT GGGGCGGAGA GGATGTGCAC CTTTATCGCA AGTATCTCCA CAGCAACCTC 1380
 15 ATAGTGGTAC GGACGCTGT GCGAGGACTC TTCCACCTCT GGCATGAGAA GCGCTGCATG 1440
 GACGAGCTGA CCCCAGGACA GTACAAGATG TGATGTCAGT CCAAGGCCAT GAACGAGGCA 1500
 TCCCAGGCC AGCTGGGCAT GCTGGTGTCT AGGCACGAGA TAGAGGCTCA CCTTCGCAAA 1560
 CAGAAACAGA AGACAAGTAG CAAAAAACA TGA

20 A186 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.11260
 Probeset Accession #: R73640
 25 Protein Accession #: NP_060841
 Signal sequence: 1-26
 Transmembrane domains: none found
 Cellular Localization: not determined

30 1 11 21 31 41 51
 MVRRLGLAWI SRVVLLVLL CCAISVLYML ACTPKGDEEQ LALPRANSPT GKEGYQAVLQ 60
 EMEQHRNYV SSLKRIQIQL KEELQERSEQ LRNGQYQASD AAGLGLDRSP PEKTDADLLA 120
 FLHSQVDRAE VNAGVKLATE YAAVFPDSFT LQKVYQLEST LTRHPEEKPV RDKRDELVE 180
 35 AIESALETLN NPAENSPNHR PYTASDFIEG IYRTERDKGT LYELTFKGDH KHEFKRLILF 240
 RPFGPIMVKV NEKLANMANTL INVIVPLAKR VDKFRQFMQN FREMCIEQDG RVHLTVVYFG 300
 KEEINEVRGI LENTSKAANF RNFTFIQLNG EFSRKGGLDV GARFWKGSNV LLPFCVDVYI 360
 FTSEPLNTRC LNTQPGKKVF YPVLFSQYNF GIIYGHHDV PPLEQQLVIK KETGFWRDFG 420
 FGMTQCYRSD FINIGGFOLD IKGWGGEDVH LYRKYLHNSL IIVRTPVRGL FHLWHEKRCM 480
 40 DELTPEQYKM CMQSKAMNEA SHGQLGMLVF RHEIEAHLRK QKQRTSSKIT

A187 DNA SEQUENCE
 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 45 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 ATGATTCTCTG TATTGACATC AAAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAGC CTGATCTTCA GAATGCTCTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 TTTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 55 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTTCTGGCTT CTGCACTCAT CAGTGTTTTA 240
 ATGCATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTTCAGT 300
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGAAAGCC ATTGTGTGGC TGAAGGAAAA TTGGAGCATA CACTTGCCCG AGACTTGGTT 420
 CCAGGTGATA CAGTTTGCTT TCTGTGTGGG GATAGAGTTC CTGCTGACTT ACCTTGTGTT 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAAC GCCTTGTCTT 540
 60 AAGGTGACAG CTCCCTCAGC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTGTCTAT TGGAAACAGGA 660
 GAAAATCTCT AATTGGGGA GGTTTTAAAT ATGATGCAAG CAGAGAGGCC ACCAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGTGATA 780
 65 ATAGGAATCA TAGGTGTGGT TGGCTGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840
 ATTAGTGTA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTTCACAGT 900
 AOGCTAGCTC TTGGTGTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCTT 960
 ATTGTGAAA CTCTGGGCTG CTGTAATGTG ATTTGTTTCA ATAAACTGG AACACTGACG 1020
 AAGAATGAAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
 GGAGTTGGCT AATATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATT 1140
 70 TATAACCCAG CTGTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
 AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
 ATGGGCTCTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
 GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
 TGTTTTATGA AAGGTGCTTA CGAACAAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
 75 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAAG GAAGGCACGC 1500
 ATGGGCTCAG CGGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGAACT GGGACAGCTG 1560
 ACATTCTCTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
 ACAACACTCA TTGCTCTCAG AGTATCAATA AAAATGATTA CTGGAGATT 1680
 80 GCAGTTGCAA TCGCCAGTCG TCTGGGATTG TATTCAAAA CTCCCAAGT AGTCTCAGGA 1740
 GAAGAAATAG ATGCAATGGA TGTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800
 TTTTACAGCA CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
 ATTGGAGTTG CGATGGGCCA GACTGTGTACA GATGTTTGA AAGAGGCAGC AGACATGATC 1980
 CTAGTGGATG ATGATTTTCA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040

5 AATAACATTA AAAATTTCGT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACITTA 2100
 ATCTCATTTG CTACATTAAT GAACTTTCCT AATCCTCTCA ATGCCATGCA GATTTTGTGG 2160
 ATCAATATTA TTATGGATGG ACCCCAGCT CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
 GATGTCAATC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTGACTAA AAACCTTGATA 2280
 CTTAAAATAC TTGTTTCATC AATAATCATT GTTTGTGGGA CTTTGTGTGT CTTCTGGCGT 2340
 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
 TTTTGTGACA TGTTCAATGC ACTAAGTICC AGATCCAGCA CCAAGTCTGT GTTTGAGATT 2460
 GGACTCTGCA GTAATAGAAT GTTTTGTCTAT GCAGTTCITG GATCCATCAT GGGACAATTA 2520
 10 CTAGTTATTT ACTTTCCTCC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
 GATCTGTTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
 AAGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
 CTGAAGTAT GA

A188 Protein sequence:

15 Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 Probeset Accession #: N51919
 Protein Accession #: AAF27813
 20 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

25 1 11 21 31 41 51
 | | | | |
 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRRA FHGWNEFDIS EDEPLWKYI 60
 SQFKNPLML LLAASVISVL MHQEDDAVSI TVAILIVTV AFVQEYRSEK SLEELSKLVP 120
 30 PECHCVREGK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSIDES SLTGETTPCS 180
 KVTAPQPAAT NGDLASRSNI AFMGTIVLRG KAGGVVITG ENSEFGEVFK MMQAEAPKT 240
 PLQKSMDLG KQLSPYSFGI IGIIMLVGWL LGKDILEMFT ISVSLAVAAI PEGPLPIVTV 300
 TLALGVMMRV KKRRAIVKLLP IVETLGCNVC ICSDKTGTLT KNEMTVTRIF TSDGLHAEVT 360
 GVGYNQFGEV IVDGQVHGF YNPAVSRIVE AGCVNDNAVI RNNITLMKPT BGALIALANK 420
 35 MGLDGLQDQY IRKAEYPPSS EQKWMVAVKV HRTQQDRPEI CFMKGAYEQV IKYCTTYQSK 480
 GQTLTLTQQQ RDVYQEKAR MGSAGLRVLA LASGPGLQL TFLGLVGIIID PPRTGVKEAV 540
 TTLIASGVI KMITGDSQET AVAIASRLGL YSKTSQSVSG EEIDAMDVQQ LSQIVPKVAV 600
 FYRASPRHKM KIIKSLQKNG SVVAMTGDGV NDAVALKAAD IGVAMGQTGT DVCKEADMI 660
 LVDDDFQTIM SAIEEGKGIY NNINNFVRPQ LSTSIALLTL ISLATLMNFP NPLNAMQILW 720
 40 INIIMDGPPA QSLGVEPVDK DVIRKPPRNW KDSILTKNLI LKILVSSIII VCGTLFVFWR 780
 ELRDNVITPR DITMTFTCFV FFDMPNALSS RSQTKSVFEI GLCSNRMFCY AVLGSIMGQL 840
 LVIIYFPPLQK VFQTESLSIL DLLFLLGLTS SVCIVAEIHK KVERSREKIQ KHVSTSSSF 900
 LEV

A189 DNA SEQUENCE

45 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 50 Coding sequence: 1-1284 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | |
 ATGGGCTACC AGAGGCAGGA GCCTGTATC COGCOGCAGA GAGGATTGCC TTATTCAATG 60
 AAGCAAGCTG GGTTCCTTTT GGAATATTG CTTTATTCT GGGTTTCATA TGTTCAGAC 120
 TTTTCCCTTG TTTTATTGAT AAAAGGAGGG GCCCTCTCTG GAACAGATAC CTACCACTCT 180
 TTGGTCAATA AAACTTTCGG CTTTCCAGGG TATCTGCTCC TCTCTGTTCT TCAGTTTTTG 240
 TATCCTTTTA TAGCAATGAT AAGTTACAAT ATAATAGCTG GAGATACTTT GAGCAAAGTT 300
 60 TTICAAAGAA TCCAGGAGT TGATCCTGAA AACCTGTTTA TTGGTGCCTA CTTCAATTAT 360
 GGACTTTCCA CAGTTACCTT TACTCTGCCT TTATCCTTGT ACCGAAATAT AGCAAAGCTT 420
 GGAAAGGTCT CCTCATCTC TACAGGTTTA ACAACTCTGA TTCTTGGAAAT TGTAAATGCA 480
 AGGGCAATTT CACTGGGTCC ACACATACCA AAACAGAAAG ACGCTGGGT ATTTGCAAGG 540
 CCAATGCCA TTCAAGCGGT CGGGTTATG TCTTTTGCAT TTATTGCGA CCATAACTCC 600
 65 TCTTAGTTT ACAGTTCTCT AGAAGAACC ACAGTAGCTA AGTGGTCCG CTTATCCAT 660
 ATGTCCATCG TGATTTCTGT ATTTATCTGT ATATTCTTG CTACATGTGG ATACTTGACA 720
 TTTACTGGCT TCACCCAAGG GGACTTATT GAAATTACT GCAGAAATGA TGACCTGGTA 780
 ACATTGGAA GATTTGTGA TGGTGTCACT GTCAATTTGA CATACCTTAT GGAATGCTTT 840
 GTGACAAGAG AGGTAATTGC CAATGTGTTT TTTGGTGGGA ATCTTTCATC GGTTTTCCAC 900
 70 ATGTGTGTA CAGTGATGT CATCACTGTA GCCAGCTTG TGTCAATGCT GATTGATTGC 960
 CTGGGATAG TTCTAGAACT CAATGGTGTG CTCTGTGCAA CTCCCTCAT TTTTATCATT 1020
 CCATCAGCCT GTTATCTGAA ACTGTCTGAA GAACCAAGGA CAACTCCGA TAAGATTATG 1080
 TCTTGTGTC TGCTTCCCAT TGGTGTCTGT GTGATGGTTT TTGGATTGCT CATGGCTATT 1140
 ACAAATAC TC AAGACTGCAC CCATGGGCAG GAAATGTTCT ACTGCTTTC TGACAAATTC 1200
 75 TCTCTCAAA ATACCTCAGA GTCTCATGTT CAGCAGACAA CACAACCTTC TACTTTAAAT 1260
 ATTAGTATCT TTCAACTCGA GTAA

A190 Protein sequence:

80 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 28-50, 66-88-112-134, 142-164, 217-239, 260-282, 298-320, 327-348, 359-381

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 | | | | |
 MG YQRQEPVI PPQRGLPYSM KQAGFPILGIL LLFVWSYVTD FSLVLLIKGG ALSGTDITYQS 60
 LVNKTGFPFG YLLLSVLQFL YPFIAMISYN IIAGDTLSKV FORIPGVDPF NVFIGRHFII 120
 GLSTVTFPLP LSLYRNIAKL GKVSLISTGL TTLILGIWMA RAISLGHPIH KTEDANVFAK 180
 10 PNAIQAVGVM SFAFICHNS FLVYSSLEBP TVAKWSRLIH MSIVISVFIC IFFATCGYLT 240
 FTGFTQGDLF ENYCRNDDL VTFGRFCYGVV VILTYPMECF VTREVIANVF FGGNLSVVFH 300
 IIVTVMTIV ATLVSLLIDC LGIVLELNGV LCATPLIFII PSACYLKLSE EPRTHSDKIM 360
 SCVMLPIGAV VMVFGFVMAI TINTQDCTHGQ EMPYCFDFNF SLINTSESHV QQTQLSTLN 420
 ISIFQLE

A191 DNA SEQUENCE

15 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 20 Coding sequence: 1-1203 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 25 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAGT TTTCCCTTGT TTTATTGATA 60
 AAGAGAGGG CCCTCTCTGG AACAGATACC TACCAGTCTT TGGTCAATAA AACITTCGGC 120
 TTTCCAGGGT ATCTGCTCCT CTCTGTCTCT CAGTTTTTGT ATCCTTTTAT AGCAATGATA 180
 AGTTACAATA TAATAGCTGG AGATACTTTG AGCAAGATTT TCAAAAGAAT CCCAGGAGTT 240
 30 GATCCCTGAAA ACCTGTTTTAT TGGTCGCCAC TTCAATTATT GACTTTCCAC AGTTACCTTT 300
 ACTCTGCCTT TATCCTTGTA CCGAAATATA GCAAAGCTTG GAAAGGTCTC CCTCATCTCT 360
 ACAGGTTTAA CAACCTCTGAT TCTTGAATTT GTAAATGGCAA GGGCAATTTC ACTGGGTCCA 420
 CACATACCAA AAACAGAAGA CGCTTGGGTA TTTGCAAAGC CCAATGCCAT TCAAGCGGTC 480
 GGGGTTATGT CTTTGTGCAAT TATTGGCCAC CATAACTCCT TCTTAGTTTA CAGTTCTCTA 540
 35 AAGAACCACA CAGTAGCTAA GTGGTCCCGC CTTATCCATA TGTCCATCGT GATTCTGTA 600
 TTTATCTGTA TATTCTTTGC TACATGTGGA TACTTGACAT TTAATGGCTT CACCCAAGGG 660
 GACTTATTG AAAATTACTG CAGAAATGAT GACCTGGTAA CATTGGAAG ATTTTGTTAT 720
 GGTGTCAGTG TCAATTTGAC ATACCTATAG GAATGCTTTG TGACAAGAGA GGTAAATGGC 780
 AATGTGTTTT TTGGTGGGAA TCCTTCATCG GTTTTCACA TTGTTGTAAC AGTGATGGTC 840
 40 ATCACTGTAG CCACGCTTGT GTCAATGCTG ATTGATTGCC TCGGGATAGT TCTAGAACTC 900
 AATGGTGTGC TCTGTGCAAC TCCCTCATTT TTTATCATTC CATCAGCCTG TTATCTGAAA 960
 CTGTCTGAAG AACCAAGGAC ACACCTCGAT AAGATTATGT CTTGTGTCAT GCTTCCCAT 1020
 GGTGCTGTGG TGATGGTTTT TGGATTGCTC ATGGCTATTA CAAATACTCA AGACTGCACC 1080
 CATGGGAGG AATGTTCTA CTGCTTTCCT GACAATTTCT CTCTACAAA TACCTCAGAG 1140
 45 TCTCATGTTT AGCAGACAAC ACAACTTTCT ACTTTAAATA TTAGTATCTT TCAACTCGAG 1200
 TAA

A192 Protein sequence:

50 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Protein Accession #: none found
 Signal sequence: 1-26
 Transmembrane domains: 45-61, 92-108, 117-132, 191-207, 274-290, 297-313, 335-351
 55 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 60 MG YQRQEPVI PPQFSLVLLI KGGALSGTDT YQSLVNKTFG FPGYLLLSVL QFLYFFIAMI 60
 SYNIIAGDTL SKVFQIRIPV DPENVFIGRH FIIGLSTVTF TLPLSLYRNI AKLGKVSLSIS 120
 TGLTTLILGI VMARAIISLP HIPKTEDAWV FAKPNAIQAV GVMSPAFICH HNSPLVYSSL 180
 EEPFVAKWSR LIHMSIVISV FICIFPATCG YLTFGTGTQG DLFPNYCRND DLVTFGRFCY 240
 65 GVTVILTYPM ECFVTREVIK NVFPGNLS VPHIVVTVMV ITVATLVSLI IDCLGIVLEL 300
 NGVLCATPLI FIIPSACYLK LSEEPRTSD KIMSCVMLPI GAVVMVFGFV MAITNTQDCT 360
 HGQEMFYCFP DNPSLNTTSE SHVQQTQLS TLNISIFQLE

A193 DNA SEQUENCE

70 Gene name: ESTs
 Unigene number: Hs.293185
 Probeset Accession #: N62096
 Nucleic Acid Accession #: N62096
 Coding sequence: 1-1140 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 75 ATGGGCTACC AGAGGCAGGA GCCTGTCATC CCGCCGCGAG TCAATAAAAC TTTCCGCTTT 60
 CCAGGGTATC TGCTCCTCTC TGTTCTTCAG TTTTGTATC CTTTATAGC AATGATAAGT 120
 80 TACAATATAA TAGCTGGAGA TACTTTGAGC AAAGTTTTTC AAAGAATCCC AGGAGTTGAT 180
 CCTGAAAACG TGTTTATTGG TCGCCACTTC ATTATTGGAC TTTCACAGT TACCTTTACT 240
 CTGCCCTTAT CCTTGTACCG AAATATAGCA AAGCTTGGAA AGGCTCTCCT CATCTCTACA 300
 GGTTTAACAA CTCTGATTCT TGAATTGTA ATGGCAAGGG CAATTTCACT GGGTCCACAC 360
 ATACCAAAAA CAGAAGACGC TTGGGTATTT GCAAAGCCCA ATGCCATTCA AGCGGTCCGG 420

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GTATGTCTT TTGCATTTAT TTGCCACCAT AACTCCTCT TAGTTTACAG TTCTCTAGAA 480
GAACCCACAG TAGCTAAGTG GTCCCGCCTT ATCCATATGT CCATCGTGAT TTCTGTATTT 540
ATCTGTATAT TCTTTGCTAC ATGTGGATAC TTGCATTTA CTGGCTTCAC CCAAGGGGAC 600
TTATTTGAAA ATTACTGCAG AAATGATGAC CTGGTAACAT TTGGAAGATT TTGTTATGGT 660
GTCACTGTCA TTTTGACATA CCCTATGGAA TGCTTTGTGA CAAGAGAGGT AATTGCCAAT 720
GTGTTTTTGT GTGGGAATCT TTCATCGGTT TTCCACATTG TTGTAACAGT GATGGTCATC 780
ACTGTAGCCA CGCTTGCTGTC ATTGCTGATT GATTGCCCTCG GGATAGTTCT AGAACTCAAT 840
GGTGTGCTCT GTGCAACTCC CCTCATTTT ATCATTTCCAT CAGCCTGTTA TCTGAAACTG 900
TCTGAAGAAC CAAGGACACA CTCGATAAG ATTATGTCTT GTGTCTGCT TCCCATTGGT 960
GCTGTGGTGA TGTTTTTTGG ATTGCTCATG GCTATTACAA ATACTCAAGA CTGCACCCAT 1020
GGGCAGGAAA TGTTCCTACTG CTTTCTCTGAC AATTTCTCTC TCACAAATAC CTCAGAGTCT 1080
CATGTTTACG AGACAACACA ACTTTCTACT TTAATATTA GTATCTTTCA ACTCGAGTAA

A194 Protein sequence:

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 24-40, 70-86, 95-111, 171-186, 253-269, 276-292, 314-330
Cellular Localization: plasma membrane

1 11 21 31 41 51
MGYQRQEPVI PPQVNKTFGF PGYLLLSVLQ FLYPFIAMIS YNIIAGDTLS KVFQRIQVGD 60
PENVFIGRHF IIGLSTVTFT LPLSLYRNIA KLGKVSLLST GLTTLILGIV MARAISLGFH 120
IPKTEDAWVF AKPNAIQAVG VMSFAPICHH NSFLVYSSLE EPTVAKWSRL IHMSIVISVF 180
ICIEFATCGY LTFTGFTQGD LFENYCRNDD LVTGFRFCYG VTVILTYPME CPVTREVIAN 240
VFFGGNLSVV FHVIVTVMVI TVATLVSLLI DCLGIVLELN GVLCATPLIF IIPSACYLKL 300
SEEPRTSDK IMSCVMLPIG AVVMVFGFVM AITNTQDCTH GQEMFYCFPD NFSLTNTSES 360
HVQQTQLST LNISIFQLB

A195 DNA SEQUENCE:

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Nucleic Acid Accession #: N62096
Coding sequence: 1-1389 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
ATGGGCTACC AGAGGCAGGA GCCTGTCTATC CGGCGCAGAG GAGATTAGA TGACAGAGAA 60
ACCTTGTTT CTGAACATGA GTATAAAGAG AAAACCTGTC AGTCTGCTGC TCTTTTAAAT 120
GTGTCAACT CGATTATAGG ATCTGTGATA ATAGGATTGC CTATTCAAT GAAGCAAGCT 180
GGGTTTCTCT TGGGAATATT GCTTTTATTC TGGGTTTCAT ATGTTACAGA CTTTCCCTT 240
GTTTTATTGA TAAAGGAGG GGCCTCTCT GGAACAGATA CCTACCAGTC TTTGGTCAAT 300
AAAACITTCG GCTTTCAGG GTATCTGCTC CTCTCTGTC TTCACTTTT GTATCCTTTT 360
ATAGCAATGA TAAGTTACAA TATAATAGCT GGAGATACTT TGAGCAAGT TTTTCAAGA 420
ATCCACAGAG TTGATCTCTG AAACGTGTTT ATTGGTCGCC ACTTCATTAT TGGACTTTCC 480
ACAGTTACCT TTAATCTGCC TTTATCTCTG TACCGAATA TAGCAAGCT TGGAAAGGTC 540
TCCCTCATCT CTACAGGTTT AACAACTCTG ATCTCTGAA TTGTAATGCC AAGGGCAATT 600
TCACCTGGTC CACACATACC AAAACAGAG GACGCTGGG TATTTGCAAA GCCCAATGCC 660
ATTCAGCGG TCGGGGTTAT GTCTTTTGCA TTTATTGCCC ACCATAACTC CTCTTAGT 720
TACAGTTCTC TAGAAGAACC CACAGTAGCT AAGTGGTCCC GCCTTATCCA TATGTCCATC 780
GTGATTCTG TATTATCTG TATATTCTT GCTACATGTG GATACTTGAC ATTACTGGC 840
TTCACCCAG GGGACTTATT TGAAATATC TGCAGAAATG ATGACCTGGT AACATTGGA 900
AGATTTGTT ATGGTGTCAC TGTCATTTT ACATACCCTA TGGAAATGCT TGTGACAAGA 960
GAGGTAATTG CCAATGTGTT TTTTGGTGGG AATCTTTTCA CGGTTTCCA CATTGTTGA 1020
ACAGTGAATG TCATCACTGT AGCCACGCTT GTGTCAATGC TGATTGATTG CCTCGGATA 1080
GTTCTAGAAC TCAATGGTGT GCTCTGTGCA ACTCCCTCA TTTTATCAT TCCATCAGCC 1140
TGTATCTGA AACTGTCTGA AGAACCAAGG ACACACTCCG ATAAGATTAT GTCTTGTGTC 1200
ATGCTTCCA TTTGCTGCTG GGTGATGGTT TTTGATTTCG TCATGGCTAT TACAAATCT 1260
CAAGACTGCA CCCATGGGCA GGAAATGTTT TACTGCTTTC CTGACAATT CTCTCTCACA 1320
AATACCTCAG AGTCTCATGT TCAGCAGACA ACACAACTTT CTACTTTAAA TATTAGTATC 1380
TTTCAATGA

A196 Protein sequence:

Gene name: ESTs
Unigene number: Hs.293185
Probeset Accession #: N62096
Protein Accession #: none found
Signal sequence: none found
Transmembrane domains: 37-53, 66-82, 109-125, 155-172, 180-196, 255-271, 338-354, 361-377, 399-415
Cellular Localization: plasma membrane

1 11 21 31 41 51
MGYQRQEPVI PPQRDLDDRE TLVSEHEYKE KTCQSAALFN VVNSIIGSGI IGLPYSMRQA 60

GFPLGILLLF WVSYVDFSL VLLIKGGALS GTDTYQSLVN KTFGFPGYLL LSVLQFLYPF 120
 IAMISYNIA GDTLSKVFQR IPGVDPENV IGRHPIIGLS TVTPTLPLSL YRNIAGLKV 180
 SLISTGLTTL ILGIVMARAI SLGPHIPKTE DAWVFAKPA IQAVGVMSFA FICHNSFLV 240
 YSSLESPTVA KWSRLIHMSI VISVPICIFF ATCGYLTFTG FTQGDLFENY CRNDDLVTFG 300
 RFCYGVTVIL TYPMECFVTR EVIANVFFGG NLSSVFHIV TVMVITVATL VSLLDICLGI 360
 VLELNGVLCA TPLIFIIPSA CYLKLSEEP THSKIMSCV MLPIGAVVMV FGFVMAITNT 420
 QDCTHGQEMF YCFDPNFSLT NTSSEHVQQT TQLSTLNI SI FQ

A197 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Nucleic Acid Accession #: NM_017636
 Coding sequence: 1-3501 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGGAGGATG CCTTCGGGGC AGCCGTGGTG ACCGTGTGGG ACACGATGC ACACACCACG 60
 GAGAAGCCCA CCGATGCGTA CGGAGAGCTG GACTTCACGG GGGCGGGCCG CAAGCACAGC 120
 AATTTCCTCC GGCCTCTCTGA CCGAACGGAT CCAGCTGCAG TTTATAGTCT GGTACACAGC 180
 ACATGGGGCT TCCGTGCCCC GAACCTGGTG GTGTCACTGC TGGGGGGATC GGGGGGCCCC 240
 GTCTCCAGA CCGGCTGCA GACCTGCTG CTGCTGGGGC TGGTGGGGC TGCCAGAGC 300
 ACAGGAGCCT GGATTGTGAC TGGGGGTCTG CACACGGGCA TCGGCGGCA TGTGGGTGTG 360
 GCTGTAGCGG ACCATCAGAT GGCCAGCACT GGGGGCACA AGGTGGTGGC CATGGGTGTG 420
 GCCCCTGGG GTGTGGTCCG GAATAGAGAC ACCCTCATCA ACCCAAGGG CTGTTCCCT 480
 GCGAGGTACC GGTGGCGCGG TGACCCGGAG GACGGGGTCC AGTTTCCCTT GGACTACAAC 540
 TACTCGGCTG TCTTCTGGT GGACGACGGC ACACACGGCT GCCTGGGGGG CGAGAACCAG 600
 TTCCGCTTGC TCCGCTGGAT CTACATCTCA CAGCAGAAGA CGGGCGTGGG AGGGACTGGA 660
 ATTGACATCC CTGTCTCTGT CTTCTCTGAT GATGGTATG AGAAGATGTT GACGCGAATA 720
 GAGAACCGCA CCGAGGCTCA GCTCCCATGT CTCTCGTGG CTGGCTCAGG GGGAGCTGCG 780
 GACTGCCTGG CGGAGACCCT GGAAGACACT CTGGCCCCAG GGAGTGGGGG AGCCAGGCAA 840
 GCGGAAGCCC GAGATCGAAT CAGGCGTTTC TTTCCTCAAG GGGACCTTGA GGTCTGCAG 900
 GCCCAGGTGG AGAGGATTAT GACCCGGAAG GAGCTCCTGA CAGTCTATT TCTGAGGAT 960
 GGGTCTGAGG AATTGAGAC CATAGTTTTG AAGGCCCTTG TGAAGCCCTG TGGGAGCTCG 1020
 GAGGCTTCAG CTTAGCTGGA TGAGCTGGT TTGGCTGTGG CTGGAAACCG CTGGACATT 1080
 GCGCAGAGTG AACTCTTTCG GGGGGACATC CAATGGCGGT CTTTCCATCT CGAAGCTTCC 1140
 CTCATGGAGC CCGTCTGTA TGACCCGGCT GAGTTCTGTC GCTTCTCAT TTCCACGGC 1200
 CTCAGCCTGG GCGCTTCTCT GACCCGATG CGCTGGCCCC AACTCTACAG CGCGCGGCC 1260
 TCCAACTGCG TCATCGCAA CCTTTTGAC CAGGCGTCCC ACAGCGCAGG CACCAAGACC 1320
 CCAGCCCTAA AAGGGGAGC TGCGGAGCTC CGCCCCCTG ACGTGGGGCA TGTCTGAGG 1380
 ATGCTGTCTG GGAAGATGTG CGCGCGAGG TACCCCTCCG GGGGCGCCTG GGACCTCAC 1440
 CCAGGCCAGG GCTTCGGGGA GAGCATGTAT CTGCTCTCGG ACAAGGCCAC CTGCGCGCTC 1500
 TCGCTGGATG TCGGCTCTGG GCAGGCCCCC TGGAGCGACC TGCTCTTTG GGCACTGTG 1560
 CTGAACAGGG CACAGATGGC CATGTACTTC TGGGAGATGG GTTCCAATGC AGTTTCTCA 1620
 GCTCTTGGG CCGTTTGTCT GCTCCGGGTG ATGCGACGCC TGGAGCTTGA CGCTGAGGAG 1680
 GCAGCACGGA GGAAGAGACT GCGGTTCAAG TTTGAGGGGA TGGGCGTTGA CCTCTTTGGC 1740
 GAGTGCTATC GCAGCAGTGA GGTGAGGGCT GCGCCCTCTC TCCTCCGTG CTGCGCGCTC 1800
 TGGGGGGATG CCACTTGTCT CCAGCTGGCC ATGCAAGCTG ACGCCCGTGC CTCTTTTGCC 1860
 CAGGATGGGG TACAGTCTCT GCTGACACAG AAGTGGTGGG GAGATATGGC CAGCACTACA 1920
 CCATCTGGG CCTGTGTTCT CGCCTTCTTT TGCCCTCCAC TCATCTACAC CGCCTCATC 1980
 ACCCTCAGGA AATCAGAAGA GGAGCCACCA CGGAGGAGC TAGAGTTTGA CATGGATAGT 2040
 GTCAATTAAT GGAAGAGGCC TGTCCGGACG CGGAGCCAG CCGAGAAGAC GCGCTGGGG 2100
 GTCCCGCGCC AGTCGGGCGC TCGGGTGTG TCGGGGGGCC GCTGCGGGGG GCGCGGTTG 2160
 CTACCGCGCT GGTTCACAT CTGGGGCGCG CCGGTGACCA TCTTCATGGG CAACGTGTC 2220
 AGCTACCTGC TGTCTCTGCT GCTTTTCTG CGGGTGTGTC TCGTGGATT CCAGCGGGG 2280
 CCGCCCGGCT CCGTGGAGCT GCTGCTCTAT TTCTGGGCTT TCAAGCTGCT GTGCGAGGA 2340
 CTGCGCCAGG GCGTGAAGCG AGGCGGGGGC AGCCTGCGCA GCGGGGGGCC CGGGCTTGGC 2400
 CATGCTCAC TGAGCCAGCG CTTGCGCTTC TACCTGCGCG ACAGCTGGA CCACTGCGAC 2460
 CTAGTGGCTC TCACCTGCTT CTTCTGGGCG GTGGCTGCG GGTGACCCC GGGTTGTAC 2520
 CACTTGGGCC CCACTGCTCT CTGCATCGAC TTTATGGTTT TCACGCTGCG GCTGCTCAC 2580
 ATCTTCACGG TCAACAAACA GCTGGGGGCC AAGATGCTCA TCGTGAAGAA GATGATGAAG 2640
 GACGTGTTCT TCTTCTCTT CTTCCTCGGC GTGTGGCTGG TAGCCTATGG CGTGGCCAG 2700
 GAGGGGCTCC TGAGGCCAAG GGAAGTGGAC TTCCCAAGTA TCCTGCGCGG GGTCTTCTAC 2760
 CGTCCCTACC TGCAGATCTT CGGGCAGATT CCCCAGGAG ACATGGACGT GGCCCTCAT 2820
 GAGCACAGCA ACTGCTCTGCT GGAGCCCGCG TTCTGGGCAC ACCCTCTGCG GCGCCAGGCG 2880
 GGCACCTGCG TCTCCAGTA TGCCAACTGG CTGGTGGTGC TGCTCTCTGT CATCTTCTG 2940
 CTGTTGCCCA ACATCTGCT GGTCAACTTG CTCATTGCCA TGTTCAGTTA CACATTGCG 3000
 AAAGTACAGG GCAACAGCGA TCTCTACTGG AAGGCGCAGC GTTACCGCTT CATCGGGAA 3060
 TTCCACTCTC GGGCGGGCT GGGCCGCGCC TTTATGCTCA TCTCCACTT GCGCCTCTG 3120
 CTGAGGCAAT TGTGACGGCG ACCCGGGAG CCCCAGCCGT CCTCCCGGCG CCGAGCAT 3180
 TTCCGGGTTT ACCTTTCTAA GGAAGCGAG CGGAAGCTGC TAAAGTGGGA ATCGGTGCAT 3240
 AAGGAGAATC TTCTGTCTGC ACGGCTAGG GACAAGCGG AGAGCGACTC CGAGCGCTG 3300
 AAGCGCAGCT CCAGAGAGT GGAAGTGGCA CTGAAACAGC TGGGACACAT CCGGAGTAC 3360
 GAACAGCGCG TGAAGTGTCT GGAGCGGGAG GTCCAGCAGT GTAGCCCGCT CCGGGGTGG 3420
 GTGGCGGAG CCGTGGCGCG CTCTGCTTGG CTGCCCCAG GTGGGCGGCC ACCCCCTGAC 3480
 CTGCTGGGT CCAAGAGCTG A

A198 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.31608
 Probeset Accession #: H18836
 Protein Accession #: none found

Signal sequence: none found
 Transmembrane domains: 214-230, 537-556, 642-662, 730-752, 760-782, 815-837, 842-864, 877-899, 973-995
 Cellular Localization: plasma membrane

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1	11	21	31	41	51	
MEDAFGA	AVV	TVWSDAHTT	EKPTDAYGEL	DFTGAGRKHS	NFLRLSDRTD	PAAVYSLVTR 60
TWGFRA	PNLV	VSVLGGSGGP	VLQTLQDQLL	RRGLVRAAQS	TGAWIVTGG	HTGIGRHVG 120
AVRDHMA	ST	GGTKVVMGV	APWGVVRNRD	TLINPKGSFP	ARYRWGDPE	DGVQFPPLDYN 180
YSAFFLV	DDG	THGCLGGENR	FRLRLESYIS	QKKTGVGGTG	IDIPVLLLLI	DGDEKMLTRI 240
ENATQAQ	LPC	LLVAGSGGAA	DCLAETLED	LAPGSGGARQ	GEARDIRRRF	FPKGDLEVLQ 300
AQVERIM	TRK	ELLTVYSSD	GSEEFETIVL	KALVKACGSS	EASAYLDEL	LAVAWNRVDI 360
AQSELFR	DI	QWRSFHLEAS	LMDALLNDRP	EFVRLISHG	LSLGHFLTPM	RLAQLYSAAP 420
SNLSIRNL	LD	QASHSAGTKA	PALKGGAEL	RPPDVGHVLR	MLLGKMCAPR	YPSGGAWDPH 480
PGQFGES	MYL	SLSDKATSP	SLDAGLGQAP	WSDLLWALL	LNRAQMAMYF	WEMGSNAVSS 540
ALGACLL	LRV	MARLEPDABE	AARRKDLAFK	FEGMGVDLFG	ECYRSSEVRA	ARLLLRRCPL 600
WGDATE	CLQLA	MQADARAFFA	QDGVQSLLTQ	KWGDMASTT	PIWALVLAF	CPPLIYTRLI 660
WFRSEEP	T	REELFPDMS	VINGEGPVTG	ADPAEKTPLG	VPRQSGRPGC	CGRCGGRRC 720
LRWFHFW	GA	PVTTFMGNV	SYLLFLLLF	RVLLVDFQPA	PPGSELELLY	FWAFTLLCEB 780
LRQFLSG	GGG	SLASGGPGP	HASLSQRLRL	YLADSWNQCD	LVALTCFLLG	VGCRLTPGLY 840
HLGRTVL	CID	FMVPTVRLH	IFTVNKQLGP	KIVIVSKMK	DVFFLPFLG	VWLVAYGVAT 900
EGLLRPR	DS	FPSILRRVY	RPYLQIFQI	PQEDMDVALM	EHSNCSSEPG	FWAHPGAQA 960
GTCVSQA	YAN	LVLVLLVIFL	LVANILLVNL	LIAMFSYTFG	KVQNSDLW	KAQRYRLIRE 1020
FHSRPA	LAPP	FIVISHRLRL	LRQLCRRPRS	PQPSSPAELH	FRVYLSKEAB	RKLLTWESVH 1080
KENFLAR	AR	DKRESDSERL	KRTSQKVDLA	LKQLGHIREY	EQRLKVLERE	VQCCSRVLGW 1140
VAELSRSA	L	LPPGGPPPPD	LPGSKD			

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A199 DNA SEQUENCE
 Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Nucleic Acid Accession #: AA054237
 Coding sequence: 1-894 (underlined sequences correspond to start and stop codons)

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1	11	21	31	41	51	
ATGGAGC	CGC	GGCGCTCGT	CACGCGCTC	AGCCTCGGCC	TCAGCCTGTG	CTCCCTGGGG 60
CTGCTCG	TCA	CGGCCATCTT	CACCGACCAC	TGGTACGAGA	COGACCCCGG	GCGCCACAAG 120
GAGAGCT	GCG	ACCGCAGCCG	CGCGGGCGCC	GACCCCCCGG	ACCAGAAGAA	CCGCCTGATG 180
CGCTGTG	CGC	ACCTGCCCTG	CGGGGACTCG	CCCCCGCTGG	GGCGCCGGCT	GCTCCCGGGC 240
GGCCCGGG	CGC	CGCGACCC	CGAGTCTCTG	CGCTCGCTCC	TGGGGCTCGG	CGGGCTGGAC 300
GCCGAGT	GCG	CGCGCCCT	CTTGGCCACC	TACTCGGGCC	TCTGGAGGAA	GTGCTACTTC 360
CTGGGCA	TG	ACCGGACAT	CGACACCTC	ATCCTGAAAG	GTATTGCGCA	CGGATGCACG 420
GCATCAAG	T	ACCACTTTTC	TCAGCCCATC	CGCTTGCGAA	ACATTCCTTT	TAATTTAACC 480
AAGACCAT	C	AGCAAGATGA	GTGGCACCTG	CTTCATTTAA	GAAGATCAC	TGCTGGCTTC 540
CTCGGCAT	G	CGTAGCCGT	CCTTCTCTGC	GGCTGCATTG	TGGCCACAGT	CAGTTTCTTC 600
TGGGAGGA	G	GCTTGACCA	GCACTGGCT	GGACTCTGT	TCCTCATGAC	AGGGATATTT 660
TGCACCAT	T	CCCTCTGTAC	TTATGCGGCC	AGTATCTCGT	ATGATTGAA	CCGGCTCCCA 720
AAGCTAA	T	ATAGCTGCC	TGCTGATGTG	GAACATGGTT	ACAGCTGGTC	CATCTTTTGC 780
GCCTGGT	G	CTTAGGCTT	TATTGTGGCA	GCTGGAGGTC	TCTGCATCGC	TTATCCGTTT 840
ATTAGCCG	G	CCAAGATTGC	ACAGCTAAAG	TCTGGCAGAG	ACTCCACGGT	ATGA

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A200 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.40808
 Probeset Accession #: AA054237
 Protein Accession #: none found
 Signal sequence: 1-18
 Transmembrane domains: 179-201, 209-231, 257-279
 Cellular Localization: plasma membrane

65
 70

1	11	21	31	41	51	
MEPRALV	TAL	SLGLSLCSLG	LLVTAIFTDH	WYBTDPRRHK	ESCERSRAGA	DPPDQKNRLM 60
PLSHLPL	RDS	PPLGRRLLP	GPGRADPEW	RSLLGLGLD	AECCRPFPAT	YSGLWRKCYF 120
LGIDRID	IDL	ILKGIAQRCT	AIKYHFSQPI	RLRNIPFNLT	KTIQDEWHL	LHLRRITAGF 180
LGMVAVL	LLC	GCIVATVSFF	WEESLTQHYA	GLLPLMTGIF	CTISLCTYAA	SISYDLNRLP 240
KLIYSLP	ADV	EHGYSWSIFC	AWCSLGFIVA	AGGLCIAYPF	ISRKTIAQLK	SGRDSTV

75
 80

A201 DNA SEQUENCE
 Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1-1134 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGAGGCG	AC	TGAATCGGAA	AAAAACTTTA	AGTTTGSTAA	AAGAGTTGGA	TGCCTTTCCG 60
AAGGTTCT	CTG	AGAGCTATGT	AGAGACTTCA	GCCAGTGGAG	GTACAGTTTC	TCTAATAGCA 120

5 TTTACAACCTA TGGCTTTATT AACCATAAAT GAATTCCTCAG TATATCAAGA TACATGGATG 180
 AAGTATGAAT AGGAAGTAGA CAAGGATTTT TCTAGCAAAAT TAAGAATTAA TATAGATATT 240
 ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTAGC AGAAACAATG 300
 GTTGATCTCG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
 AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
 CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480
 GATGATTCAT CACAGTCTCC AAATGCATGC AGAATTCTAT GCCATCTATA TGTCATAAAA 540
 GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCTCTG TGGTCATGCA 600
 10 CATTGCGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTGT 660
 TCTTTTGGAG AGCTTGTTC AGCAATTAAT AATCCTTTAG ATGGAACTGA AAAAATTGCT 720
 ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCCAACAA ACTACATACA 780
 TATAAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840
 CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTTATGA AATATGATCT CAGTCTCTCT 900
 15 ATGGTGACAG TTAATGAGGA GCACATGCCA TCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
 ATTGTTGGAG GAATCTTTTC AACCAACAGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020
 GAAATAATTT GCTGTCGTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCTCTTT 1080
 GAGGATGGCC ACACAGACAA CCATTACCT CTTTTAGAAA ATAATACACA TGA

20 A202 Protein sequence:

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 25 Protein Accession #: NP_057654
 Signal sequence: none found
 Transmembrane domains: none found
 Cellular Localization: nuclear

30 1 11 21 31 41 51
 | | | | | |
 MRRLNRKKTSLVVKELDAFVKVPESEVETSASGGTVSLIAFTTMALLTIM EFSVYQDTWM 60
 KVEYEVDRDFSSKLRLINIDITVAMKQYVGVADVLDAETMVASADGLVYEPTVFDLSPPQ 120
 35 KEWQRMQLQISRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPNACRIHGHLYVNK 180
 VAGNFHITVGA KALPHPRGRHHLAALVNHESYNFSHRIDHLSFGELVPAIINFLDGTETKIA 240
 IDHNGMFQYF ITVVPFKLHET YKISADTHQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
 MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKPIV EIIICRFRLG SYKPVNSVPP 360
 EDGHTDNHLP LLENNTHT

40 A203 DNA SEQUENCE

Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 Probeset Accession #: S79876
 45 Nucleic Acid Accession #: NM_001935.1
 Coding sequence: 76-2301 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
 | | | | | |
 CGCGCGTCTC CGCGCGCCCG GTGACTTCTG CTTGCGCTCC TTCTCTGAAC GCTCACTTCC 60
 GAGGAGAGCG CGACGATGAA GACACCGTGG AAGATTCTTC TGGGACTGCT GGGTGTGCT 120
 CGCGCTGTCA CCATCATCAC CGTGCCCGTG GTTCTGCTGA ACAAGGCAC AGATGATGCT 180
 55 ACAGCTGACA GTGCGAAAC TTACACTCTA ACTGATTACT TAAAAAATAC TTATAGACTG 240
 AAGTTATACT CCTTAAGATG GATTTCAGAT CATGAATATC TCTACAAACA AGAAAAATAA 300
 ATCTTGGTAT TCAATGCTGA ATATGGAAAC AGCTCAGTTT TCTTGGAGAA CAGTACATTT 360
 GATGAGTTTG GACATTTCTAT CAATGATTAT TCAATATCTC CTGATGGGCA GTTTATTCTC 420
 TTAGAATACA ACTACGTGAA GCAATGGAGG CATTCTCTACA CAGCTTCATA TGACATTTAT 480
 60 GATTTAAATA AAAGGCAGCT GATTACAGAA GAGAGGATTC CAAACACAC ACAGTGGGTC 540
 ACATGGTCA CAGTGGGTCA TAAATTGGCA TATGTTTGGG ACAATGACAT TTATGTTAAA 600
 APTGAACCAA ATTATCCAA TACAGAAATC ACATGGACGG GGAAGAAGA TATAATATAT 660
 AATGGAATAA CTGACTGGGT TTATGAAGAG GAAGTCTTCA GTGCTACTFC TGCTCTGTGG 720
 TGCTCTCCAA ACGGCCTTT TTTAGCATAT GCCCAATTTA ACGACACAGA AGTCCCACTT 780
 ATTGAATACT CCTTCTACTC TGATGAGTCA CTGCACTACC CAAAGACTGT ACGGTTTCCA 840
 65 TATCCAAAGG CAGGAGCTGT GAATCCAACT GTAAAGTTCT TTGTTGTAAA TACAGACTCT 900
 CTCAGCTCAG TCACCAATGC AACTTCCATA CAAATCACTG CTCTGCTTC TATGTTGATA 960
 GGGGATCACT ACTTGTGTGA TGTGACATGG GCAACACAG AAAGAATTTT TTTGCACTGG 1020
 CTCAGGAGGA TTCAGAACTA TTCGGTCATG GATATTTGTG ACTATGATGA ATCCAGTGGG 1080
 70 AGATGGAATC GCTTAGTGGC ACGGCAACAC ATTGAAATGA GTACTACTGG CTGGGTTGGA 1140
 AGATTTAGGC CTTCAGAAAC TCATTTTACC CTGATGGTGA ATAGCTTCTA CAAGATCATC 1200
 AGCAATGAAG AAGGTTACAG ACACATTTGC TATTTCCAAA TAGATAAAAA AGACTGCACA 1260
 TTTATTACAA AAGGCACCTG GGAAGTCATC GGGATAGAA GCTTAACCA TGAATTATCTA 1320
 TACTATGATA GTAATGAATA TAAAGGAATG CCAGGAGGAA GGAATCTTTA TAAAAATCAA 1380
 75 CTATTAGTCT ATACAAAAGT GACATGCCTC AGTTGTGAGC TGAATCCGGA AAGGTGTCAG 1440
 TACTATTCTG TGTCATTCTG TAAAGAGGCG AAGTATTATC AGCTGAGATG TTCCGGTCTC 1500
 GGTCTGCCCC CTATACTCT ACACAGCAGC GTGAATGATA AAGGCTGAG AGTCTGGAAA 1560
 GACAAATTCAG CTTTGGATAA AATGCTGCAG AATGTCCAGA TGCCCTCCAA AAAACTGGAC 1620
 TTCATTATTT TGAATGAAAC AAAATTTTGG TATCAGATGA TCTTGCCTCC TCATTTTGAT 1680
 80 AATCCACAGA AATATCTCTC ACTATTAGAT GTGTATGCAG GCCCATGTAG TCAAAAAGCA 1740
 GACACTGTCT TCAGACTGAA CTGGGCCACT TACCTTGCAA GCACAGAAAA CATTATAGTA 1800
 GCTAGCTTTG ATGGCAGAGG AAGTGGTTAC CAAGGAGATA AGATCATGCA TGCAATCAAC 1860
 AGAAGACTGG GAACATTGGA AGTTGAAGAT CAAATTGAAG CAGCCAGACA ATTTTCAAAA 1920
 ATGGGATTTG TGGACAACAA ACGAATTGCA ATTTGGGGCT GGTCAATAGG AGGGTACGTA 1980
 ACCTCAATGG TCTGGGATC GGAAGATGGC GTGTTCAAGT GTGGAATAGC CGTGGCGCCT 2040

5 GTATCCCGGT GGGAGTACTA TGACTCAGTG TACACAGAAC GTTACATGGG TCTCCCAACT 2100
 CCAGAGAGACA ACCTTGAGCCA TTACAGAAAT TCAACAGTCA TGAGCAGAGC TGAATAATTTT 2160
 AAACAGAGTTG AGTACCTCCT TATTCATGGA ACAGCAGATG ATAAAGTTCA CTTCAGCAG 2220
 TCAGCTCAGA TCTCCAAAGC CCTGGTCGAT GTTGGAGTGG ATTTCCAGGC AATGTGGTAT 2280
 ACTGATGAAG ACCATGGAAT AGCTAGCAGC ACAGCACACC AACATATATA TACCCACATG 2340
 AGCCACTTCA TAAAACAATG TTTCTCTTTA CCTTAGCACC TCAAAATACC ATGCCATTTA 2400
 AAGCTTATTA AAACCTATT TGTGTTTCAT TATCTCAAAA CTGCACTGTC AAGATGATGA 2460
 TGATCTTTAA AATACACACT CAAATCAAGA AACTTAAGGT TACCTTTGTT CCCAAATTTT 2520
 10 ATACCTATCA TCTTAAGTAG GGACTTCTGT CTTCACAACA GATTATTACC TTACAGAAGT 2580
 TTGAATTATC CGGTGGGTTT TTATTGTTTA AAATCATTTT TGCATCAGCT GCTGAAACAA 2640
 CAAATAGGAA TTGTTTATTTAT GGAGGCTTTG CATAGATTCC CTGAGCAGGA TTTTAATCTT 2700
 TTTCTAACTG GACTGGTTCA AATGTTGTTT TCTTCTTTAA AGGGATGGCA AGATGIGGGC 2760
 AGTGATGTCA CTAGGGCAGG GACAGGATAA GAGGGATTAG GGAGAGAAGA TAGCAGGSCA 2820
 15 TGGCTGGGAA CCCAAGTCCA AGCATAACCA CACGAGCAGG CTACTGTCAG CTCCTCTCGG 2880
 AGAAGAGCTG TTCACCAAGA GACTGGCACA GTTTTCTGAG AAAGACTATT CAAACAGTCT 2940
 CAGGAAATCA AATATCGAAA GCACTGACTT CTAAGTAAAC CACAGCAGTT GAAAGACTCC 3000
 AAAGAAATGT AAGGGAATCT GCCAGCAACG CAGCCCCCAG GTGCCAGTTA TGGCTATAGG 3060
 TGCTACAAAA ACACAGCAAG GGTGATGGGA AAGCATTGTA AATGTGCTTT TAAAAAATAA 3120
 20 TACTGATGTT CCTAGTGAAA GAGGCAGCTT GAAACTGAGA TGTGAACACA TCAGCTTGCC 3180
 CTGTTAAAG ATGAAATAT TGTATCACA AATCTTAAT TGAAGGAGTC CTGTCATCAA 3240
 TTTTCTTAT TTCTTTCTT TGAGTGCTT AATTAAGA ATATTTAAC TTCCTGGAC 3300
 TCATTTTAAA AAATGGAACA TAAATACAA TGTATGTAT TATTATCCC ATTCTACATA 3360
 CTATGGAATT TCTCCAGTC ATTTAATAAA TGTGCTTCA TTTTTC

25

A204 Protein sequence:
 Gene name: dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
 Unigene number: Hs.44926
 30 Probeset Accession #: S79876
 Protein Accession #: NP_001926.1
 Signal sequence: none found
 Transmembrane domains: 6-28
 DPPIV_N_term domain: 43-557
 35 Peptidase_S9 domain: 558-635
 Cellular Localization: plasma membrane

40 1 11 21 31 41 51
 MKTPWKILLG LLGAAALVTI ITVPVVLNKG GTDDATADSR KTYTLTDYLK NTYRLKLYSL 60
 RWISDHEIYLY KQENNILVFN AEYGNSSVPL ENSTFDEFHG SINDYSISPD GQFILLEYN 120
 VKQWRHSYTA SYDIYDLNKR QLITEERIPN NTQWVTNSPV GHKLAYVMNN DIYVKIEPNL 180
 PSYRIWTGK EDIYINGITD WYEESEVESA YSALWSPNG TFLAYAQFND TEVPLIEYSP 240
 45 YSDESLQYPK TVRVYPYKAG AVNPTVKFPV VNTDSLSSVT NATSIQITAP ASMLIGDHYL 300
 CDVTWATQGR ISLQWLRIQ NYSVMDICDY DESSGRWNCL VARQHIEMST TGVVGRFRPS 360
 EPHFTLDGNS FYKIIISNEEG YRHICYFQID KDCCTFITKG TWEVIGIEAL TSDYLYIISN 420
 EYKGMPOGRN LYKIQILIDYT KVTCLSCBLN PERQYYSVS FSKEAKYQVL RCGSGPLPLY 480
 TLHSSVMDRG LRVLEDMSAL DKMLQNVQMP SKKLDPIILN ETKFWYQML PPHFDKSKKY 540
 50 PLLLDVYAGP CSQADTVFR LNWATYLAST ENIIIVASEFDG RGSQYQGDKI MHAINRRLGT 600
 FEVEDQIEAA RQFSKMGFVD NKRIAINGWS YGGYVTSMLV GSGSGVFKCG IAVAPVSRWE 660
 YDSVYTRY MGLPTPEDNL DEYRNSTVMS RAENFKQVEY LLIEGTADDN VHFQQAQIS 720
 KALVDVGVPD QAMWYTEDDH GIASSTARQH IYTHMSHPK QCFSLP

55 **A205 DNA SEQUENCE**
 Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 Nucleic Acid Accession #: none found
 60 Coding sequence: 1-261 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 ATGGCTCTGG CGAAGGTGAG GGAGCCAAAC GCAATGACA ATGCCATCAG AGTTGACAAC 60
 AGAAGTGTGA TTAAGTGGC TGCTAACCAAG TGTTCCTGCG ATGAGGCAGA AAGTGAATCC 120
 AGAAACCCCTC AGGAGCTCTG GATGGGCCCTG CTCCTCTTGA TGGGGGTCCT AGAAGCATGT 180
 GTGGAAATGA GGCCTCTGTC AGTCTGGTCC CTGAGAGATG ACAAGGAGCA GAGCCCCCAC 240
 CAGCCACAC TGGATGTCTA A

70

A206 Protein sequence:
 Gene name: predicted exon
 Unigene number: none found
 Probeset Accession #: none found
 75 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 46-68
 Cellular Localization: not determined

80

1 11 21 31 41 51
 MALAKVREPN ANDNAIRVDN RSVIKVRANQ CSLHEASES RNPQELWMGL LLLMGVLEAC 60
 VEMRPLSVMS LRDDKQSPH QPTLDV

A207 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Nucleic Acid Accession #: none found
 Coding sequence: 1-462 (underlined sequences correspond to start and stop codons)

```

10      1      11      21      31      41      51
      |      |      |      |      |      |
      ATGCCAAATG CTGAGTTAGA AGCAAAGAGC CTTGGAAGCA GTAAATGTTT AAAAACTGCT 60
      CTCATACCTG CTGTATGTTG TGGATCAGCA AATATAGTCA GCCCTCTACT TGAGCAAAAT 120
      ATTGATGTAT CTTCTCAAGA TCTGGACAGA CGGCCAGAGA GTATGCTGTT TCTAGTCATC 180
15      ATCATGTGGA CCAGTTTGTG GGAAGACAAT CTTTCCATGG GCTGGGGGAA GCTAGAAGAT 240
      TTTATGGCTA TTGAAGAAGA AATGAAGAAG CACGGAAGTA CTATGTGGG ATTCCCAGAA 300
      AACCAGACTA ATGGTGCCCG TGCTGGCAAT GGTGATGATG GATTAAATCC TCCAAGGAAG 360
      AGCAGAACAC CTGAAAGCCA GCAATTTCCT GACACTGAGA ATGAAGAGTA TCACAGGTTT 420
      GTCAAGATC AGATAGTTGT AGATATGCGG CGTTATTTCT GA
  
```

A208 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.222886
 Probeset Accession #: AI672225
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 16-38
 Cellular Localization: not determined

```

30      1      11      21      31      41      51
      |      |      |      |      |      |
      MPNAELEAKS LGSSKCLKTA LILAVCCGSA NIVSPLLBQN IDVSSQDLDR RPESMLFLVI 60
      IMWTSFVEDN LSMGWGKLED FMAIEEEMKK HGSTHVGFPE NLINGAAAGN GDDGLIPPRK 120
35      SRTPEQQPFP DTENEYHRF VKDQIVVDMR RYF
  
```

A209 DNA SEQUENCE

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Nucleic Acid Accession #: NM_014253
 Coding sequence: 65-8242 (underlined sequences correspond to start and stop codons)

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45      1      11      21      31      41      51
      |      |      |      |      |      |
      GACTGCTTGC ATTAAAGGAC TTCTCATCC TTTTTCAT GAAACTGAGC TTGCTTAATC 60
      AGAGATGGAG CAAACTGACT GCAAAACCTA CCAGCCTCTA CCAAAAGTCA AGCATGAAAT 120
      GGATCTAGCT TACACCAAGT CTTCTGATGA GAGTGAAGAT GGAAGAAAC CAAGACAGTC 180
50      ATACAACCTC AGGGAGACCC TGCAACGAGTA TAACCAAGGAG CTGAGGATGA ATTACAATAG 240
      CCAGAGTAGA AAGAGGAAGA AAGTAGAAAA ATCTACTCAA GAGATGGAAT TCTGTGAAAC 300
      CTCTCAGACT CTGTGCTCTG GCTACCAAC AGACATGCAC AGCGTTTCTC GGCATGGCTA 360
      CCAGCTAGAG ATGGGATCTG ATGTGGACAC AGAGACAGAA GGTGCTGCCT CACCTGACCA 420
      TGCACTAAGA TTCTCTCTCTG TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 480
55      GGCCAACTCT GCATTATCCT TGAATGACAC TGACCATGAA AGGAAGTCTG ATGGGGAAAA 540
      TGGTTTCAAA TTCTCTCTCTG TTTGTTGTGA CATGGAGGCT CAAGCTGGGT CTACTCAAGA 600
      TGTGAGAGGC AGCCACACAC ACCAGTTCAC CTTGAGACCC CTCOCACGCC CACCTCCGCC 660
      TCCTCATGCC TGCACCTGTG CCAGGAAGCC ACCCCCTGCA GCGACTCTCT TTCAGAGGAG 720
      ATCAATGACT ACCCGAGCCC AGCCGAGCCC AGCTGCTCCA GCTCCCCCAA CCAGCAGGCA 780
60      GGATTCAGTC CATCTGCATA ACAGCTGGGT CCTGAACAGC AACATACCAT TGGAGACCGA 840
      GCATTCCCTG TTCAACATG GATCTGGTTC CTCTGCGATC TTCAGTGCAG CCAGTCAGAA 900
      CTACCCCTCG ACATCCAATA CCGTGTACTC GCCCCCTCCG AGGCCTCTTC CTCGAAGCAC 960
      CTTTTCOAGA CTGCTCTTTA CCTTTAACA ACCTTACAGG TGCTGCAACT GGAAGTGCAC 1020
      AGCATGTAGG GCCACTGCAG TCACAGTGAC TTTGGCCCTG TTAAGAGCCT ATGTGATTGC 1080
65      AGTGCATTGT TCGGCCCTGA CTTGGCAGTT GCAACCAAGT GAAGGAGAGC TGTATGCAAA 1140
      TGGAGTTAGC AAAGGGAACA GGGGGACCGA GTCCATGGAC ACTACTTACT CTCCAATTGG 1200
      AGGAAAGATT TCTGATAAAT CAGAGAAAAA AGTGTTCAG AAGGGACGGG CGATAGACAC 1260
      TGGAGAAGTT GACATTGGTG CACAGGTCAT GCAGACCATT CCACCTGGTT TATTCTGGCG 1320
      TTTCCAGATT ACTATCCACC ATCCAATATA TCTGAAGTTC AATATTTCCT TAGCCAAGGA 1380
70      CTCTCTGCTG GGAATTATG GCAGAGAAAA CATTCACCTT ACACATACTC AGTTTGATTT 1440
      TGTAAAACCTA CTGATGGGCA AACAGCTGGT CAAGCAGGAC TCCAAGGGCT CTGATGATAC 1500
      ACAGCACTCC CCTGGAACCC TGATCTTAAC TTGCTTCAG GAGACAGGTT TCATAGAGTA 1560
      TATGGATCAA GGACCTTGGT ATCTGGCGTT TTACAATGAT GGAAGAAAGA TGGAGCAAAT 1620
      ATTGCTGTGA ACTACAGCAA TTGAAATATG GGATGACTGT TCAACCAATT GCAATGGAAA 1680
75      TGGAGAGTGT ATCTCTGGCC ATTGTCAATG TTTCCAGGTA TTCCTTGAC CTGACTGTGC 1740
      TAGAGATTCC TGCCCTGTGC TGTGTGGTGG GAATGGAGAA TACGAGAAAG GACACTGTGT 1800
      CTGCGGCGAT GGCCTGGAAG GGCAGAGTG TGACGTTCOG GAAGAACAAAT GCATTGATCC 1860
      AACATGCTTT GGCACGGCA CCTGCATCAT GGGAGTCTGC ATCTGTGTGC CAGGATACAA 1920
      AGGAGAAATA TGGAGGGAAG AGGACTGCCT AGACCCAAAT TGTTCACACC ATGGCATCTG 1980
      TGTAAAGGA GAATGTCACT GTTCTACTGG CTGGGGAGGA GTTAACTGTG AAACACCACT 2040
      TCCTGTATCC CAGAGCAGT GCTCAGGACA CGGAACCTTT CTTCTGAGCG CTGAGTATG 2100
      CAGCTGTGAT CCCAAGTGA CAGGATCTGA CTGCTCAACA GAGCTGTGTA CCATGGAGTG 2160
      TGGTAGCCAT GGAGTCTGCT CAAGAGGAAT TTGCCAGTGT GAAGAGGCT GGGTAGGACC 2220
80      AACATGTGAG GAAGCTCTCT GTCAATCTCA TTGTACTGAG CATGGCCAAT GCAAGAGATG 2280
  
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	AAAAATGTGAG	TGTAGCCCTG	GATGGGAGGG	CGACCACTGC	ACAATTGCTC	ACTACTTAGA	2340
	TGCTGTCCGA	GATGGCTGCC	CAGGGCTCTG	CTTTGGAAAT	GGACGATGTA	CCCTGGATCA	2400
	AAATGGTTGG	CACCTGTGTG	GTGAGGTGGG	TTGGAGTGGG	ACAGGCTGCA	ATGTTGTGTCAT	2460
5	GGAAATGCTT	TGTGGAGATA	ACTTGGACAA	TGATGGAGAT	GGTTTAACCG	ACTGTGTGGA	2520
	TCCTGACTGT	TGTCAACAAA	GCAACTGTTA	TATAAGTCCT	CTCTGCCAGG	GCTCACCAGA	2580
	TCCTCTTGAC	CTCATTGACG	AAAGCCAAAC	TCCTCTCTCT	CAGCACACTT	CAAGACTTTT	2640
	TTATGATCGA	ATCAAATTCC	TCATTGGCAA	GGACAGTACT	CATGTCAATC	CTCCTGAGGT	2700
	GTCAATTGAC	AGCAGGCGTG	CCTGTGTGAT	TCGAGGCCAA	GTGGTGGCCA	TAGATGGAAC	2760
10	TCCTCTAGTG	GGAGTGAATG	TCAGTTTCTT	GCACCAAGT	GATTATGGGT	TTACCATCAG	2820
	CCGGCAAGAT	GGAAGCTTTG	ACCTCGTGGC	CATCGGTGGC	ATCTCTGTCA	TCTTAATCTT	2880
	CGACCGATCC	CCTTTCCTGC	CTGAGAAGAG	AACACTCTG	TTGCCTTGA	ATCAGTTTAT	2940
	TGTGGTAGAG	AAAGTCACCA	TGCAGAGAGT	TGTATCAGAC	CCGCCATCCT	GCGATATCTC	3000
	CAACTTTATC	AGCCCCAAAC	CTATTGTGCT	TCCTTCAACG	CTCACATCAT	TTGGAGGGTG	3060
15	CTGTCCAGAG	AGGGGAACCTA	TTGTTCTGTA	GCTGCAGGTT	GTACAGGAGG	AAATTCCCAT	3120
	TCCCTCCAGC	TTTGTGAGGC	TGAGTTACCT	GAGCAGCCGC	ACCCCTGGGT	ATAAAACCTC	3180
	GCTACGGATC	CTTCTGACAC	ATTCACAGAT	TCCCGTAGGC	ATGATAAAAG	TACACCTCAC	3240
	AGTAGCTGTG	GAAGGGCGAC	TCACACAGAA	GTGGTTTCCC	GCCGCAATTA	ATCTTGTCTA	3300
	CACATTGTCT	TGGAAACAAG	CCGATATCTA	TGGACAGAAG	GTTTGGGGCC	TGGCAGAGGC	3360
20	TTTGGTATCT	GGGGGATATG	AATATGAAAC	GTGCCCTGAC	TTTATTCTCT	GGGAGCAAGG	3420
	GACAGTGTGT	TTACAAGGTT	TTGAGATGGA	TGCTTCTAAC	CTAGGAGACT	GGTCTTTGAA	3480
	TAAGCATCAC	ATTTTGAATC	CTCAAAGTGG	AATCATACAT	AAAGGGAATG	GAGAAAATAT	3540
	GTTCATTCCC	CAGCAGCCCC	CAGTCAATATC	AACCATAAATG	GGTAATGGAC	ACCAAAGGAG	3600
	TGTAGCCTGC	ACCAACTGCA	ATGGCCACGC	CCACAACAAC	AAACTCTTTG	CTCCTGTGCG	3660
25	CTTAGCTTCT	GCGCCTGATG	GCAGTGTGTA	TGTTGGCGAC	TTCAATTTTG	TAAGGAGAAT	3720
	ATTTCCCTCG	GGAACCTCCG	TTAGTATTTT	GGAATTAAGC	ACAAGTCTGT	CTCACAATA	3780
	CTATCTGGCT	ATGGACCCCTG	TGCTGAATC	ACTCTATCTA	TCAGACACCA	ATACTCGCAA	3840
	AGTCTACAAG	TTGAAATCTC	TTGTGGAGAC	GAAAGATCTG	TCCAAGAATT	TTGAAGTGGT	3900
	GGCAGGAATC	GGTGATCAGT	GCCTTCCCTT	TGACCAGAGT	CATTGTGGAG	ATGGTGGGAG	3960
30	AGCATCGGAA	GCTCTCACTGA	ATAGCCCTCG	AGGCATCACA	GTTGATAGGC	ATGGATTAT	4020
	TTACTTTGTG	GATGGGACTA	TGATTCCGAA	AATTGATGAG	AATGCTGTGA	TCACAACCTG	4080
	AATGGCTCA	AATGGTCTGA	CTTCCACACA	ACCCTGAGC	TGTGACTCAG	GAATGGACAT	4140
	CACCTAGGTT	CGATTAGAGT	GGCCAAACAGA	CCTTGCAGTA	AATCCTATGG	ACAATTCAAT	4200
	GTATGCTTGT	GATAACAACA	TTGTGCTGCA	AATTTCTGAG	AACAGGCGTG	TTCCGATCAT	4260
35	CGCAGGACCG	CCCTGCTGCT	GCCAGGTGCC	AGGCATCGAT	CATTTCCTGT	TCAGCAAGGT	4320
	AGCAATTCAC	TCCACTCTAG	AGTCAGCGAG	GGCCATCAGT	GTCTCCACCA	GCGGGCTGCT	4380
	CTTCATAGCT	GAAACAGACG	AGAGGAAAGT	AAACCGCATT	CAGCAAGTAA	CCACCAATGG	4440
	GGAGATCTAC	ATCATCGCTG	GTGCCCCAC	TGACTGTGAC	TGCAAAATTG	ATCCAACTG	4500
	TGACTGTTTT	TCAGGTGATG	GTGGCTATGC	CAAGATGCA	AAGATGAAAG	CCCTTCTCTC	4560
40	CTTAGCAGTG	TCGCTGATG	GAACCTCTA	TGTGGCAGAC	CTCGGAATG	TTCGAATTGG	4620
	TACCATCAGC	AGGAACCAAG	CCCACCTGAA	TGACATGAAC	ATTTATGAGA	TTGCTTCACC	4680
	CGCTGATCAG	GAAGTGTACC	AGTTCACGT	AAATGGAACC	CACCTACACA	CCCTGAACCT	4740
	GATAACAAAG	GACTATGTTT	ATAACTTCAC	CTACAATTCT	GAAGGTGACT	TGGGCGCGAT	4800
	TACCAGCAGC	AATGGCAATT	CAGTGACAT	TCGCCGTGAT	GCAAGCGGAA	TGCCGCTATG	4860
45	GCTTGAGTGA	CCCTGGCGAG	AAGTATAGT	GCTGACTATA	AGCAGCAATG	GAGTCTTGAA	4920
	AAGAGTGTCA	GCCCCAAGCT	ATAATCCGGC	CTTAATGACC	TATCCAGGAA	ACACAGGGCT	4980
	TCTGGCTACC	AAAAGTAAAG	AAAATGGATG	GACAACCGTT	TATGAGTATG	ACCCCGAGGT	5040
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A210 Protein sequence:

Gene name: odz (odd Oz/ten-m, Drosophila) homolog 1
 Unigene number: Hs.23796
 Probeset Accession #: NM_014253
 Protein Accession #: NP_055068
 Signal sequence: none found
 Transmembrane domains: 318-340
 Cellular Localization: plasma membrane

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A211 DNA SEQUENCE:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Nucleic Acid Accession #: NM_000441
 Coding sequence: 225-2567 (underlined sequences correspond to start and stop codons)

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 GCACAGATAT CTACAAAAGT ACCAAGAATT ACAAACCAT TGAAGAACCT CAAGGAGTGA 1860
 AGATTCTTAG ATTTTCCAGT CCTATTTTCT ATGGCAATGT CGATGGTTT AAAAATGTGA 1920
 TCAAGTCCAC AGTTGGATTG GATGCCATTA GAGTATATAA TAAGAGGCTG AAAGCGCTGA 1980
 GGAAATACCA GAAACTAATA AAAAGTGGAC AATTAAGAGC AACAAAGAAAT GGCATCATAA 2040
 30 GTGATGCTGT TGACACAAAC AATGCTTTTG AGCCTGATGA GGAATATTGA GATCTGGAGG 2100
 AACTTGATAT CCAACCAAG GAAATAGAGA TTCAAGTGGG TTGGAACCTC GAGCTTCCAG 2160
 TCAAGTAGAA CGTTCACAA GTGCCAATCC ATAGCCTTGT GCTTGACTGT GGAGCTATAT 2220
 CTTTCTGGGA CGTTGTTGGA GTGAGATCAC TGCGGTGAT TGTCAAAGAA TTCCAAAGAA 2280
 TTGATGTGAA TGTGTAATTT GCATCACTTC AAGATTATGT GATAGAAAAG CTGGAGCAAT 2340
 35 GGGGTTCTT TGACAGCAAC ATTAGAAAGG ACACATTCTT TTTGACGGTC CATGATGCTA 2400
 TACTCTATCT ACAGAACCAA GTGAAATCTC AAGAGGGTCA AGGTTCCATT TTAGAAAAGCA 2460
 TCACCTCTAG TCAGGATGTT AAAGATAACC TTGAATTAAT AGAAACAGAG CTGACGGAAG 2520
 AAGAACCTGA TGTCCAGGAT GAGGCTATGC GTACACTTGC ATCTGAAAG TGGGTTCCGG 2580
 AGGTCTCTAT GAGCAGGAA TACAAGACAA AACTTCTCTA ATGCATTGAC TATTTCTTCA 2640
 40 GACTCAAAAC ACTCATCTT TTTTCTATTA AGCATTGAA AGAGAAGCAC TAAGACTGCT 2700
 TCTAGGCTTT ATTTATAAAA TAAACACCTT ATCCCTAACA TGGGCAAAAT GGCTAGAATT 2760
 ATTCAGAGAA TTTGGCAGG TCCAGGGTAA GCTGGTGTTA TAATACGCTG CTGATCTACA 2820
 TCACAGATTT GCTAATAATG TTCACGTGGG CCCTGGCATA TCTCTGTTCA GTTAGAGTGA 2880
 GTGCTGACCC AACAGCCTCT GTGGTCAAGC GAGTCAAGAA TGATTAATCA TAAAGAAAAA 2940
 45 TCAGTTCTTG ACTCATCTGG ATATCCATGA GCTGCATGTA TCACCATGTA AGGTCACTT 3000
 TAGTAAATGC TGAATAAAA TGATTAATGC ATTTATCAAT AAAGCCCTTT GAAATACTT 3060
 TGGATAATAA ATTGAGTTGT TAAAAATGCA AATTGCTTA GTATCTAATA ATGAAGTGT 3120
 ATTACATATA GCCGGAATTG AGGATCTCTT TGATCTGGA AATGGTTTAC CTAAGAGCTA 3180
 CAGAACCAGG CCAATATATT TTGAATATT GATGCAGACA AATGAATATA TAAAGAGATT 3240
 50 TTCACTGTTT ATAAAAATCT TTTTGTATAT GATAAATACT ATGATCACA CTGAGATCAA 3300
 AAAAAATATG CACAGATTAT TTTGTTTAAA AATGCAGTTT TAATTATCTT AGTCTATAGA 3360
 AATGATCATT GCATGGAGGC ATGTATAGST ATGATCTGTG TAAATCTGA CATAAAAAACA 3420
 GTGCTATCTT GAGTGAAAT TTTTGTGATG TGCTTACATA ACCATGGTGA TTAAGATGAG 3480
 TTTATATTTT TTCTCAAAAA TTTTAGCAGT GTGTAAGTA AGTAATCTTT AACTGAACTC 3540
 55 TGACCACTTA AAAAAAATC TAAAAATTGA ACTACCTATA GTAGTCTGTG TTTAAAGTGA 3600
 ATTTTAAAG ACAAGCATTT CTAAATGAAC TCAATATAAA AACATTCTT TGGAAATGAC 3660
 ATACTGAAAA ATACAGGTTT TTTTGACCAA AAGTTTTTAT ATCTTTCTT TTTATTTATT 3720
 TTTTCTCTAA GTGCCAACAA TTTTCTAGAT ATTATATACA ACACAGGCTT TGATCTTGGG 3780
 GACTTTTCCC ATATATTTCA CACTGGAGTG AATGAAGTTG TACTTCATT CTAGAGAAAA 3840
 60 GTTATACCCA GGTCCCCAAT TGAGAAATGTC TTGCTTGATT GAAAAACGACA TCATCCCTTG 3900
 GTATACTCCA GGGATTGGTT TCAGGACCCC TGCAATTACC AAAATTGTG CACACTCAAG 3960
 TCCTGCAATG ACCCTGCTCT AAAGATAGAA TGGCTTCTCT GTTTTCTTC TGAATAACAA 4020
 CCAGAACCAA TGTGTCTATT TCTGAAAGAA TAGGATTAAT GATCATACAA ATGGGTTAAT 4080
 CCTGAATCTT GGTGTAAAT CTGGTTACAG CATAACTAGG ATTATAATGC TGCTCATTT 4140
 65 TCACAGCACT ACTTGCTTAT ATTGACAACA AATCATCTCG CTAAGAGAGT AATGTAGGCC 4200
 AGGCGCGGTG GCTCATGCCCT GTAATCCAG CACTTTGGGA GGCCGAGGCG GGTGGATCAC 4260
 GAGGTCAGGA GATCGAGACC ATCCTGGCTA ACATGGTAAA ACCCGTCTC TACTAAAAAT 4320
 AGAAAAAAG AAATTAGCCT AGCGTGGTGG CTGGCGGCGG CCTGTAGTCC CAGCTATTTG 4380
 GGAGGCTAAG GCAGGAGAT GGCCTGAACC CGGGAGGCGG AGCTTCAGT GAGCCGAGGT 4440
 70 CGTGCCACTG CACTCCAGCC TGGCGACAG AGCAAGACTC CGTCTCAAAA AAAAAAATAA 4500
 AAAAAAATAA AGAGTGAATG TAATAGTCTT GCAGAAAATG AATGAATACC TTTGTTCAAT 4560
 AAAGGAATAA TGCACTGCTC ACTTTTGA AGGAAATGCC AAAGTTACGT TTTACAACAA 4620
 GGCTAGAGTT TGTAAATCTT GGGTTCATTT GTGATGACAT AAGTCAGCAA ACTGCGGGA 4680
 TACTGTCTCT TCTATGATT TTGTGAATAG TAAGCATAAT TTTAGTTTGG TATTATCAAT 4740
 75 GAAATTTTCA CTTGAAATTA AAGCTGCCTT TTGTTATATT TTTAACCTAT AGGATAAGAT 4800
 TCCAGTATTG TATATGAGTT TTAACAAAT AAAAAATCAA ATCATGTACA TTTGAAATA 4860
 TTTGCACACA TTTAAAAATA AATGTAAGT TGTCTTTTAA ACTACTCGGA TGTGCTCTT 4920
 CTGAACAAA

A212 Protein sequence:

Gene name: Solute carrier family 26, member 4
 Unigene number: Hs.159275
 Probeset Accession #: AF030880
 Protein Accession #: O43511
 Signal sequence: none found

Transmembrane domains: 81-103, 109-131, 136-158, 185-207, 221-243, 245-267, 270-291, 295-317,
347-369, 386-408, 420-442, 448-470, 486-508
Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MAAPGGRSEP PQLPEYSCSY MVSRFVYSEL AFQQQHERRL QERKTLRESL AKCCSCSRKR 60
AFGLVKTLVP ILEWLKPYRV KEWLLSDVIS GVSTGLVATL QGMAYALLAA VPVGYGLYSA 120
FFPILTYFIF GTSRHSIVSGP FPVVSMLVGS VVLSMAPDEH FLVSSSNGTV LNTTMDTAA 180
RDTARVLIAS ALTLVLGIIQ LIFGGLQIGF IVRYLADPLV GGFTTAAAFQ VLVSQLKIVL 240
NVSTKNYNGV LSIYITLVEI FQNIQDNLNLA DFTAGLLTIV VCMVAVKELND RFRHKIPVPI 300
PIEVIVTIIA TAIISYGANLE KQYNAGIVKS IPRGFLPPEL PPVSLFSEML AASPSIAVVA 360
YAIASVGVKV YATKYDYTID GNQEFIAFGI SNIFSGFFSC FVATTALSRT AVQESTGGKT 420
QVAGIISAAI VMIALALGK LLEPLQKSVL AAVVIANLKG MFMQLCDIPR LWRQNKIDAV 480
IWVFTCIYSI ILGLDLGLLA GLIFGLLTIV LRVQFPFVNG LGSIPSTDYI KSTKNYKNIE 540
EPQGVKILRF SSPIFYGNVD GFKKCIKSTV GFDAIRVYNK RLKALRKIQK LIKSGQLRAT 600
KNGIISDAVS TNNAFEPDED IEDLEELDIP TKEIEIQVDW NSELPVKVNV PKVPIHSLVL 660
DCGALISLDV VGVRSRLRVV KEFQRIDVNV YFASLQDYVI EKLEQCGFFD DNIRKDTFFL 720
TVHDAIYLQ NQVKSQEGQG SILETITLIQ DCKDTLELIE TELTEBELDV QDEAMRTLAS 780
QDEAMRTLAS

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A213 DNA SEQUENCE:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Nucleic Acid Accession #: NM_021614
Coding sequence: 458-2197 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
CGGCGGCAGC AGCCCATGCC TCCGGTGCAA CAGCTGCGCC TCCTCCGGTG CCCCAGCGGC 60
GGGGGCGGGA GATAACCTGT CCTGCTGCTC CGGCACCTCC TCGCCCGGCG GCGCCTTCGG 120
GACCCGCACC TCCTGCGCGC TGTCGGGCTC GTCTGCTGCT TGCTGCTGCT GCTCGTCGCG 180
CGGGGCGCAG CAGCTCAATG TGAGCGAGCT GACGCGCTCC AGCCATGCCA GTGCGCTCCG 240
GCAGCAGTAC GCGCAGCAGT CCGCGCAGCA GTCGGCGTCC GCCTCCAGT ACCACCAATG 300
CCACAGCCTG CAGCCCGCGC CCAGCCCCAC GGCAGCCTC GGCAGTCTGG GCTCCGCGCC 360
CCCGCTCTCG CACCACCACC ACCACCCGCA CCGCGGCAC CACCAGCACC ACCAGCCCCA 420
GGCGCGCGCC GAGAGCAACC CCTTCACCGA AATAGCCATG AGCAGCTGCA GGTACAAACG 480
GGCGCTCATG CGCCCGCTCA GCAACTTGAG CGCGTCCCGC CGGAACCTCC ACGAGATGGA 540
CTCAGAGGCG CAGCCCTGTC AGCCCCCGGC GTCTGTGGGA GGAGGTGGCG GCGCGTCTCT 600
CCGCTCTGCA GAGCTGCGCG CCGCCGCGCG TGTTTGTGTC TCAGCCCGCG AGATCGTGGT 660
GTCTAAGCCC GAGCACAACA ACTCCAACAA CCTGGGCTCT TATGGAACCG GCGCGGAGG 720
CAGCACTGGA GGAGGCGGCG GCGGTGGAGG GAGCGGGCAC GGCAGCAGCA GTGGCACCAA 780
GTCCAGCAAA AAGAAAAACC AGAACATCGG CTACAAGCTG GGCCACCGCG GCGCCCTGTT 840
CGAAAAAGCG AAGCGGCTCA GCGACTACGC GCTCATCTTC GGCATGTTCT GCATCGTGGT 900
CATGTCTATC GAGACCGAGC TGTCGTGGGG CGCCTACGAC AAGGCGTTCG TGATTCCCTT 960
AGCTCTGAAA TGCCCTTATC GTCTCTCCAC GATCATCTCG CTCGGTCTGA TCATCGTGTA 1020
CCACGCCAGG GAAATACAGT TGTTCATGGT GGCAATGGA GCAGATGACT GGAGAATAGC 1080
CATGACTTAT GAGCGTATT TCTTCATCTG CTTGGAATAA CTGGTGTGTG CTATTCTATC 1140
CATACCTGGG AATTATACAT TCACATGGAC GGCCCGGCTT GCCTTCTCCT ATGCCCATC 1200
CACAAACCCG GCTGATGTGG ATATTATTTT ATCTATACCA ATGTTCTTAA GACTCTATCT 1260
GATTGCCAGA GTCATGCTTT TACATAGCAA ACTTTTCACT GATGCCTCCT CTAGAAGCAT 1320
TGGAGCACTT AATAAGATAA ACTTCAATAC ACGTTTTGTT ATGAAGACTT TAATGACTAT 1380
ATGCCCAGGA ACTGTACTCT TGGTTTTAG TATCTCATTA TGGATAATTG CCGCATGGAC 1440
TGTCGAGCTG TGGAAGAGT ACCATGATCA ACAGGATGTT ACTAGCAACT TCCTTGGAGC 1500
GATGTGGTTG ATATCAATAA CTTTCTCTC CATTGGTTAT GGTGACATGG TACCTAACAC 1560
ATACTGTGGA AAGGAGTCT GCTTACTTAC TGGAAATTAT GGTGCTGGTT GCACAGCCCT 1620
GGTGGTAGCT GTAGTGGCAA GGAAGCTAGA ACTTACCAAA GCAGAAAAAC ACGTGACACA 1680
TTTCATGATG GATACTCAGC TGACTAAAAG AGTAAAAAAT GCAGCTGCCA ATGTACTCAG 1740
GGAAACATGG CTAATTATCA AAAATACAAA GCTAGTGAAA AAGATAGATC ATGCAAAAGT 1800
AAGAAAAACAT CAACGAAAT TCCTGCAAGC TATTTCATCA TTAAGAAAGT TAAAAATGGA 1860
GCAGAGGAAA CTGAATGACC AAGCAACAC TTTGGTGGAC TTGGCAAGA CCCAGAACAT 1920
CATGTATGAT ATGATTTCTG ACTTAAACGA AAGGAGTGAA GACTTCGAGA AGAGGATTGT 1980
TACCTGGGAA ACAAAACTAG AGACTTTGAT TGGTAGCATC CACGCCCTCC CTGGGCTCAT 2040
AAGCCAGACC ATCAGGCAGC AGCAGAGAGA TTTCAATTAG GCTCAGATGG AGAGCTACGA 2100
CAAGCAGCTC ACTTACAATG CTGAGCGGTC CCGGTCTCTG TCCAGGAGGC GCGGTCTCTC 2160
TTCCACAGCA CCACCAACTT CATCAGAGAG TAGCTAGAAG AGAATAAGTT AACCACAAAA 2220
TAAGACTTTT TGCCATCATA TGGTCAATAT TTTAGCTTTT ATTGTAAAGC CCCTATGGTT 2280
CTAATCAGCG TTATCCGGGT TCTGATGTCA GAATCCTGGG AACCTGAACA CTAAGTTTAA 2340
GGCCAAAATG AGTGAATACT CTTTTTTTTT CTTTCAGATG CACAGGGAAT GCACCTATTA 2400
TTGCTATATA GATTGTTCCT CCGTGAATTT CACTAACCTT TTATTCATGC ACTTCAACAA 2460
AACTTTACTA CTACATTATA TGATATATAA TAAAAAAGT TAATTTGGGA

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A214 Protein sequence:

Gene name: ESTs, Highly similar to calcium-activated potassium channel rSK2 [R.norvegicus]
Unigene number: Hs.98280
Probeset Accession #: AA418000
Protein Accession #: NP_067627
Signal sequence: none found
Transmembrane domains: 135-157, 168-190, 208-230, 254-276, 306-328, 342-364, 373-394

Calmodulin binding domain: 412-488
Cellular Localization: plasma membrane

5
1 11 21 31 41 51
| | | | |
MSSCRYNGGV MRPLSNLSAS RRNLHMDSE AQPLQPPASV GGGGGASSPS ADAAAAAAS 60
SSAPEIVSVK PEHNNSNNLA LYGTGGGGST GGGGGGGGGG HGSSSGTKSS KKKQNIGYK 120
10 LGHRRALPEK RKRLSDYALI FGMFGIVVMV IETELSWGAY DKASLYSLAL KCLISLSTII 180
LLGLIIVYHA REIQLFMVDN GADDWRIAMT YERIFFICLE ILVCAIHPIF GNYTFTWTAR 240
LAFSYAPSTT TADVDIILSI PMFLRLYLIA RVMLLHSLKF TDASSRSIGA LNKINFNTRF 300
VMKTLMTICP GTVLLVFSIS LWIIAAWTVR ACERYHDQDQ VTSNFLGAMW LISITFLSIG 360
YGDMVPNTYC GKGVCLLTGI MGAGCTALVV AVVARKLELT KAEKHVHNFM MDTQLTKRVK 420
15 NAAANVLRET WLIYKNTKLK KKIDHAKVRK HQRKFLQATH QLRSVKMEQR KLNDQANTLV 480
DLAKTQNMV DMISDLNERS EDFEKRIVTL ETKLETIGS IHALPGLISQ TIRQQQRDFI 540
EAQMSYDKH VTNAERSRS SSRRRSSST APPTSSESS

A215 DNA SEQUENCE:

Gene name: CGI-86 protein
Unigene number: Hs.109201
Probeset Accession #: AW161450
Nucleic Acid Accession #: NM_016029
Coding sequence: 228-1097 (underlined sequences correspond to start and stop codons)

25
1 11 21 31 41 51
| | | | |
CTGCGATCCC GCAGGGCAGC GACGCGACTC TGGTGCGGGC CGTCTTCTTC CCCCCGAGCT 60
GGGCGTGGGC GGCOCGCAATG AACTGGGAGC TGCTGCTGTG GCTGCTGGTG CTGTGCGCGC 120
30 TGCTCTCTGT CTGTGTGCGC CTGCTGCGCT TCCTGAGGGC TGACGGCGAC CTGACGCTAC 180
TATGGCGCGA GTGGCAGGGA CGACGCCAG AATGGGAGCT GACTGATATG GTGGTGTGGG 240
TGACTGAGAG CTGAGTGGGA ATTGGTQAGG AGCTGGCTTA CCAATTGTCT AACTAGGAG 300
TTTCTCTGTG GCTGTGAGCC AGAAGAGTGC ATGAGCTGGA AAGGGTGAAA AGAAGATGCC 360
35 TAGAGAATGG CAATTAAAA GAAAAAGATA TACTTGTGTT GCCCCTTGAC CTGACCGACA 420
CTGGTTCCTCA TGAAGCGGCT ACCAAGCTG TTCTCCAGGA GTTTGGTAGA ATCGACATTC 480
TGGTCAACAA TGGTGGAAATG TCCACGCGTT CTCTGTGCAT GGATACCAGC TTGGATGTCT 540
ACAGAAAGCT AATAGAGCTT AACTACTTAG GACGCGTGTC CTTGACAAAA TGTGTTCTGC 600
CTCACATGAT CGAGAGGAAG CAAGGAAAGA TTGTACTGTG GAATAGCATC CTGGGTATCA 660
40 TATCTGTACC TCTTTCATT GGATACTGTG CTAGCAAGCA TGCTCTCCGG GGTGTTTTTA 720
ATGGCCTTCG AACAGAACTT GCCACATACC CAGGTATAAT AGTTTCTAAC ATTTGCCCGG 780
GACCTGTGCA ATCAAAATATT GTGGAGAATT CCCTAGCTGG AGAAGTCACA AAGACTATAG 840
GCAATAATGG AGACCACTGC CACAAGATGA CAACCACTGC TTGTGTGCGG CTGATGTTAA 900
TCAGCATGGC CAATGATTTG AAAGAAGTTT GGATCTCAGA ACAACCTTTC TTGTTAGTAA 960
45 CATATTGTGG GCAATACATG CCAACCTGGG CCTGGTGGAT AACCAACAAG ATGGGGAAGA 1020
AAAGGATTGA GAACTTTAAG AGTGGTGGG ATGCAGACTC TTCTATTGTT AAAATCTTTA 1080
AGACAAAACA TGACTGAAA GAGCACCTGT ACTTTTCAAG CCATCGGAGG GAGAAATGGA 1140
AAACATGAAA ACAGCAATCT TCTTATGCTT CTGAATAATC AAAGACTAAT TTGTGATTTT 1200
ACTTTTAAAT AGATATGACT TTGCTTCCAA CATGGAATGA AATAAAAAAT AAATAATAAA 1260
50 AGATTGCCAT GAATCTTGCA AA

A216 Protein sequence:

Gene name: CGI-86 protein
Unigene number: Hs.109201
55 Probeset Accession #: AW161450
Protein Accession #: NP_057113
Signal sequence: 1-26
Transmembrane domains: 183-206, 221-243
60 Cellular Localization: plasma membrane

65
1 11 21 31 41 51
| | | | |
MNWELLWLWL VCALLLLLV QLLRFLRADG DLTLLWAEWQ GRRPEWELTD MVVWVTGASS 60
GIGEELAYQL SKLGVSLVLV ARRVHELERY KRRCLENGSL KEKDILVLPL DLTDTGSHEA 120
ATKAVLQEFQ RIDILVNNGS MSQRSLCMDT SLDVYRKLIE LNYLGTVSLT KCVLPHEMER 180
KQGRIVTVNS ILGIISVPLS IGYCASKHAL RGPFFNGLRTE LATYPGIIVS NICPGPVQSN 240
IVENSLAGEV TKTIGNNGDQ SHKMTTSCV RLMLISMAND LKEVWISBP PLLVTYLWQY 300
70 MPTWAWWITN KMGKKRIENF KSGVDADSSY FKIFKTKHD

A217 DNA SEQUENCE:

Gene name: Homo sapiens mRNA; cDNA DKFPZp56401763 (from clone DKFPZp56401763)
Unigene number: Hs.27373
75 Probeset Accession #: F13036
Nucleic Acid Accession #: AC012478
Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

80
1 11 21 31 41 51
| | | | |
ATGCGCGCGG TGCGCGCTGC CGCCCGGCTC CTGCGGCTGC TGCTGCTGCG GCTCTGGGCC 60
GCTCCCGCGG CCCGCGCCAG CAGAGCGGAG TCCGTCTCCG CGCCGTGGCC CGAACCCGAG 120
CGCGAGTCGC GGCACCGGCC CGGCCGGGGG CCGGGGAACA CCACCCGTTT TGGGTCTGGG 180
GCGGCGGGCG GCAGCGGCGC CTCCAGCTCC AACAGCAGTG GCGACGCTT GGTGACCGCG 240

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ATTTCACATCC TCCTCCGCGA CCTACCCACC CTCAAGGCAG CCGTGATCGT GCGGTTCCGC 300
TTTACACACC TCCTCATCGC CTGCGTGTCT CTGCGCGTCT TCAGGTCGGG AAAGAGGTTA 360
AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGGG AATGGCGCCA 420
CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCTCT 540
GTGCCCCAC CTTCATCCT CGACATTGAC CTTCCAGCAA GATGCAGTGG AAGGCCTGAT 600
GGTGGAAATCA GACCTGGTAA AACCTGTTTC CCAGCCTGGT GSCATCCTGT GGAAGTTGG 660
TCAGCTGCAA CTGGGGTGT GAAGGACTGG ACCTGGAAGC CCTCTTGCTG CGGAGGTGTT 720
GAAACCAAAA CGAAGCTTAT GTATAAAACC CCAGCTCCAT CGTGCCTGTC AGGCATCTGC 780
TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
TTTGGGCATC CTTTAAAGT GCCCCTACT TCTACTCCC ATGTTTTCG ACAACTGCAG 900
CTGAATCTCA TGGAAAAGCT GGATTCCTCT GCCTTACGCA GAAACACCCG GGCCTCATCT 960
GCCAGGTGCT TGCCACTGGT CCTGGCAGAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
CCTTGGTGGC ACTTCAGGCG CACAGGCTCT CCAATAAAAA CCTTTACAC ACAAAACCATG 1080
AGTACCTTGG GCTTGGATGT TTTCTGTGT GCGGCGCAGC GGGCACCTT TTGTGAAGAC 1140
AGAGCAGTGA CTAAGGTTCT CCAGGCTAGC TCTTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
ACCCATCTGT TCAGGTTGGC TCGTTCAGAT GCCCGGGGAC AAGCCAGCCT GACCGGGAGG 1320
AGGGTGTTC GCGCTCCGCG GCAGTCTCTG CATGGCGGAG GGTCAAGCGG TACCGCAACT 1380
TGCTTTTGG TTTTGAAGAT TCTGTGAGG GCGCATCCTC ACCTTGACCT CTTCTACAA 1440
ATCTGTCTCC CTTGTCTGTC CGTGGAAAC CTACGGGAAG CCAAGAGAAG CTCACTGACT 1500
GTCTTGTGCT CATTTGAGCA GAGCCCAACA AAGGCAGCTG CTGCCACCGG GGAGCCTGTC 1560
AAACGAGGGC CCAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
CGGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCCAGCTGA GGATGTCACT 1680
CACCTTGAGG GAGACTTGGG TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
GATGGCAGAT GCCAGAAGAT GGTCTGTATG TCTGAGGAAG GCGCACCTAG TTTGACAGGA 1800
TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCTTCCTTT 1860
TCCCCCGAC AGCCCTGTT TCTGTCCAGG CCTTGA
  
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A218 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFpZ56401763 (from clone DKFpZ56401763)
 Unigene number: Hs.27373
 Probeset Accession #: F13036
 Protein Accession #: FGENESH predicted
 Signal sequence: 1-27
 Transmembrane domains: 94-115, 448-469
 Cellular Localization: not determined

1 11 21 31 41 51
 | | | | |
 MRVPLPAPL LPLLLALLA APAARASRAE SVSAPWPEPE RESRPPPGPG PGNTTRFGSG 60
 AAGSGSSSSS NSSGDALVTR ISILLRDLP LKAAVIVAF FTLIIACL LRVFRSGKRL 120
 KTRKYDIIT TPAERVMAP LNEEDDEDED STVFDIKYRV SLPAALRRQL PGCTLLTVP 180
 VPPFPILID LPARCSGRPD GGIRPGKTCF PAWHPVESH SAATWGVKDW TNKPSVGVG 240
 ETKTNVMYKT PAPSCVSGIC SDCHWQARFH VITMELLPP FGHFPKVPP STPHGPRQLQ 300
 LNLMERLDSS ALRNRTRAPS ARCLPLVLAE MAAABSDLPN PMWHFSATGS PIKTLTYQTM 360
 STLGLDVFCG AGQRTFCED RAVTKVLQGS SPSKQLRWKP ALESFPHHL RLLRECPPLS 420
 THPVRLARSD ARQASLTGR RVFRRPRQSL HGGGSAGTAT CLLVLKILLR RHPHLDLFYK 480
 ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAAGPEPV KRGPSSQLTR HTPCGWGIH 540
 ANLQTIPTDQ GQEGPREDTV HPGGDLGVA NFYLEEEGFG DGRQCKMVLN SEEGPPSLTG 600
 CERLTGSHHF SSKSKSWSFL SPRQPLFLSR P

A219 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTA AGAGAGTGGG 60
 GCTTGTCTT ACAACACCTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 CAGCAAAGGT ACACACACCT GGTGCAATT CAAAACAAG AAGAGATTGA GTACCTAAAC 180
 TCCATATTGA GCTATTCACT AAGTTATTAC TGGATTGGAA TCAGAAAAGT CAACAATGTG 240
 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAGAAG CCAAGAACTG GGCTCCAGGT 300
 GAAACCAACA ATAGGCAAAA AGATGAGGAC TCGTGGAGA TCTACATCAA GAGAGAAAAA 360
 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCTGTA CCAATACATC CTGCAGTGGC CACGCTGAAT GTGTAGAGAC CATCAATAAT 480
 TACACTGCA AGTGTACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAAGTGT 540
 ACAGCCCTGG AATCCCTGTA GCATGGAAGC CTGTTTGCA GTCAACCACT GGGAAACTTC 600
 AGCTACAATT CTTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGA 780
 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGA ACTAATGGGA 840
 GCCCAGAGCC TTCACTGTAC CTATCTGGG AATTGGGACA ACAGAGAGCC AACGTGTAAA 900
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CCTGCTGGAG AGTTCACTCT CAAATCATCC TGCAACTTCA CTGTGAGGA AGGCTTCATG 1020
 TTGCAGGAG CAGCCAGGT TGAATGCACC ACTCAAGGCG AGTGCACACA GCAATCCCA 1080
 GTTTGTGAAG TTTTCACTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
 CTTCTAGTG CTTCTGCGAG TTTCCGTTAT GGGTCCAGCT GTGAGTCTC CTGTGAGCAG 1200
 GGTTTTGTGT TGAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260

5 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 GTGAGGTGTG CTCAATCCCC TATTGGAGAA TTCACCTACA AGTCCTCTTG TGCCCTCAGC 1380
 TGTGAGGAGG GATTTGAAAT ATATGGATCA ACTCACTTG AGTGACATC TCAGGGACAA 1440
 TGGACAGAAG AGGTTCTCTC CTGCCAAGTG GTAAAAATGT CAAGCCTGGC AGTTCCGGGA 1500
 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTTTGCCA CTGTGTGCAA GTTCGCCTGT 1560
 CCTGAAGGAT GGACGCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 CTTTCTGCTG CTGGACTCTC CTTCTTGACA TTAGCACCAT TTCTCTCTG GCTTCGGAAA 1740
 10 TGCTTACGGA AAGCAAAGAA ATTTGTTCCT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
 GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

A220 Protein sequence:

15 Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 20 Transmembrane domains: 555-573
 C-lectin domain: 23-139
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QORYTHLVAI QNKKEIEYLN 60
 SILSYSPSYW WIGIRKVNNV WVVVGTKRPL TEEAKNWAPG EPNNRQKDED CVEIYIKREK 120
 DVGMMNDERC SKKLLALCYT AACTNTSCSG HGECVETINN YTKCDPGFS GLKCEQIVNC 180
 30 TALESPHEGS LVCSEHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSSGEW SAPIACNVV 240
 ECDAVTNPAN GFVECFQNPQ SFPWNITCTF DCEGFELMG AQSLQCTSSG NWDNEKFTCK 300
 AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEGFM LQGPQVVECT TQGWTOQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSFRY GSSCEFSCEQ GFVLKSGSKRL QCGPTGEWDN 420
 EKPTCEAVRC DAVHQFPKGL VRCASHPIGE PTYKSSCAPS CEEGFELYGS TQLECTSQQQ 480
 35 WTEVEVPSQV VKCSSLAVPG KINMSCSGEP VPGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 SGLLPTECAP TESNIPLVAG LSAAGLSLIT LAPFLWLWRK CLRKAKKFPV ASSCQSLES 600
 GSYQRPSYIL

Taxol Prostate

A221 DNA SEQUENCE

40 Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 Probeset Accession #: N51002
 Nucleic Acid Accession #: N51002
 45 Coding sequence: 1-3793 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGATGTGTG AAGTGATGCC CACGATTAAT GAGGACACCC CAATGAGCCA AAGGGGGTCC 60
 CAAAGCAGTG GCTCGGACTC AGACTCCCAT TTTGAGCAGC TGATGGTGAA TATGCTAGAT 120
 50 GAAAGGGGAT GTCTTCTAGA CACCCTTGGG GAGACCCAGG AAAGCCTCTC ACTTGCCAG 180
 CAAAGACTTC AGGATGTCAT CTATGACCGA GACTCACTCC AGAGACAGCT CAATTGAGCC 240
 CTGCCACAGG ATATCGAATC CCTAACAGGA GGGCTGGCTG GTTCTAAGGG GGCTGATCCA 300
 CCGGAATTGG CTGCACTGAC AAAAGAAATTA AATGCCCTGA GGGAAACAAT TCTAGAAAAG 360
 55 GAAGAAGAAA TCTCTGAATC TAAAGCTGAA AGAAACAACA CAAGACTATT ACTGGAGCAT 420
 TTGGAGTGCC TTGTGTACAG ACATGAAAGA TCACTAAGAA TGACGGTGGT AAAACGGCAA 480
 GCCCATGCTC CCTCAGAGGT ATCCAGTGAA GTTGAAGTTC TCAAGGCATC GAAATCTTTG 540
 TTTGAGCACC ACAGGCCTT GGATGAAAAG GTAAGGGAGC GACTGAGGGT TTCTTTAGAA 600
 AGAGTCTCTG CACTGGAAGA AGAACTAGCT GCTGCTAATC AGGAGATTGT TGCTTTGCGT 660
 60 GAACAAAATG TTTATATACA AAGAAAAATG GCATCAAGCG AGGGATCCAC AGAGTCAGAA 720
 CATCTTGAAG GGATGGAACC TGGACAGAAA GTCCATGAGA AGCGTTTGTC CAATGGTTCT 780
 ATAGACTCAA CGATGAAAC TAGTCAAATA GTTGAATCAC AAGAAITGCT TGAAGAGCAA 840
 AACTATGAAA TGGCCAGAT GAAAGAACGT TTAGCAGCCC TTTCTTCCCG AGTGGGAGAG 900
 GTGGAACAGG AAGCAGAGAC AGCAAGAAAG GATCTCATT AACAAGAGA AATGAACACC 960
 65 AAGTATCAAA GGGACATTAG GGAGGCCATG GCACAAAAGG AAGATATGGA AGAAAGAATT 1020
 ACAACCCCTT AAAAGCGTTA CCTCAGTGCT CAGAGAGAAT CTACCTCCAT ACATGACATG 1080
 AATGATAAAC TAGAAAATGA GTTAGCAAAT AAAGAAGCTA TCCTACGGCA GATGGAAGAG 1140
 AAAAAAGAGC AGTTACAAGA ACGTCTTGAG CTAGCTGAAC AAAAGTTGCA GCAGACCATG 1200
 AGAAAGGCTG AAACCTTGCC TGAAGTAGAG GCTGAACCTG CTCAGAGAA TGCAGCCCTA 1260
 70 ACCAAGGCTG AAGAGAGACA TGGAAATATT GAAGAACGTA TGAGACATTT AGAGGGTCAA 1320
 CTGGAAGAGA AGAATCAAGA ACTTCAAAGA GCTAGGCAAA GAGAGAAAAT GAATGAGGAG 1380
 CATAACAGA GATTATCGGA TACGGTTGAT AGACTTCTGA CTGAATCCAA TGAACGCCCTA 1440
 CAACTACACT TAAAGGAAAG AATGGCTGCT CTAGAAGAAA AGAATGTTTT AATTCAAGAA 1500
 TCAGAAACTT TCAGAAAGAA TCTTGAAGAA TCTTTACATG ATAAGGAAAG ATTAGCAGAA 1560
 75 GAAATTGAAA ATGATGATGA TGAACCTGAC CAATTGAAAA TGAGAACTCG CTCTTTAATT 1620
 GAACCCACAA TACCAGAAC TCATCTAGAC ACCTCAGCTG AGTTGCGGTA CTCAGTGGGA 1680
 TCCCTAGTGG ACAGCCATGC TGATTACAGA ACAACTAAAG TAATAAGAAG ACCAAGGAGA 1740
 GGCCGATGGS GTGTGCGAAG AGATGAGCCA AAGGTGAAAT CTCTTGGGGA TCACGAGTGG 1800
 AATGAAACTC AACAGATTGG AGTACTAAGC AGCCACCTTT TTGAAAGTGA CACTGAAATG 1860
 80 TCTGATATTG ATGATGATGA CAGAGAAACA ATTTTATGCT CAATGGATCT TCTCTCTCCA 1920
 AGTGTGCTAT CCGATGCCCA GACGCTAGCC ATGATGCTTC AGGAACAATT GGATGCCATC 1980
 AACAAAGAAA TCAGGCTAAT TCAGGAAGAA AAAGAATCTA CAGAGTTGGG TGCTGAAGAA 2040
 ATTGAAAATA GAGTGGCTAG TGTGAGCCTC GAAGGCTCGA ATTTGGCAAG GGTCCACCCA 2100

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GGTACCTCCA TTA CTGCTC TGTTACAGCT TCATGCTGG CAGTTTCATC TCCCCCAGT 2160
GGCACTCAAA CTCCAAGCT CACCCCTCGA AGCCCTGCCA GGGAAATGGA TCGGATGGGA 2220
GTCATGACAC TGCCAAAGTGA TCTGAGGAAA CATCGGAGAA AGATTGCACT TGTGGAAGAA 2280
GATGGTCGAG AGGACAAAGC AACAAATTAAT TGTGAAACTT CTCCTCTCC TACCCCTAGA 2340
GCCCTCAGAA TGACTCAGAC TCTCCCTTCT TCCTACCACA ATGATGCTCG AAGTAGTTTA 2400
TCTGTCTCTC TTGAGCCAGA AAGCCTCGGG CTTGGTAGTG CCAACAGCAG CCAAGACTCT 2460
CTTCACAAAG CCCCCAAGAA GAAAGGAATC AAGTCTTCAA TAGGACGTTT GTTTGGTAAA 2520
AAAGAAAAAG CTCGACTTGG GCAGCTCCGA GGCTTTATGG AGACTGAAGC TGCAGCTCAG 2580
GAGTCCCTGG GGTTAGGCAA ACTCGGAAC CAAGCTGAGA AGGATCGAAG ACTAAAGAAA 2640
AAGCATGAAC TTCTTGAAGA AGCTCGGAGA AAGGGATTAC CTTTGGCCCA GTGGGATGGG 2700
CCAAGTGGG TCGCATGGCT AGAGCTTTGG TTGGGAATGC CTGCGTGGTA CGTGGCAGCC 2760
TGCCGAGCCA AGCTGAAGAG TGGTGCCATC ATGTCTGCTT TATCTGACAC TGAGATCCAG 2820
AGAGAAATGG GAATCAGCAA TCCACTGCAT CGCTTAAAC TCGATTAGC AATCCAGGAG 2880
ATGGTTTCCG AAATAGGTCC TTCACTCTCT CCAACATCTC GAACTCCTTC AGGCAACGTT 2940
TGGGTGACTC ATGAAGAAAT GGAATATCTT GCAGCTCCAG CAAAAACGAA AGAATCTGAG 3000
GAAGGAAGCT GGGCCCAAGT TCCGTTTCTT CTACAGACCC TGGCTTATGG AGATATGAAT 3060
CATGAGTGGG TTGGAATAGA ATGGCTTCCC AGCTTGGGGT TACCTCAGTA CAGAAGTTAC 3120
TTTATGGAAT GCTTGGTAGA TGCAAGAATG TTAGATCACC TAACAAAAAA AGATCTCCGT 3180
GTCCATTGAA AAATGGTGGG TAGTTTCCAT CGAACCAAGT TACAATATGG AATTATGTGC 3240
TTAAAGAGGT TGAATATAGA CAGAAAAGAA CTAGAAAAGAA GACGGGAAGC AAGCCAACAT 3300
GAAATAAAAG ACGTGTGGT GTGAGCAAT GACCGAATTA TTCGCTGGAT ACAAGCAATT 3360
GGACTTCGAG AATATGCAAA TAATATACTT GAGAGCGGTG TGCATGGCTC ACTTATAGCC 3420
CTGGATGAAA ACTTTGACTA CAGCAGCTTA ACTTTATTAT TACAGATTCC AACACAGAAC 3480
AGCCAGGCAA GGCAGATTCT TGAAGAGAGAA TACAATAACC TCTTGGCCCT GGAAGCTGAA 3540
AGGCGACTGG ATGAAGTGA TGACAAGAAC TTCAGACGTG GATCAACCTG GAGAAGGCAG 3600
TTTCTCTCTC GTGAAGTACA TGAATCAGC ATGATGCCCT GGTCTCTAGA AACATTACCA 3660
GCTGGATTGA GGTAAACCA ACCTCTGGG CAATCAAGAA AATGACAAC AGATGTTGCT 3720
TCATCAAGAC TGCAGAGGTT AGACAACCTC ACTGTTCCGA CATACTCATG TCTCGAGTAA 3780
GGGCGCGCTT TAA

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A222 Protein sequence:

Gene name: ESTs; Liprin A2
 Unigene number: Hs.306480
 Probeset Accession #: N51002
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: none found
 AAA domain: 286-539
 SAM domains: 895-964, 1017-1084, 1105-1177
 Cellular Localization: not determined

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1 11 21 31 41 51
| | | | |
MMCEVMPTIN EDTPMSQRGS QSSGSDSDSH FEQLMVNMLD ERDRLLDTLR ETQESLSLAQ 60
QRLQDVYDR DSLQRQLNSA LPQDIESLTG GLAGSKGADP PEFAALTKEI NACREQLLEK 120
EEEISELKAE RNNTRLLEH LECLVSRHER SLRMTVVKQV AQSPSGVSSS VEVLKALKSL 180
FEHHKALDEK VRERLRVSLR RVSALEBELA AANQEIVALR BQNVHIQRKM ASSEGSTESE 240
HLEGMEPQOK VHEKRLSNGS IDSTDTSQI VELQELLEKQ NYEMAQMKER LAALSSRVGE 300
VEQEASTARK DLIKTEEMNT KYQRDIREAM AQKEDMEERI TTLEKRYLSA QRESTSIHDM 360
NDKLENELAN KEAILRQMEZ KNRQLQERLE LAEQKLOQTH RKAETLPEVE AELAQRIAAL 420
TKAEERHNGI EERMRHLEGQ LEEKNQELQR ARQREKMNES HNKRLSDTVD RLLTESNERL 480
QLHLKERMMA LEEKNVLIQE SETFRKNLEE SLHDKERLAE EIEKLRSLED QLKMRGTSLI 540
BPTIPRTHLD TSAELRYSVG SLVDSQSDYR TTKVIRPRR GRMGVRRDEP KVKSLGDHEW 600
NRTQQIGVLS SHPFESDTEM SDIDDDRET IFSSMDLLSP SGHSDAQTLA MMLQEQLDAI 660
NKEIRLIQEE KESTELRAEE IENRVASVSL EGLNLARVHP GTSITASVTA SSLASSSPPS 720
GHSTPKLTPR SPAREMDRMG VMTLPSDLRK HRRKIAVVEE DGRDQKATIK CETSPPTPTP 780
ALRMTHTLPS SYHNDARSSL SVSLEPESLG LGSANSSQDS LHKAPKKKGI KSSIGRLFGK 840
KEKARLGQLR GFMEETAAAG ESLGLGLGT QAEKDRRLKK KHELLEEAR KGLPFAQWDG 900
PTVVANLELM LGMPAWYVAA CRANVKSAGI MSALSDTEIQ REIGISNPLH RLKLRLAIQE 960
MVSILTSPSP PTSRTPSGNV WVTHEEMENL AAPAKTKESE EGSWAQCPVF LQTLAYGDMN 1020
HEWIGNEWLP SLGLPQYRSY FMECLVDARM LOHLTKKDLR VHLKMDVSPH RTSIQYGYMC 1080
LKRLNYDRKE LERRREASQH EIKDVLVWSN DRIIRWIOAI GLREYANNIL ESGVHGSLLA 1140
LDENFDYSSL TLLQLIPTQN TQARQILERE YNNLLALGTE RRLDESDDKN FRRGSTWRRQ 1200
PPPREVHGHS MPMGSSETLP AGFRLTTTSG QSRKMTTDAV SSRQLRLDNS TVRTYSCLC

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A223 DNA SEQUENCE

Gene name: CDA14
 Unigene number: Hs.26813
 Probeset Accession #: N32912
 Nucleic Acid Accession #: NM_016570
 Coding sequence: 1- 1134 (underlined sequences correspond to start and stop codons)

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80

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1 11 21 31 41 51
| | | | |
ATGAGGCGAC TGAATCGGAA AAAAACTTTA AGTTTGGTAA AAGAGTTGGA TGCCTTTCCG 60
AAGGTTCTCG AGAGCTATGT AGAGACTTCA GCGAGTGGAG GTACAGTTTC TCTAATAGCA 120
TTTAACTAAT TGGCTTTATT AACCATAATG GAATTCCTAG TATATCAAGA TACATGGATG 180
AAGTATGAAT ACGAAGTAGA CAAGGATTTT TCTAGCAAAT TAAGAATTAA TATAGATATT 240
ACTGTTGCCA TGAAGTGTCA ATATGTTGGA GCGGATGTAT TGGATTTAGC AGAAACAATG 300
GTGCACTCTG CAGATGGTTT AGTTTATGAA CCAACAGTAT TTGATCTTTC ACCACAGCAG 360
AAAGAGTGGC AGAGGATGCT GCAGCTGATT CAGAGTAGGC TACAAGAAGA GCATTCACTT 420
CAAGATGTGA TATTTAAAG TGCTTTTAAA AGTACATCAA CAGCTCTTCC ACCAAGAGAA 480

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GATGATTTCAT CACAGTCTCC AAATGCATGC AGAATTCATG GCCATCTATA TGTCAATAAA 540
GTAGCAGGGA ATTTTCACAT AACAGTGGGC AAGGCAATTC CACATCCTCG TGGTCATGCA 600
CATTTGGCAG CACTTGTCAA CCATGAATCT TACAATTTT CTCATAGAAT AGATCATTG 660
TCTTTGGAG AGCTTGTTC AGCAATTATT AATCCTTTAG ATGGAACCTGA AAAAAATTGCT 720
ATAGATCACA ACCAGATGTT CCAATATTTT ATTACAGTTG TGCCAACAAA ACTACATACA 780
TATAAATAT CAGCAGACAC CCATCAGTTT TCTGTGACAG AAAGGGAACG TATCATTAAAC 840
CATGCTGCAG GCAGCCATGG AGTCTCTGGG ATATTATGA AATATGATCT CAGTTCTCTT 900
ATGGTGACAG TTAGTGAGGA GCACATGCCA TTCTGGCAGT TTTTGTAAAG ACTCTGTGGT 960
ATTGTTGAG GAATCTTTTC AACACAGGC ATGTTACATG GAATTGGAAA ATTTATAGTT 1020
GAAATAATTT GCTGTCGTTT CAGACTTGA TCCTATAAAC CTGTCAATTC TGTTCTCTTT 1080
GAGGATGCC ACACAGACAA CCATTAACCT CTTTATAGAA ATAATACACA TTGA

A224 Protein sequence:

Gene name: CDA14
Unigene number: Hs.26813
Probeset Accession #: N32912
Protein Accession #: NP_057654
Signal sequence: none found
Transmembrane domains: none found
Cellular Localization: nuclear

1 11 21 31 41 51
| | | | |
MRLNRKKTLL SLVKELDAFP KVPESYVETS ASGGTVSLIA FTTMALLTIM EFSVYQDTWM 60
KYEYEVKDF SSKLRINIDI TVAMKQYVG ADVLDLAETM VASADGLVYE PTFVDLSPQQ 120
KEWQMLQLI QSRLEEEHSL QDVIFKSAFK STSTALPPRE DDSSQSPNAC RINGHLYVNK 180
VAGNFHITVG KAIPHPRGHA HLAALVNHES YNFSHRIDHL SFGLVPAII NPLDGTEDIA 240
IDHNMFPQYF ITVVTKLHT YKISADTEQF SVTERERIIN HAAGSHGVSG IFMKYDLSSL 300
MVTITEHMP FQPFVRLCG IVGGIFSTTG MLHGIGKFIV EIICCRFRLG SYKPVNSVFP 360
EDGTDNHLPL LLENNTNTH

UterineA225 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCACAG TTCTCTCCAA CCTTGCCATT 120
GCAATAAAAA AGAATAAAGAG GCCTCCTCAG ACATCTCAA GAGGATGGGG AGATGACATC 180
ACTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACTCTGA GGATTGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAAATT ATCACTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTACC CCTATTGATA GAAACATGA AGAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAA AGCCTTCACT TCAAAGAAGT CAAATTTTAT 600
GAAGAAAAAC TCTGGCAGAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAA 660
TTACTATTTA GTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
TCTGAAAAAA AAAAAA AAAA

A226 Protein sequence:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

1 11 21 31 41 51
| | | | |
MMLHSALGLL LLLVTVSSNL AIAIKKEKRP PQTLRSGWGD DITVQTYEE GLFYAQKSKK 60
PLMVIHLED QYQALKKV FAQNEEIQEM AQNKFIIMNL MHETTDKNLS PDGQYVPRIM 120
FVDFSLTVRA DIAGRSNRL YTYEPDLPL LIEMKKALR LIQSEL

A227 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
Unigene number: Hs.285529
Probeset Accession #: AA460530
Nucleic Acid Accession #: NM_003667
Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
5  GTGGCGGCAA CCGGCACCTC AGTCCCCGCC GCGCTTCTCC TCGCCGCCCA CCGCGTGGGG 60
   TCAGGAACGC GGGGTCTGGC GCTGCAGACG CCGCTGAGT  TGCAGAAAGCC CACGGAGCGG 120
   CGCCCGGCGC GCCACGGCCC GTAGCAGTCC GGTGCTGCTC TCCGCCCGCG TCCGGCTCGT 180
   GGGCCCCCTAC TTGGGGCACC ATGGACACCT CCGGCTCGG  TGTGCTCCTG TCCTTGCTCT 240
   TGCTGCTGCA GCTGGCGACC GGGGGCAGCT CTCCAGGTC  TGGTGTGTGT CTGAGGGGCT 300
   GCGCCACACA CTGTATTGCG GAGCCCGACG GCAGGATGTT GCTCAGGGTG GACTGCTCCG 360
   ACCTGGGGCT CTGGGAGCTG CCTTCCAACC TCAGCGTCTT CACCTCTAC CTAGACCTCA 420
10  GTATGAACAA CATCAGTCAG CTGCTCCCGA ATCCCTGCCG CAGTCTCCGC TTCCTGGAGG 480
   AGTTAGCTCT TCGGGGAAAC GCTCTGACAT ACATTCCCAA GGGAGCATTG ACTGGCCTTT 540
   ACAGTCTTAA AGTTCCTATG CTGCAGAATA ATCAGCTAAG ACAGTACCC ACAGAAGCTC 600
   TGCAGAAATT GCGAAGCCTT CAATCCCTGC GTCTGGATGC TAAACCAATC AGCTATGTGC 660
   CCCCAGCTG TTTCACTGGC CTGCAATCCC TGAGGCACCT GTGGCTGGAT GACATGCGT 720
15  TAACAGAAAT CCCCGTCCAG GCTTTTAGAA GTTTATCGGC ATTGCAAGCC ATGACCTTGG 780
   CCTTGAACAA AATACACCAC ATACCAGACT ATGCTTTGG AAACCTCTCC AGCTTGGTAG 840
   TTCTACATCA AATTAACAAT AGAATCCAAT CCTGGGAAA GAAATGCTTT GATGGGCTCC 900
   ACAGCCTAGA GACTTTAGAT TTAATTTACA ATAACCTTGA TGAATTCCTC ACTGCAATTA 960
   GGACACTCTC CAACCTTAAA GAACTAGGAT TTCATAGCAA CAATATCAGG TCGATACCTG 1020
20  AGAAAGCATT TGTAGGCAAC CCTTCTCTTA TTACAATACA TTTCTATGAC AATCCCATCC 1080
   AATTTGTGTT GAGATCTGCT TTTCAACATT TACCTGAACT AAGAACACTG ACTCTGAATG 1140
   GTGCCCTACA AATTAACGAA TTTCTGATT TAACTGGAAC TGCAAACTCG GAGAGCTGTA 1200
   CTTTAACTGG AGCAGACATG TCATCTCTTC CTCAAACCGT CTGCAATCAG TTACCTAATC 1260
   TCCAAGTGTG AGATCTGCTT TACAACCTAT TAGAAGATT ACCCAGTTT TCAGTCTGCC 1320
25  AAAAGCTTCA GAAATTTGAC CTAAGACATA ATGAAATCTA CGAAATTTAA GTTGACACTT 1380
   TCCAGCAGTT GCTTAGCCTC CGATCGCTGA ATTGGCTTG GAACAAAATT GCTATTATTC 1440
   ACCCCAAATG ATTTTCCACT TTGCCATCCC TAATAAGCT GGACCTATCG TCCAACCTCC 1500
   TGTGCTCTTT TCCTATAACT GGGTTACATG GTTTAACTCA CTTAAATTA ACAGGAAATC 1560
   ATGCCCTTAC GAGCTTGATA TCATCTGAAA ACTTCCAGA ACTCAAGGTT ATAGAAATGC 1620
30  CTTATGCTTA CCAGTGTCTG GCATTTTGGAG TGTGTGAGAA TGCCCTATAAG ATTTCTAATC 1680
   AATGGAATAA AGGTGACAAC AGCAGTATGG ACGACCTTCA TAAGAAAGAT GCTGGAATGT 1740
   TTCAGGCTCA AGATGAACGT GACCTTGAAG ATTTCTGCT TGACTTTGAG GAAGACCTGA 1800
   AAGCCCTTCA TTCAGTGACG GTTTCACCTT CCGCAGGCCC CTTCAAACCC TGTGAACACC 1860
   TGCTTGATGG CTGCTGATC AGAATTGGAG TGTGACCAT AGCAGTTCTG GCACCTTACT 1920
35  GTAATGCTTT GGTGACTTCA ACAGTTTTCG GATCCCCCTT GTACATTTC CCAATTAAC 1980
   TGTTAATTTG GGTGATCGCA GCAGTGAACA TGCTCACGGG AGTCTCCAGT GCGTGTCTGG 2040
   CTGGTGTGGA TGGCTTCACT TTTGGCAGCT TTGCACGACA TGGTGCCTGG TGGGAGAATG 2100
   GGGTTGGTTG CCATGTCAAT GTTTTTTTGT CCATTTTTCG TTCAGAAATCA TCTGTTTTCC 2160
   TGCTTACTCT GCGACCCCTG GAGCGTGGGT TCTCTGTGAA ATATTCTGCA AAATTTGAAA 2220
40  CGAAAGCTCC ATTTTCTAGC CTGAAAGTAA TCATTTTGCT TGTGCCCCTG CTGGCCTTGA 2280
   CCATGGCCCG AGTTCCTCTG CTGGGTGGCA GCAAGTATGG CGCTCCCTCT CTCTGCTGTC 2340
   CTTTGGCTTT TGGGAGCCCG AGCACCATGG GCTACATGGT CGCTCTCATC TTGCTCAATT 2400
   CCCTTTGCTT CCTCATGATG ACCATTGCTT ACACCAAGCT CTACTGCAAT TTGGACAAGG 2460
   GAGACCTTGA GAATATTGCG GACTGCTCTA TGTAAACA CAATGCCCCTG TTGCTCTTCA 2520
45  CCAACTGCAT CCTAACTGCG CTGTGTGCTT TCTTGTCTT CTCTCTTTTA ATAAACCTTA 2580
   CATTTATCAC TCCTGAAGTA ATTAAGTTTA TCCTTCTGGT GGTAGTCCCA CTCTCTGATC 2640
   GTCTCAATCC CCTTCTCTAC ATCTTGTTC ATCCTCACTT TAAGGAGGAT CCGGTGAGCC 2700
   TGAGAAAGCA AACCTACGTC TGGACAAGAT CAAACACCCC AAGCTTGATG TCAATTAAC 2760
50  CTGATATGCT CGAAACACG TCCTGTGACT CAACTCAAGC CTTGGTAACC TTTACCAGCT 2820
   CCAGCATCAC TTATGACCTG CCTCCAGTT CCGTGCATC ACCAGCTTAT CCAGTGACTG 2880
   AGAGCTGCCA TCTTCTCTCT GTGGCATTGT TCCCATGTCT CTAATTAATA TGTGAAGGAA 2940
   AATGTTTTCA AAGGTTGAGA ACCTGAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000
   ATAAGAAGAG CTGAGGTGAA ACTCGTTTAA AA

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A228 Protein sequence

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 Cellular Localization: plasma membrane

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65  1      11      21      31      41      51
   |      |      |      |      |      |
   MDTSLRGVLL SLFVLLQLAT GGSSPRSGVL LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
   PSNLSVFTSY LDLSMNNISQ LLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
   LQNNQLRHVP TEALQNLRSQ QSLRLDANHI SYVFPSCFSG LHSRLRLWLD DNALTBIQVQ 180
   AFRSLALQA MTLALNKHKH IPDYAFGNLS SLVVLHLHNN RIHSLGKKCF DGLHSLLETD 240
70  LNYNNLDBFP TAIRTLNMLK ELGFHSNNIR SIPEKAFVGN PSLITIHFDY NPIQFVGRSA 300
   FQHLPELRTL TLNGASQITE FPDLTGTANL BSLTLTGAQI SSLPQTVCNQ LPNLQVLDSL 360
   YNLLDELPSF SVCQLKQKID LRHNEIYEIK VDTFQQLSL RSLNLAWNKI AIHPNAFST 420
   LPSLIKLDLS SNLLSFPFIT GLHGLTHLKL TGNHALQSLI SSFNFPPELV IEMFYAYQCC 480
   AFGVCENAYK ISNQMNKGDN SSMDDLHKKD AGMFQAQDER DLEDFLLDFE EDLKLHVSQ 540
75  CSPSPGPFKP CEHLLDGWL I RIGVWTIAVL ALTCNALVTS TVFRSPLYIS PIKLLIGVIA 600
   AVNMLTGVSS AVLAVGDAFT PGSFARHGAW WENGVGCEVI GFSLIFASES SVFLTLAAL 660
   ERGFSVYSYA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGGSKYGASP LCLPLPFGEF 720
   STMGMVVALI LLNSLCFLAM TIAYTKLYCN LDKGDLLENW DCSMKVHIAL LLFTNCLINC 780
   FVAFLSFSLL INLTFTSPEV IKFILLVVVP LPACLNPLLY ILFNPHEKED LVSLRQQTIV 840
80  WTRSKHPSLM SINSDDVERQ SCDSTQALVT FTSSSITYDL PPSSVPSPAY PVTESCHLSS 900
   VAFVPCIL

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Table 75: See Table 1

Table 76A depicts Seq ID No; UnigeneID; UnigeneTitle; PKey; Predicted Cellular Localization; and Exemplar Accession for each of the sequences in Table 78. The information in

Table 76A is linked by SeqID No to Table 78.

Seq ID No: Pkey: ExAccn: UnigeneID: Unigene Title: Pred Subcell Loc:	Sequence ID No for sequences in table Unique Eos probe/seq identifier number Exemplar Accession number, Genbank accession number Unigene number Unigene gene title Predicted sub-cellular localization				
Seq ID No	Pkey	ExAccn	UnigeneID	Unigene Title	Pred Subcell Loc
Seq ID 1 & 2	425023	AW956889	Hs.154210	endothelial differentiation, sphingolipid	plasma membrane
Seq ID 3 & 4	424503	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	plasma membrane
Seq ID 5 & 6	429423	AI016712	Hs.287797	Integrin, beta 1 (fibronectin receptor,	plasma membrane
Seq ID 7 & 8	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	secreted
Seq ID 9 & 10	419172	AW338625	Hs.22120	ESTs; similar to TRANSMEMBRANE 4 SUPERF	plasma membrane
Seq ID 11 & 12	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 13 & 14	418007	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	secreted
Seq ID 15 & 16	407836	T79340	Hs.200272	B-cell CLL/lymphoma 6, member B, zinc fi	intracell
Seq ID 17 & 18	414577	AK056548	Hs.72116	hypothetical protein FLJ20992 similar to	secreted
Seq ID 19 & 20	418738	AW388633	Hs.6682	solute carrier family 7, (cationic amino	plasma membrane
Seq ID 21 & 22	428368	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	secreted
Seq ID 23 & 24	415138	C18356	Hs.295944	tissue factor pathway inhibitor 2	secreted
Seq ID 25 & 26	429276	AF056085	Hs.198612	G protein-coupled receptor 51	plasma membrane
Seq ID 27 & 28	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	plasma membrane
Seq ID 29 & 30	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	secreted
Seq ID 31 & 32	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	intracell
Seq ID 33 & 34	418506	AA084248	Hs.85339	G protein-coupled receptor 39	plasma membrane
Seq ID 35 & 36	423961	D13666	Hs.136348	perforin (OSF-2os)	secreted
Seq ID 37 & 38	414812	X72755	Hs.77367	monokine induced by gamma interferon	secreted
Seq ID 39 & 40	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 41 & 42	417433	BE270266	Hs.82128	ST4 oncofetal trophoblast glycoprotein	plasma membrane
Seq ID 43 & 44	424399	AI905687		AI905687:IL-BT095-190199-019 BT095 Homo	secreted
Seq ID 45 & 46	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	secreted
Seq ID 47 & 48	428227	AA321649	Hs.2248	small inducible cytokine subfamily B (Cy	secreted
Seq ID 49 & 50	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	secreted
Seq ID 51 & 52	439569	AW602166	Hs.222399	CEGP1 protein	secreted
Seq ID 53 & 54	411558	AA102670	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
Seq ID 55 & 56	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	plasma membrane
Seq ID 57 & 58	411789	AF245505	Hs.72157	Adican	secreted
Seq ID 59 & 60	428698	AA852773	Hs.334838	KIAA1866 protein	plasma membrane
Seq ID 61 & 62	450098	W27249	Hs.8109	hypothetical protein FLJ21080	intracell
Seq ID 63 & 64	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	secreted
Seq ID 65 & 66	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	plasma membrane
Seq ID 67 & 68	415539	AI733881	Hs.72472	BMP-R1B	plasma membrane
Seq ID 69 & 70	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 71 & 72	416636	N32536	Hs.42645	solute carrier family 16 (monocarboxylic	plasma membrane
Seq ID 73 & 74	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	plasma membrane
Seq ID 75 & 76	442082	R41823	Hs.7413	ESTs	plasma membrane
Seq ID 77 & 78	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278	plasma membrane
Seq ID 79 & 80	451398	AI793124	Hs.144479	ESTs	intracell
Seq ID 81 & 82	429220	AW207206		ESTs	plasma membrane
Seq ID 83 & 84	421524	AA312082	Hs.105445	GDNF family receptor alpha 1	plasma membrane
Seq ID 85 & 86	423242	AL039402	Hs.125783	DEME-6 protein	plasma membrane
Seq ID 87 & 88	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 89 & 90	423242	AL039402	Hs.125783	DEME-6 protein	intracell
Seq ID 91 & 92	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 93 & 94	452190	H26735	Hs.91668	Homo sapiens clone PP1498 unknown mRNA	intracell
Seq ID 95 & 96	325372			Phase 2 & 3 Exons	cytoplasmic
Seq ID 97 & 98	450375	AA009647		a disintegrin and metalloproteinase doma	plasma membrane
Seq ID 99 & 100	426215	AW963419	Hs.155223	stanniocalcin 2	secreted
Seq ID 101 & 102	425247	NM_005940	Hs.155324	matrix metalloproteinase 11 (stromelysin	secreted
Seq ID 103 & 104	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 105 & 106	429353	AL117406	Hs.335891	ATP-binding cassette transporter MRP8	plasma membrane
Seq ID 107 & 108	432201	AI538613	Hs.298241	Transmembrane protease, serine 3	plasma membrane
Seq ID 109 & 110	427585	D31152	Hs.179729	collagen, type X, alpha 1 (Schmid metaph	secreted
Seq ID 111 & 112	446163	AA026880	Hs.25252	prolactin receptor	plasma membrane
Seq ID 113 & 114	442117	AW664964	Hs.128899	ESTs; hypothetical protein for IMAGE:447	plasma membrane
Seq ID 115 & 116	428179	AI127772	Hs.279696	serum/glucocorticoid regulated kinase-II	intracell
Seq ID 117 & 118	431211	M86849	Hs.323733	gap junction protein, beta 2, 26kD (conn	plasma membrane
Seq ID 119 & 120	447033	AJ357412	Hs.157601	ESTs	secreted
Seq ID 121 & 122	447033	AJ357412	Hs.157601	ESTs	secreted
Seq ID 123 & 124	447033	AJ357412	Hs.157601	ESTs	secreted
Seq ID 125 & 126	115522	BE614387	Hs.333893	c-Myc target JPO1	intracell
Seq ID 127 & 128	452679	Z42387	Hs.83983	transmembrane, prostate androgen induced	plasma membrane
Seq ID 129 & 130	446051	BE048061	Hs.37054	ephrin-A3	plasma membrane
Seq ID 131 & 132	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	secreted
Seq ID 133 & 134	410418	D31382	Hs.63325	transmembrane protease, serine 4	plasma membrane
Seq ID 135 & 136	446342	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr	plasma membrane
Seq ID 137 & 138	422260	AA315993	Hs.105484	regenerating gene type IV	secreted

5	Seq ID 139 & 140	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 141 & 142	409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	secreted
	Seq ID 143 & 144	111929	AF027208	Hs.112350	prominin (mouse)-like 1	plasma membrane
	Seq ID 145 & 146	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 147 & 148	111929	AF027208	Hs.112360	prominin (mouse)-like 1	plasma membrane
	Seq ID 149 & 150	104888	AW939591	Hs.5940	mucln 13, epithelial transmembrane	plasma membrane
	Seq ID 151 & 152	420159	AI572490	Hs.59785	Homo sapiens cDNA: FLJ21245 fis, clone C	plasma membrane
	Seq ID 153 & 154	422330	D30783	Hs.115263	epiregulin	plasma membrane
10	Seq ID 155 & 156	452461	N78223	Hs.108106	transcription factor	intracell
	Seq ID 157 & 158	413324	V00571	Hs.75294	corticotropin releasing hormone	secreted
	Seq ID 159 & 160	412420	AL035668	Hs.73853	bone morphogenetic protein 2	secreted
	Seq ID 161 & 162	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	secreted
	Seq ID 163 & 164	407811	AW190902	Hs.40098	cysteine knot superfamily 1, BMP antagon	secreted
15	Seq ID 165	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 166 & 167	402230			Fgenesh predicted: CYTOCHROME P450 4F5 (intracell
	Seq ID 168 & 169	432829	W60377	Hs.57772	ESTs	intracell
	Seq ID 170 & 171	425721	AC002115	Hs.159309	uroplakin 1A	plasma membrane
	Seq ID 172 & 173	420370	Y13645	Hs.97234	uroplakin 2	plasma membrane
20	Seq ID 174 & 175	437852	BE001836	Hs.256897	ESTs, Weakly similar to dJ365012.1 [H.s	plasma membrane
	Seq ID 176 & 177	402075			ENSP00000251056*:Plasma membrane calcium	secreted
	Seq ID 178 & 179	421110	AJ250717	Hs.1355	cathepsin E	secreted
	Seq ID 180 & 181	451668	Z43948	Hs.326444	cartilage acidic protein 1	plasma membrane
	Seq ID 182 & 183	451668	Z43948	Hs.326444	cartilage acidic protein 1	secreted
25	Seq ID 184 & 185	451668	Z43948	Hs.326444	cartilage acidic protein 1	intracell
	Seq ID 186 & 187	408243	Y00787	Hs.624	interleukin 8	secreted
	Seq ID 188 & 189	422282	AF019225	Hs.114309	apolipoprotein L	secreted
	Seq ID 190 & 191	425852	AK001504	Hs.159651	death receptor 6, TNF superfamily member	plasma membrane
	Seq ID 192 & 193	439738	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig),	plasma membrane
30	Seq ID 194 & 195	404875			NM_022819*:Homo sapiens phospholipase A2	intracell
	Seq ID 196 & 197	425883	AL137708	Hs.161031	Homo sapiens mRNA; cDNA DKFZp434K0322 (I	plasma membrane
	Seq ID 198 & 199	404977			Insulin-like growth factor 2 (somatomedi	secreted
	Seq ID 200 & 201	420876	AA918425	Hs.177744	ESTs	plasma membrane
	Seq ID 202 & 203	427747	AW411425	Hs.180655	serine/threonine kinase 12	intracell
35	Seq ID 204 & 205	420281	AI623693	Hs.323494	Predicted cation efflux pump	plasma membrane
	Seq ID 206 & 207	446673	NM_016361	Hs.15871	LPAP for lysophosphatidic acid phosphata	intracell
	Seq ID 208	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 209 & 210	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
	Seq ID 211 & 212	437553	AI829935	Hs.130497	ESTs, Weakly similar to MAT8_HUMAN CHLOR	plasma membrane
40	Seq ID 213 & 214	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 215 & 216	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 217 & 218	426900	AW163564	Hs.142375	ESTs	plasma membrane
	Seq ID 219 & 220	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0	intracell
	Seq ID 221 & 222	405932			C15000305:gi3806122[gb]AAC69198.1] (AF0	intracell
45	Seq ID 223 & 224	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 225 & 226	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 227 & 228	424008	R02740	Hs.137555	putative chemokine receptor; GTP-binding	plasma membrane
	Seq ID 229 & 230	444342	NM_014398	Hs.10887	similar to lysosome-associated membrane	secreted
	Seq ID 231 & 232	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	secreted
50	Seq ID 233 & 234	417079	U65590	Hs.81134	interleukin 1 receptor antagonist	secreted
	Seq ID 235 & 236	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 237 & 238	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 239 & 240	412986	X81120	Hs.75110	cannabinoid receptor 1 (brain)	plasma membrane
	Seq ID 241 & 242	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	intracell
55	Seq ID 243 & 244	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	secreted
	Seq ID 245 & 246	419723	AL120193	Hs.339810	longevity assurance (LAG1, S. cerevisiae	plasma membrane
	Seq ID 247 & 248	430890	X54232	Hs.2699	glypican 1	plasma membrane
	Seq ID 249 & 250	456759	BE259150	Hs.127792	della (Drosophila)-like 3	plasma membrane
	Seq ID 251	429466	M85835	Hs.12827	ESTs	
60	Seq ID 252	429466	M85835	Hs.12827	ESTs	
	Seq ID 253 & 254	419721	NM_001650	Hs.288650	aquaporin 4	plasma membrane
	Seq ID 255 & 256	407034	U84540		gb:Human dystrobrevin isoform DTN-3 (DTN	secreted
	Seq ID 257 & 258	413472	BE242870	Hs.75379	solute carrier family 1 (glial high affi	plasma membrane
	Seq ID 259 & 260	438380	T06430	Hs.6194	chondroitin sulfate proteoglycan BEHAB/b	secreted & plasma membrane
65	Seq ID 261 & 262	426271	AF026547	Hs.169047	chondroitin sulfate proteoglycan 3 (neur	secreted
	Seq ID 263 & 264	419704	AA429104	Hs.45057	ESTs	intracell
	Seq ID 265 & 266	444471	AB020684	Hs.11217	KIAA0877 protein	plasma membrane
	Seq ID 267 & 268	409395	U46745	Hs.336678	dystrobrevin, alpha	secreted
	Seq ID 269 & 270	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	secreted
70	Seq ID 271 & 272	433800	AJ034361	Hs.135150	lung type-I cell membrane-associated gly	plasma membrane
	Seq ID 273	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 274	458435	AI418718	Hs.144121	ESTs, Weakly similar to T46916 hypotheti	
	Seq ID 275 & 276	424343	AW956360	Hs.4748	adenylate cyclase activating polypeptide	
	Seq ID 277 & 278	424998	U58515	Hs.154138	chitinase 3-like 2	plasma membrane
75	Seq ID 279 & 280	412709	AL022327	Hs.74518	KIAA0027 protein	secreted
	Seq ID 281 & 282	435615	Y15065	Hs.4975	potassium voltage-gated channel, KOT-like	plasma membrane
	Seq ID 283 & 284	404049			NM_018937*:Homo sapiens protocadherin be	plasma membrane
	Seq ID 285 & 286	418932	L34059	Hs.89484	cadherin 4, type 1, R-cadherin (retinal)	plasma membrane
	Seq ID 287 & 288	404029			NM_018936*:Homo sapiens protocadherin be	plasma membrane
80	Seq ID 289 & 290	436480	AJ271643	Hs.87469	putative acid-sensing ion channel	intracell
	Seq ID 291 & 292	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 293 & 294	452401	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	secreted
	Seq ID 295 & 296	436895	AF037335	Hs.5338	carbonic anhydrase XII	plasma membrane
	Seq ID 297 & 298	421471	U90545	Hs.327179	solute carrier family 17 (sodium phospho	plasma membrane

5	Seq ID 299 & 300	428296	NM_003058	Hs.183572	solute carrier family 22 (organic cation	plasma membrane
	Seq ID 301 & 302	423508	AW604297	Hs.129711	hepatitis A virus cellular receptor 1	plasma membrane
	Seq ID 303 & 304	450001	NM_001044	Hs.406	solute carrier family 6 (neurotransmitter	plasma membrane
	Seq ID 305 & 306	410407	X65839	Hs.63287	carbonic anhydrase IX	plasma membrane
	Seq ID 307 & 308	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	plasma membrane
	Seq ID 309 & 310	420737	L08096	Hs.99899	CD70 ; tumor necrosis factor (ligand) s	plasma membrane
	Seq ID 311 & 312	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	plasma membrane
	Seq ID 313 & 314	412719	AW016610	Hs.816	ESTs	intracell
10	Seq ID 315 & 316	417034	NM_006183	Hs.80962	neurotensin	secreted
	Seq ID 317 & 318	430486	BE062109	Hs.241551	chloride channel, calcium activated, fam	plasma membrane
	Seq ID 319 & 320	413753	U17760	Hs.75517	laminin, beta 3 (nicein (125kD), kalinin	secreted
	Seq ID 321 & 322	425650	NM_001944	Hs.1925	desmoglein 3 (pemphigus vulgaris antigen	plasma membrane
	Seq ID 323 & 324	423673	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	secreted
15	Seq ID 325 & 326	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 327 & 328	418663	AK001100	Hs.41690	desmocollin 3	plasma membrane
	Seq ID 329 & 330	429610	AB024937	Hs.211092	LUNX protein; PLUNC (palate lung and nas	secreted
	Seq ID 331 & 332	406690	M29540	Hs.220529	carcinoembryonic antigen-related cell ad	plasma membrane
	Seq ID 333 & 334	431846	BE019924	Hs.271580	uroplakin 1B	plasma membrane
	Seq ID 335 & 336	422158	L10343	Hs.112341	protease inhibitor 3, skin-derived (SKAL	secreted
20	Seq ID 337 & 338	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	plasma membrane
	Seq ID 339 & 340	437044	AL035864	Hs.69517	differentially expressed in Fanconi's an	plasma membrane
	Seq ID 341 & 342	428484	AF104032	Hs.184601	solute carrier family 7 (cationic amino	plasma membrane
	Seq ID 343 & 344	429211	AF052693	Hs.198249	gap junction protein, beta 5 (connexin 3	plasma membrane
25	Seq ID 345 & 346	417389	BE260964	Hs.82045	nidkin (neurite growth-promoting factor	secreted
	Seq ID 347 & 348	431009	BE149762	Hs.48956	gap junction protein, beta 6 (connexin 3	plasma membrane
	Seq ID 349 & 350	417542	J04129	Hs.82269	progestagen-associated endometrial prote	secreted
	Seq ID 351 & 352	449230	BE613348	Hs.211579	melanoma cell adhesion molecule	plasma membrane
	Seq ID 353 & 354	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
30	Seq ID 355 & 356	410555	U92649	Hs.64311	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 357 & 358	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	secreted
	Seq ID 359 & 360	418462	BE001596	Hs.85266	Integrin, beta 4	plasma membrane
	Seq ID 361 & 362	410274	AA381807	Hs.61762	hypoxia-inducible protein 2	secreted
	Seq ID 363 & 364	439606	W79123	Hs.58561	G protein-coupled receptor 87	plasma membrane
35	Seq ID 365 & 366	404877			NM_005365:Homo sapiens melanoma antigen,	intracell
	Seq ID 367 & 368	444781	NM_014400	Hs.11950	GPI-anchored metastasis-associated prote	plasma membrane
	Seq ID 369 & 370	109424	NM_005329	Hs.85962	hyaluronan synthase 3	plasma membrane
	Seq ID 371 & 372	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 373 & 374	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
40	Seq ID 375 & 376	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 377 & 378	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 379 & 380	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 381 & 382	415817	U88967	Hs.78867	protein tyrosine phosphatase, receptor-t	plasma membrane
	Seq ID 383 & 384	421817	AF146074	Hs.108660	ATP-binding cassette, sub-family C (CFTR	plasma membrane
45	Seq ID 385 & 386	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 387 & 388	418678	NM_001327	Hs.87225	cancer/testis antigen (NY-ESO-1)	intracell
	Seq ID 389 & 390	409420	Z15008	Hs.54451	laminin, gamma 2 (nicein (100kD), kalini	secreted
	Seq ID 391 & 392	332180	AF134160	Hs.7327	claudin 1	plasma membrane
	Seq ID 393 & 394	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
50	Seq ID 395 & 396	408790	AW580227	Hs.47860	neurotrophic tyrosine kinase, receptor,	plasma membrane
	Seq ID 397 & 398	439223	AW238299	Hs.250618	UL16 binding protein 2	plasma membrane
	Seq ID 399 & 400	409757	NM_001898	Hs.123114	cystatin SN	secreted
	Seq ID 401 & 402	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 403 & 404	428969	AF120274	Hs.194689	artemin	secreted
55	Seq ID 405 & 406	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 407 & 408	428969	AF120274	Hs.194689	artemin	secreted
	Seq ID 409 & 410	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 411 & 412	450701	H39960	Hs.288467	hypothetical protein XP_098151 (leucine-	secreted
	Seq ID 413 & 414	414774	X02419	Hs.77274	plasminogen activator, urokinase	secreted
60	Seq ID 415 & 416	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 417 & 418	407944	R34008	Hs.239727	desmocollin 2	plasma membrane
	Seq ID 419 & 420	428486	AW583497	Hs.184604	pancreatic polypeptide	secreted
	Seq ID 421 & 422	457489	AI693815	Hs.127179	cryptic gene	secreted
	Seq ID 423 & 424	432874	W94322	Hs.279651	melanoma inhibitory activity	secreted
65	Seq ID 425 & 426	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 427 & 428	445891	AW391342	Hs.199460	DPCR1 protein	plasma membrane
	Seq ID 429 & 430	404682			C9001188*gt[12738842]ref[NP_073725.1] p	secreted
	Seq ID 431 & 432	429547	AW009166	Hs.99376	ESTs	secreted
	Seq ID 433 & 434	425921	NM_007231	Hs.162211	solute carrier family 6 (neurotransmitter	plasma membrane
70	Seq ID 435 & 436	407242	M18728		gb:Human nonspecific crossreacting anti	plasma membrane
	Seq ID 437 & 438	407242	M18728		gb:Human nonspecific crossreacting anti	plasma membrane
	Seq ID 439 & 440	407242	M18728		gb:Human nonspecific crossreacting anti	plasma membrane
	Seq ID 441 & 442	432596	AJ224741	Hs.278461	matrilin 3	secreted
	Seq ID 443 & 444	444006	BE395085	Hs.10086	type I transmembrane protein Fn14	plasma membrane
75	Seq ID 445 & 446	423685	BE350494	Hs.49753	uveal autoantigen with coiled coil domai	intracell
	Seq ID 447 & 448	428392	H10233	Hs.2265	secretory granule, neuroendocrine protel	secreted
	Seq ID 449 & 450	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	plasma membrane
	Seq ID 451 & 452	448030	N30714	Hs.325960	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 453 & 454	422109	S73265	Hs.1473	gastrin-releasing peptide	secreted
80	Seq ID 455 & 456	419235	AW470411	Hs.288433	neurotrophin	plasma membrane
	Seq ID 457 & 458	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	plasma membrane
	Seq ID 459 & 460	427333	AF067797	Hs.176658	aquaporin 8	plasma membrane
	Seq ID 461 & 462	417931	W95642	Hs.82961	trefoil factor 3 (intestinal)	secreted
	Seq ID 463 & 464	419216	AU076718	Hs.164021	small inducible cytokine subfamily B (Cy	secreted

5	Seq ID 465 & 466	431629	AU077025	Hs.265827	Interferon, alpha-inducible protein (clo	secreted
	Seq ID 467 & 468	413554	AA319146	Hs.75426	secretogranin II (chromogranin C)	secreted
	Seq ID 469 & 470	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 471 & 472	452194	AI694413	Hs.332649	Ubiquitin-like protein FAT10777	plasma membrane
	Seq ID 473 & 474	426322	J05068	Hs.2012	transcobalamin I (vitamin B12 binding pr	secreted
	Seq ID 475 & 476	429010	Y18198	Hs.194725	one cut domain, family member 2	intracell
	Seq ID 477 & 478	431462	AW583672	Hs.256311	granin-like neuroendocrine peptide precu	secreted
	Seq ID 479 & 480	448243	AW369771	Hs.52620	Integrin, beta 8	plasma membrane
10	Seq ID 481 & 482	426427	M86699	Hs.169840	TTK protein kinase	intracell
	Seq ID 483 & 484	428187	AI687303	Hs.285529	G protein-coupled receptor 49	plasma membrane
	Seq ID 485 & 486	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 487 & 488	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 489 & 490	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
15	Seq ID 491 & 492	428579	NM_005756	Hs.184942	G protein-coupled receptor 64	plasma membrane
	Seq ID 493 & 494	445537	AJ245671	Hs.12844	EGF-like domain, multiple 6	secreted
	Seq ID 495 & 496	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	plasma membrane
	Seq ID 497 & 498	424620	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum corn	secreted
	Seq ID 499 & 500	406400			kallikrein 8 (neurosin/ovasin) (KLK8)	secreted
20	Seq ID 501 & 502	431130	NM_006103	Hs.2719	HE4; epididymis-specific, whey-acidic pr	secreted
	Seq ID 503 & 504	420440	NM_002407	Hs.97644	mammaglobin 2	secreted
	Seq ID 505 & 506	428450	NM_014791	Hs.184339	KIAA0175 gene product	intracell
	Seq ID 507 & 508	446519	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	secreted
	Seq ID 509 & 510	436982	AB018305	Hs.5378	spondin 1, (f-spondin) extracellular mat	secreted
25	Seq ID 511 & 512	453392	U23752	Hs.32964	SRY (sex determining region Y)-box 11	intracell
	Seq ID 513	431989	AW972870	Hs.291069	ESTs	
	Seq ID 514	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	
	Seq ID 515 & 516	409178	BE393948	Hs.50915	kallikrein 5	secreted
	Seq ID 517 & 518	426514	BE616833	Hs.170195	bone morphogenetic protein 7 (osteogenic	secreted
30	Seq ID 519 & 520	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 521 & 522	421478	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos	plasma membrane
	Seq ID 523 & 524	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 525 & 526	425776	U25128	Hs.159499	parathyroid hormone receptor 2	plasma membrane
	Seq ID 527 & 528	452097	AB002364	Hs.27916	a disintegrin-like and metalloprotease (secreted
35	Seq ID 529 & 530	416530	U62801	Hs.79361	kallikrein 6 (neurosin, zyme)	secreted
	Seq ID 531 & 532	431515	NM_012152	Hs.258583	endothelial differentiation, lysophospha	plasma membrane
	Seq ID 533 & 534	419452	U33635	Hs.90572	PTK7 protein tyrosine kinase 7	plasma membrane
	Seq ID 535 & 536	412078	X69699	Hs.73149	paired box gene 8	intracell
	Seq ID 537 & 538	412078	X69699	Hs.73149	paired box gene 8	intracell
40	Seq ID 539 & 540	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	secreted
	Seq ID 541 & 542	407792	AI077715	Hs.39384	putative secreted ligand homologous to f	secreted
	Seq ID 543 & 544	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypothi	plasma membrane
	Seq ID 545 & 546	452792	AB037765	Hs.30652	KIAA1344 protein	plasma membrane
	Seq ID 547 & 548	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	plasma membrane
45	Seq ID 549 & 550	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 551 & 552	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 553 & 554	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 555 & 556	432653	N62096	Hs.293185	ESTs, Weakly similar to JC7328 amino aci	plasma membrane
	Seq ID 557 & 558	400290	H18836	Hs.31608	hypothetical protein FLJ20041	plasma membrane
50	Seq ID 559 & 560	410001	AB041036	Hs.57771	kallikrein 11	secreted
	Seq ID 561 & 562	418396	AI765805	Hs.26691	ESTs	plasma membrane
	Seq ID 563 & 564	451027	AW519204	Hs.40808	ESTs	plasma membrane
	Seq ID 565 & 566	446057	AW20227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	plasma membrane
	Seq ID 567 & 568	433466	AA508353	Hs.105314	relaxin 1 (H1)	secreted
55	Seq ID 569 & 570	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 571 & 572	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	plasma membrane
	Seq ID 573 & 574	414569	AF109298	Hs.118258	prostate cancer associated protein 1	plasma membrane
	Seq ID 575 & 576	413435	XS1405	Hs.75360	carboxypeptidase E	secreted
	Seq ID 577 & 578	426501	AW043782	Hs.293616	ESTs	plasma membrane
60	Seq ID 579 & 580	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	plasma membrane
	Seq ID 581 & 582	408369	R38438	Hs.182575	solute carrier family 15 (H777) transport	plasma membrane
	Seq ID 583 & 584	412628	AI972402	Hs.306051	hypothetical protein MGC2648	secreted
	Seq ID 585 & 586	403047			NM_005656:Homo sapiens transmembrane pr	plasma membrane
	Seq ID 587 & 588	403047			NM_005656:Homo sapiens transmembrane pr	plasma membrane
65	Seq ID 589 & 590	408430	S79876	Hs.44926	dipeptidyl/peptidase IV (CD26, adenosine	plasma membrane
	Seq ID 591 & 592	445413	AA151342	Hs.12677	CGI-147 protein	secreted
	Seq ID 593 & 594	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp564O1763 (f	intracell
	Seq ID 595 & 596	427958	AA418000	Hs.98280	potassium intermediate/small conductance	plasma membrane
	Seq ID 597 & 598	421887	AW161450	Hs.109201	CGI-86 protein	plasma membrane
70	Seq ID 599 & 600	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	secreted
	Seq ID 601 & 602	432101	AI918950	Hs.123642	EphA3	plasma membrane
	Seq ID 603 & 604	407786	AA687538	Hs.38972	tetraspan 1	plasma membrane
	Seq ID 605 & 606	416836	D54745	Hs.80247	cholecystokinin	secreted
	Seq ID 607 & 608	416539	Y07909	Hs.79368	epithelial membrane protein 1	plasma membrane
75	Seq ID 609 & 610	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 611 & 612	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 613 & 614	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 615 & 616	131083	Y09763	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	plasma membrane
	Seq ID 617 & 618	422424	AI186431	Hs.296638	prostate differentiation factor	secreted
80	Seq ID 619 & 620	428970	BE276891	Hs.194691	retinoic acid induced 3	plasma membrane
	Seq ID 621 & 622	428330	L22524	Hs.22556	matrix metalloproteinase 7 (matrilysin,	secreted
	Seq ID 623 & 624	439018	AW300887	Hs.26638	membrane-spanning 4-domains, subfamily A	plasma membrane
	Seq ID 625 & 626	420610	AI683183	Hs.99348	distal-less homeo box 5	intracell
	Seq ID 627 & 628	425723	NM_014420	Hs.159311	clckopt (Xenopus laevis) homolog 4	secreted

Seq ID 629 & 630	456662	NM_002448	Hs.1494	msh (Drosophila) homeo box homolog 1 (fo	intracell
Seq ID 631 & 632	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	secreted
Seq ID 633 & 634	429903	AL134197	Hs.93597	cyclin-dependent kinase 5, regulatory su	intracell

5 Table 76B:

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

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Pkey	CAT Number	Accession
424399	238961_1	AI905687 AI905624 AI905837 AI905623 AA340069 R75793 W72837 BE074512 AI905633 W72838 BE092421 AI127172 BE186013 AW070916 AI139456 AW176044 AW291950
429220	301384_1	AW207206 AW341473 AA448195 AI951341
450375	83327_1	AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067

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Table 76C:

20 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 25 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402075	8117407	Plus	121907-122035,122804-122921,124019-124161,124455-124610,125672-126076
402230	9966312	Minus	29782-29932
403047	3540153	Minus	59793-59968
404029	7671252	Plus	108716-111112
404049	3688074	Minus	75765-78155
404682	9797231	Minus	40977-41150
404875	9801324	Plus	96588-96732,97722-97831
404877	1519284	Plus	1095-2107
404977	3738341	Minus	43081-43229
405932	7767812	Minus	123525-123713
406400	9256298	Plus	1553-1712,1878-2140,4252-4385,5922-6077

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Table 77 provides Pkey; Seq ID No; Disease Indications; and Preferred Utility for sequences in Table 78. Seq ID No links the information in Table 77 to Table 78.

	Seq ID No:	Sequence ID No for sequences in table		
	Pkey:	Unique Ecos probeset identifier number		
5	Disease Indications:	Diseases designated for coverage as described in Table 1		
	Preferred Utility:	Preference of utility, based partly upon predicted localization (Ab is antibody; sm is small molecule target; CTL is vaccine target)		
	Seq ID No	Pkey	Disease Indications	Preferred Utility
10	Seq ID 1 & 2	425023	angiogenesis	Ab, sm, CTL, imaging
	Seq ID 3 & 4	424503	pancreas, prostate, angiogenesis, bladder, lung	Ab, sm, imaging
	Seq ID 5 & 6	429423	angiogenesis	Ab, sm
	Seq ID 7 & 8	400289	angiogenesis, bladder, lung, cervical, ovarian, head & neck	Ab, sm, CTL, diagnostic
15	Seq ID 9 & 10	419172	angiogenesis, renal	Ab, sm, CTL, imaging
	Seq ID 11 & 12	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 13 & 14	418007	angiogenesis, lung, bladder, fibrosis, head & neck, pancreas, stomach, colon, ovarian	Ab, sm, diagnostic
	Seq ID 15 & 16	407836	angiogenesis	CTL
	Seq ID 17 & 18	414577	angiogenesis	Ab, CTL, diagnostic
20	Seq ID 19 & 20	418738	angiogenesis, lung, ovarian, bladder & stomach, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 21 & 22	428368	angiogenesis, head & neck, stomach	Ab, sm, diagnostic
	Seq ID 23 & 24	415138	angiogenesis, pancreas, stomach, lung, uterine	Ab, CTL, diagnostic
	Seq ID 25 & 26	429276	angiogenesis, bladder, glioblastoma	Ab, sm, imaging
	Seq ID 27 & 28	418994	prostate, angiogenesis	Ab, CTL, imaging
25	Seq ID 29 & 30	407975	angiogenesis, renal	Ab, CTL, diagnostic
	Seq ID 31 & 32	429113	angiogenesis, bladder and stomach	sm, CTL
	Seq ID 33 & 34	418506	angiogenesis, ovarian, glioblastoma, uterine, lung, bladder, pancreas	Ab, sm, imaging
	Seq ID 35 & 36	423961	breast, colon, bladder, lung, fibrosis, pancreas, head and neck, ovarian	Ab, sm, diagnostic
	Seq ID 37 & 38	414812	breast, bladder, lung, Fibrosis, pancreas, colon, head and neck, cervical, stomach, renal, ovarian	Ab, CTL, diagnostic
30	Seq ID 39 & 40	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 41 & 42	417433	pancreas, breast, bladder, lung, head & neck, cervical, uterine, ovarian, stomach, renal	Ab, CTL, imaging
	Seq ID 43 & 44	424399	breast, uterine, head & neck	Ab, CTL, diagnostic
	Seq ID 45 & 46	422867	breast, ovarian, prostate, pancreas, lung, colon, uterine	Ab, CTL, diagnostic
	Seq ID 47 & 48	428227	breast, lung, bladder, ovarian, head & neck, fibrosis, colon, stomach, cervical	Ab, CTL, diagnostic
35	Seq ID 49 & 50	444381	breast, colon, bladder, lung, pancreas, head & neck, ovarian, stomach, uterine, renal, angiogenesis	Ab, CTL, diagnostic
	Seq ID 51 & 52	439569	breast, androgen withdrawal prostate, prostate, bladder	Ab, CTL, diagnostic
	Seq ID 53 & 54	411558	pancreas, prostate, stomach, breast, uterine, cervical, ovarian	Ab, sm, imaging
	Seq ID 55 & 56	400303	breast, ovarian, pros, stomach, uterine, bladder lung head & neck	Ab, sm, CTL, imaging
	Seq ID 57 & 58	411789	pancreas, lung, breast, stomach, head & neck, ovarian, uterine	Ab, CTL, diagnostic
40	Seq ID 59 & 60	428698	breast, colon, lung, pancreas, stomach, head & neck, ovarian	Ab, sm, imaging
	Seq ID 61 & 62	450098	breast, lung, stomach, uterine	CTL
	Seq ID 63 & 64	421652	breast, ovarian, pancreas, cervical, uterine, prostate, lung, stomach, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 65 & 66	452747	breast, bladder, lung, head & neck, ovarian, stomach, uterine, pancreas	Ab, imaging
	Seq ID 67 & 68	415539	breast, prostate, ovarian, cervical, uterine	Ab, sm, CTL, imaging
45	Seq ID 69 & 70	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 71 & 72	416636	breast, pancreas, uterine	Ab, sm, CTL, imaging
	Seq ID 73 & 74	409079	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 75 & 76	442082	breast, prostate, ovarian	Ab, imaging
	Seq ID 77 & 78	400297	breast, bladder, colon, prostate	Ab, sm, CTL, imaging
50	Seq ID 79 & 80	451398	breast, ovarian	CTL
	Seq ID 81 & 82	429220	breast, prostate, benign prostatic hyperplasia	Ab, CTL, imaging
	Seq ID 83 & 84	421524	breast	Ab, sm, CTL, imaging
	Seq ID 85 & 86	423242	breast, renal, ovarian, prostate, colon	Ab, CTL, imaging
	Seq ID 87 & 88	423242	breast, renal, ovarian, prostate, colon	CTL
55	Seq ID 89 & 90	423242	breast, renal, ovarian, prostate, colon	CTL
	Seq ID 91 & 92	452190	breast, stomach, pancreas	CTL
	Seq ID 93 & 94	452190	breast, stomach, pancreas	CTL
	Seq ID 95 & 96	325372	breast	CTL
	Seq ID 97 & 98	450375	breast, ovarian, head & neck, pancreas, lung, colon	Ab, sm, CTL, imaging
60	Seq ID 99 & 100	426215	breast, lung, renal, colon, ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 101 & 102	425247	breast, ovarian, lung, colon, pancreas, head & neck, stomach, uterine, cervical, bladder	Ab, sm, CTL, diagnostic
	Seq ID 103 & 104	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 105 & 106	429353	breast, prostate	Ab, sm, CTL, imaging
	Seq ID 107 & 108	432201	breast, colon, lung chemo, ovarian, stomach, pancreas, uterine, cervical	Ab, sm, CTL, imaging
65	Seq ID 109 & 110	427585	breast, lung, head & neck, pancreas, stomach, colon, ovarian, cervical	CTL
	Seq ID 111 & 112	446163	breast, cervical, uterine	Ab, sm, imaging
	Seq ID 113 & 114	442117	breast, lung, bladder, pancreas, head & neck, stomach, ovarian, prostate	Ab, CTL, imaging
	Seq ID 115 & 116	428179	breast	sm, CTL
	Seq ID 117 & 118	431211	colon, bladder, lung, pancreas, head & neck	Ab, sm, imaging
70	Seq ID 119 & 120	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 121 & 122	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 123 & 124	447033	colon, prostate, fibrosis, breast, lung pancreas	Ab, CTL, diagnostic
	Seq ID 125 & 126	115522	colon, lung, bladder, pancreas	CTL
	Seq ID 127 & 128	452679	prostate, colon, pancreas, Taxol prostate	Ab, CTL, imaging
75	Seq ID 129 & 130	446051	colon, breast	Ab, sm, CTL, imaging
	Seq ID 131 & 132	422048	colon, pancreas, prostate	diagnostic
	Seq ID 133 & 134	410418	colon, bladder, lung, ovarian, pancreas, head & neck	Ab, sm, CTL, imaging
	Seq ID 135 & 136	446342	uterine, colon, prostate	Ab, sm, CTL, imaging
	Seq ID 137 & 138	422260	colon, ovarian mucinous	Ab, sm, CTL, diagnostic
80	Seq ID 139 & 140	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 141 & 142	409041	uterine, ovarian, lung, colon, stomach, head & neck, breast, pancreas	Ab, CTL, diagnostic
	Seq ID 143 & 144	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 145 & 146	111929	colon, breast, fibrosis	Ab, sm, imaging
	Seq ID 147 & 148	111929	colon, breast, fibrosis	Ab, sm, imaging

	Seq ID 149 & 150 104888	colon, stomach, uterine	Ab, imaging
	Seq ID 151 & 152 420159	bladder, stomach	Ab, sm, CTL, imaging
	Seq ID 153 & 154 422330	pancreas, colon, bladder	Ab, sm, CTL, imaging, diagnostic
5	Seq ID 155 & 156 452451	bladder, lung, head & neck, ovarian, glioblastoma, stomach, colon, cervical	CTL
	Seq ID 157 & 158 413324	bladder	Ab, sm, CTL, diagnostic
	Seq ID 159 & 160 412420	bladder, glioblastoma, lung, stomach	Ab, diagnostic
	Seq ID 161 & 162 416658	lung, ovarian, uterine, bladder	Ab, CTL, diagnostic
	Seq ID 163 & 164 407811	bladder, pancreas, stomach, uterine, lung	Ab, sm, diagnostic
10	Seq ID 165 402230	bladder	sm, CTL
	Seq ID 166 & 167 402230	bladder	sm, CTL
	Seq ID 168 & 169 432829	bladder	CTL
	Seq ID 170 & 171 425721	bladder	Ab, imaging
	Seq ID 172 & 173 420370	bladder	Ab, CTL, imaging
15	Seq ID 174 & 175 437852	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 176 & 177 402075	bladder, lung, head & neck, cervical	diagnostic
	Seq ID 178 & 179 421110	bladder, pancreas, stomach, ovarian, lung	Ab, sm, diagnostic
	Seq ID 180 & 181 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 182 & 183 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
20	Seq ID 184 & 185 451668	bladder, ovarian, lung	Ab, sm, CTL, diagnostic
	Seq ID 186 & 187 408243	bladder, stomach, head & neck, cervical	Ab, diagnostic
	Seq ID 188 & 189 422282	bladder, lung, head & neck	CTL, diagnostic
	Seq ID 190 & 191 425852	bladder, lung, head & neck	Ab, sm, CTL, imaging
	Seq ID 192 & 193 439738	bladder, lung, cervical	Ab, sm, CTL, imaging
25	Seq ID 194 & 195 404875	bladder	sm, CTL
	Seq ID 196 & 197 425883	bladder, pancreas	Ab, CTL, imaging
	Seq ID 198 & 199 404977	bladder, ovarian	Ab, sm, CTL, diagnostic
	Seq ID 200 & 201 420876	pancreas, bladder	Ab, sm, CTL, imaging
	Seq ID 202 & 203 427747	bladder, lung, ovarian, stomach	sm, CTL
30	Seq ID 204 & 205 420281	lung, bladder, ovarian, pancreas	Ab, sm, imaging
	Seq ID 206 & 207 446673	bladder	sm, CTL
	Seq ID 208 437553	bladder	Ab, CTL, imaging
	Seq ID 209 & 210 437553	bladder	Ab, CTL, imaging
	Seq ID 211 & 212 437553	bladder	Ab, CTL, imaging
35	Seq ID 213 & 214 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 215 & 216 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 217 & 218 426900	bladder, prostate	Ab, CTL, imaging
	Seq ID 219 & 220 405932	bladder, lung, head & neck, cervical	Ab, CTL, imaging
	Seq ID 221 & 222 405932	bladder, lung, head & neck, cervical	sm
40	Seq ID 223 & 224 424008	bladder, head & neck, stomach, cervical	sm
	Seq ID 225 & 226 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 227 & 228 424008	bladder, head & neck, stomach, cervical	Ab, sm, CTL, imaging
	Seq ID 229 & 230 444342	hepatitis C, lung, fibrosis, bladder	Ab, CTL, diagnostic
	Seq ID 231 & 232 421379	breast, pancreas, head & neck, lung, stomach, bladder, cervical, colon	Ab, CTL, diagnostic
45	Seq ID 233 & 234 417079	bladder, lung, head & neck, cervical	Ab, diagnostic
	Seq ID 235 & 236 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 237 & 238 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 239 & 240 412986	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 241 & 242 447072	glioblastoma, pancreas	sm, CTL
50	Seq ID 243 & 244 419723	glioblastoma	Ab, CTL, diagnostic
	Seq ID 245 & 246 419723	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 247 & 248 430890	glioblastoma, lung, cervical, bladder	Ab, CTL, imaging, diagnostic
	Seq ID 249 & 250 456759	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 251 429466	glioblastoma, uterine	
55	Seq ID 252 429466	glioblastoma, uterine	
	Seq ID 253 & 254 419721	glioblastoma, lung	Ab, sm, CTL, imaging
	Seq ID 255 & 256 407034	glioblastoma	Ab, CTL, diagnostic
	Seq ID 257 & 258 413472	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 259 & 260 438380	glioblastoma	Ab, CTL, diagnostic, imaging
60	Seq ID 261 & 262 426271	glioblastoma	Ab, CTL, diagnostic, imaging
	Seq ID 263 & 264 419704	glioblastoma	Ab, CTL, diagnostic
	Seq ID 265 & 266 444471	glioblastoma, lung, colon	sm, CTL
	Seq ID 267 & 268 409395	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 269 & 270 413063	glioblastoma, ovarian, bladder, lung	Ab, CTL, diagnostic
65	Seq ID 271 & 272 433800	glioblastoma, lung	Ab, CTL, diagnostic
	Seq ID 273 458435	glioblastoma	Ab, CTL, imaging
	Seq ID 274 458435	glioblastoma	
	Seq ID 275 & 276 424343	glioblastoma, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 277 & 278 424998	glioblastoma	Ab, CTL, diagnostic
70	Seq ID 279 & 280 412709	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 281 & 282 435615	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 283 & 284 404049	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 285 & 286 418932	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 287 & 288 404029	glioblastoma	Ab, sm, CTL, imaging
	Seq ID 289 & 290 436480	glioblastoma	sm, CTL
75	Seq ID 291 & 292 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 293 & 294 452401	bladder, breast, pancreas, head & neck, stomach, lung, arthritis, renal	Ab, CTL, diagnostic
	Seq ID 295 & 296 436895	breast, renal, ovarian, glioblastoma	Ab, sm, imaging
	Seq ID 297 & 298 421471	renal	Ab, sm, CTL, imaging
80	Seq ID 299 & 300 428296	renal	Ab, sm, CTL, imaging
	Seq ID 301 & 302 423508	renal, colon	Ab, CTL, imaging
	Seq ID 303 & 304 450001	renal, lung	Ab, CTL, imaging
	Seq ID 305 & 306 410407	renal, lung, colon, stomach, ovarian, uterine	Ab, sm, CTL, imaging
	Seq ID 307 & 308 453496	renal, prostate	Ab, sm, CTL, imaging

	Seq ID 309 & 310 420737	renal	Ab,sm, CTL, imaging
	Seq ID 311 & 312 309931	lung	Ab,sm, CTL, imaging
	Seq ID 313 & 314 412719	lung, head & neck, bladder, glioblastoma, cervical	CTL
5	Seq ID 315 & 316 417034	lung, head & neck, a couple cervical	Ab, CTL, diagnostic
	Seq ID 317 & 318 430486	lung, bladder, head & neck, cervical	Ab,sm, imaging
	Seq ID 319 & 320 413753	lung, bladder, head & neck, pancreas, cervical, colon	CTL, diagnostic
	Seq ID 321 & 322 425650	lung, head & neck, cervical, bladder	Ab, imaging
	Seq ID 323 & 324 423673	bladder, lung, head & neck, ovarian, pancreas, colon, stomach, uterine, cervical	Ab, CTL, diagnostic
10	Seq ID 325 & 326 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 327 & 328 418663	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 329 & 330 429610	lung	CTL, diagnostic
	Seq ID 331 & 332 406690	lung, head & neck, pancreas, stomach, bladder, colon, cervical	Ab, imaging
	Seq ID 333 & 334 431846	lung, bladder, head & neck, uterine, cervical, stomach, ovarian	Ab, imaging
15	Seq ID 335 & 336 422158	head & neck, bladder, lung, cervical, stomach	diagnostic
	Seq ID 337 & 338 431958	lung, bladder, cervical, head & neck, ovarian, colon, prostate, pancreas, breast	Ab, CTL, imaging
	Seq ID 339 & 340 437044	head & neck, cervical, lung, bladder, breast, prostate, ovarian, stomach	Ab, imaging
	Seq ID 341 & 342 428484	lung, glioblastoma, bladder, head & neck, colon, cervical	Ab, sm, imaging
	Seq ID 343 & 344 429211	lung, bladder, head & neck, cervical, stomach	Ab, imaging
20	Seq ID 345 & 346 417389	ovarian, lung, bladder, uterine, cervical, pancreas, stomach	Ab, diagnostic
	Seq ID 347 & 348 431009	lung, bladder, head & neck	Ab, sm, imaging
	Seq ID 349 & 350 417542	lung	CTL, diagnostic
	Seq ID 351 & 352 449230	lung, cervical, head & neck, bladder, ovarian, colon	Ab, imaging
	Seq ID 353 & 354 410555	lung	Ab, sm, imaging
25	Seq ID 355 & 356 410555	lung	Ab, sm, imaging
	Seq ID 357 & 358 424687	head & neck, pancreas, lung, uterine, cervical, colon, stomach	Ab, sm, diagnostic
	Seq ID 359 & 360 418462	lung, bladder	Ab, imaging
	Seq ID 361 & 362 410274	lung, renal	diagnostic
	Seq ID 363 & 364 439606	lung, bladder, head & neck, cervical	Ab, sm, imaging
30	Seq ID 365 & 366 404877	lung, bladder	CTL
	Seq ID 367 & 368 444781	lung, bladder, head & neck, cervical	Ab, imaging
	Seq ID 369 & 370 109424	bladder, lung	Ab, sm, CTL, imaging
	Seq ID 371 & 372 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 373 & 374 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
35	Seq ID 375 & 376 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 377 & 378 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 379 & 380 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 381 & 382 415817	lung, glioblastoma, head & neck, cervical, fibrosis	Ab,sm, CTL, imaging
	Seq ID 383 & 384 421817	lung, cervical, head & neck & bladder	Ab,sm, CTL, imaging
40	Seq ID 385 & 386 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL
	Seq ID 387 & 388 418678	lung, bladder, stomach, ovarian, pancreas & cervical	CTL, diagnostic
	Seq ID 389 & 390 409420	lung, head & neck, pancreas, stomach, cervical, bladder	Ab, sm, imaging
	Seq ID 391 & 392 332180	lung	Ab,sm, CTL, imaging
	Seq ID 393 & 394 408790	lung	Ab,sm, CTL, imaging
45	Seq ID 395 & 396 408790	lung	Ab, CTL, imaging
	Seq ID 397 & 398 439223	lung, head & neck, cervical, bladder & colon	Ab, CTL, diagnostic
	Seq ID 399 & 400 409757	pancreas, stomach, lung, bladder, stomach	Ab, CTL, diagnostic
	Seq ID 401 & 402 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 403 & 404 428969	lung, cervical	Ab, CTL, diagnostic
50	Seq ID 405 & 406 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 407 & 408 428969	lung, cervical	Ab, CTL, diagnostic
	Seq ID 409 & 410 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 411 & 412 450701	lung, head & neck, pancreas, breast, stomach, ovarian, colon	Ab, CTL, diagnostic
	Seq ID 413 & 414 414774	lung, bladder, head & neck, pancreas, stomach, ovarian	Ab, sm, diagnostic
55	Seq ID 415 & 416 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 417 & 418 407944	lung, head & neck	Ab, sm, imaging
	Seq ID 419 & 420 428486	pancreas	Ab, CTL, diagnostic
	Seq ID 421 & 422 457489	pancreas, prostate, lung	Ab, CTL, diagnostic
	Seq ID 423 & 424 432874	pancreas, stomach	Ab, CTL, diagnostic
60	Seq ID 425 & 426 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 427 & 428 445891	stomach, pancreas, ovarian	Ab, CTL, imaging
	Seq ID 429 & 430 404682	pancreas	Ab, CTL, diagnostic
	Seq ID 431 & 432 429547	pancreas, head & neck, lung, ovarian	Ab, CTL, diagnostic
	Seq ID 433 & 434 429521	stomach, pancreas	Ab,sm, CTL, imaging
65	Seq ID 435 & 436 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 437 & 438 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 439 & 440 407242	pancreas, colon, bladder, head & neck, stomach, lung, ovarian, cervical	Ab,sm, CTL, imaging
	Seq ID 441 & 442 432596	pancreas, breast	CTL
	Seq ID 443 & 444 444006	pancreas, colon, lung, ovarian & cervical	Ab, CTL, imaging
70	Seq ID 445 & 446 423685	pancreas, uterine, colon	CTL
	Seq ID 447 & 448 426392	pancreas	Ab, CTL, diagnostic
	Seq ID 449 & 450 429597	pancreas, colon, stomach, lung	Ab,sm, CTL, imaging
	Seq ID 451 & 452 448030	pancreas, renal and stomach,	Ab,sm, imaging
	Seq ID 453 & 454 422109	pancreas, lung, colon	Ab, CTL, diagnostic
75	Seq ID 455 & 456 419235	pancreas, fibrosis, head & neck & lung	Ab, CTL, imaging
	Seq ID 457 & 458 449048	pancreas, ovarian, uterine, glioblastoma, head & neck & lung	Ab, CTL, imaging
	Seq ID 459 & 460 427333	pancreas, colon	Ab, sm, imaging
	Seq ID 461 & 462 417931	ovarian, pancreas, stomach, colon, uterine, prostate	Ab, diagnostic
	Seq ID 463 & 464 419216	pancreas, lung, stomach, cervical, prostate, head & neck	Ab, CTL, diagnostic
80	Seq ID 465 & 466 413629	pancreas, uterine, cervical, stomach	Ab, CTL, diagnostic
	Seq ID 467 & 468 413554	pancreas, glioblastoma	Ab, CTL, diagnostic
	Seq ID 469 & 470 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 471 & 472 452194	stomach, pancreas, renal, colon	Ab,sm, CTL, imaging
	Seq ID 473 & 474 426322	pancreas, bladder, stomach	Ab, diagnostic

	Seq ID 475 & 476 429010	pancreas	sm, CTL
	Seq ID 477 & 478 431462	pancreas, lung, glioblastoma	Ab, diagnostic
	Seq ID 479 & 480 448243	ovarian, uterine, lung, stomach, head & neck, glioblastoma, pancreas	Ab, sm, imaging
	Seq ID 481 & 482 426427	ovarian, lung, head & neck, cervical, colon, uterine, stomach	sm, CTL
5	Seq ID 483 & 484 428187	ovarian, uterine, colon, stomach	Ab, sm, CTL, imaging
	Seq ID 485 & 486 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 487 & 488 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 489 & 490 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
	Seq ID 491 & 492 428579	ovarian, Ewing, uterine, pancreas	Ab, sm, CTL, imaging
10	Seq ID 493 & 494 445537	ovarian, bladder, uterine, breast, lung, head & neck, renal, fibrosis, pancreas, cervical	Ab, CTL, diagnostic
	Seq ID 495 & 496 422278	ovarian, head & neck, bladder, cervical, lung	Ab, sm, imaging
	Seq ID 497 & 498 424620	ovarian	Ab, CTL, diagnostic
	Seq ID 499 & 500 406400	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 501 & 502 431130	ovarian, uterine	Ab, CTL, diagnostic
15	Seq ID 503 & 504 420440	ovarian, uterine, cervical	Ab, CTL, diagnostic
	Seq ID 505 & 506 428450	ovarian, cervical, pancreas, lung	sm
	Seq ID 507 & 508 446619	ovarian, fibrosis, pancreas, head & neck, lung, colon	Ab, diagnostic
	Seq ID 509 & 510 436982	ovarian, fibrosis	Ab, CTL, diagnostic
	Seq ID 511 & 512 453392	ovarian, lung, glioblastoma	CTL
20	Seq ID 513 431989	ovarian	
	Seq ID 514 439820	ovarian, uterine, cervical, breast, prostate	
	Seq ID 515 & 516 409178	ovarian, breast	Ab, CTL, diagnostic
	Seq ID 517 & 518 426514	ovarian, colon, bladder, lung, cervical	Ab, CTL, diagnostic
25	Seq ID 519 & 520 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 521 & 522 421478	ovarian, bladder	Ab, CTL, imaging
	Seq ID 523 & 524 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 525 & 526 425776	ovarian, uterine, lung	Ab, sm, CTL, imaging
	Seq ID 527 & 528 452097	ovarian	Ab, sm, diagnostic
30	Seq ID 529 & 530 416530	ovarian, uterine	Ab, CTL, diagnostic
	Seq ID 531 & 532 431515	ovarian, prostate, lung	Ab, sm, CTL, imaging
	Seq ID 533 & 534 419452	ovarian, prostate, lung, breast, uterine	Ab, sm, CTL, imaging
	Seq ID 535 & 536 412078	ovarian	CTL
	Seq ID 537 & 538 412078	ovarian	CTL
35	Seq ID 539 & 540 411773	ovarian	Ab, sm, CTL, diagnostic
	Seq ID 541 & 542 407792	ovarian, uterine, cervical, pancreas	Ab, CTL, diagnostic
	Seq ID 543 & 544 431616	prostate, pancreas, colon	Ab, sm, CTL, imaging
	Seq ID 545 & 546 452792	prostate, uterine, breast	Ab, CTL, imaging
	Seq ID 547 & 548 400294	prostate, taxol prostate	Ab, sm, CTL, imaging
40	Seq ID 549 & 550 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 551 & 552 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 553 & 554 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 555 & 556 432653	prostate, lung	Ab, sm, CTL, imaging
	Seq ID 557 & 558 400290	prostate, colon	Ab, sm, CTL, imaging
45	Seq ID 559 & 560 410001	ovarian, prostate, uterine, cervical, lung	Ab, CTL, diagnostic
	Seq ID 561 & 562 418396	prostate	Ab, sm, CTL, imaging
	Seq ID 563 & 564 451027	prostate, uterine, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 565 & 566 446057	prostate	Ab, sm, CTL, imaging
	Seq ID 567 & 568 433466	prostate	Ab, CTL, diagnostic
50	Seq ID 569 & 570 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 571 & 572 453370	prostate	Ab, sm, CTL, imaging
	Seq ID 573 & 574 414569	prostate	Ab, sm, CTL, imaging
	Seq ID 575 & 576 413435	prostate, glioblastoma, pancreas	Ab, sm, diagnostic
	Seq ID 577 & 578 426501	prostate, breast, glioblastoma, lung	Ab, CTL, imaging
55	Seq ID 579 & 580 448999	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 581 & 582 408369	prostate, lung, fibrosis, uterine, glioblastoma, cervical, ovarian	Ab, sm, CTL, imaging
	Seq ID 583 & 584 412628	prostate	Ab, CTL, diagnostic
	Seq ID 585 & 586 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
	Seq ID 587 & 588 403047	prostate, bladder, colon	Ab, sm, CTL, imaging
60	Seq ID 589 & 590 408430	prostate	Ab, sm, CTL, imaging
	Seq ID 591 & 592 445413	prostate, colon, uterine, ovarian, lung, pancreas	diagnostic
	Seq ID 593 & 594 451982	prostate, bladder	CTL
	Seq ID 595 & 596 427958	prostate, glioblastoma	Ab, sm, CTL, imaging
	Seq ID 597 & 598 421887	prostate	Ab, CTL, imaging
65	Seq ID 599 & 600 425071	prostate, colon, stomach, uterine, cervical, head & neck, pancreas	Ab, diagnostic
	Seq ID 601 & 602 432101	prostate, pancreas	Ab, sm, imaging
	Seq ID 603 & 604 407786	prostate, colon, uterine, stomach, inflammatory bowel disease, ovarian	Ab, sm, imaging
	Seq ID 605 & 606 416836	Prostate, Ewing, glioblastoma	Ab, CTL, diagnostic
	Seq ID 607 & 608 416539	ZD1839 resistant cancers, head & neck	Ab, sm, CTL, imaging
70	Seq ID 609 & 610 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 611 & 612 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 613 & 614 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 615 & 616 131083	androgen withdrawal prostate	Ab, sm, CTL, imaging
	Seq ID 617 & 618 422424	bladder, pancreas, prostate, angiogenesis, colon, stomach, lung	Ab, CTL, diagnostic
75	Seq ID 619 & 620 428970	stomach, pancreas, colon	Ab, sm, imaging
	Seq ID 621 & 622 428330	uterine, ovarian, fibrosis, prostate, pancreas, lung, bladder, head & neck	Ab, sm, CTL, diagnostic
	Seq ID 623 & 624 439018	uterine, stomach, prostate	Ab, sm, CTL, imaging
	Seq ID 625 & 626 420610	uterine, ovarian endometrioid, lung	CTL
	Seq ID 627 & 628 425723	ovarian endometrioid, uterine, colon	Ab, CTL, diagnostic
80	Seq ID 629 & 630 456662	uterine, ovarian	CTL
	Seq ID 631 & 632 418261	uterine, ovarian	Ab, CTL, diagnostic
	Seq ID 633 & 634 429903	lung	sm

Table 78

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM_001400

Coding sequence: 251..1399

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	AAAGCTACAC	AAAAAGCCTG	GATCACTCAT	CGAACCACCC	CTGAAGCCAG	TGAAGGCTCT	180
	CTCGCCTCGC	CCTCTAGCGT	TCGTCTGGAG	TAGCGCCACC	CCGGCTTCTC	GGGGACACAG	240
	GGTTGGCACC	ATGGGGCCCA	CCAGCGTCCC	GCTGGTCAAG	GCCACCGCA	GCTCGGTCTC	300
	TGACTACGTC	AACTATGATA	TCATCGTCCG	GCATTACAAC	TACAOGGGAA	AGCTGAATAT	360
15	CAGCGCGGAC	AAGGAGAACA	GCATTAAACT	GACCTCGGTG	GTGTTCAATC	TCATCTGCTG	420
	CTTTATCATC	CTGGAGAACA	TCCTTGTCTT	GCTGACCATT	TGGAAAACCA	AGAAATTTCA	480
	COGACCATAG	TACTATTTTA	TTGGCAATCT	GGCCCTCTCA	GACCTGTTGG	CAGGAGTAGC	540
	CTACACAGCT	AACCTGCTCT	TGTCTGGGCG	CACCACCTAC	AAGCTCACTC	CCGCCCACTG	600
	GTTTCTGCGG	GAAGGGAGTA	TGTTTGTGGC	CCTGTGAGCC	TCCGTGTTC	GTCTCTCTCG	660
20	CATCGCCATT	GAGCGCTATA	TCACAATGCT	GAAAAAGAAA	CTCCACAACG	GGAGCAATAA	720
	CTTCGCGCTC	TTCTTGCTAA	TCAGCGCGCT	CTGGGTCAAT	TCCCTCATCC	TGGGTGGGCT	780
	GGCTATCATG	GGCTGGAATC	GCATCAGTGC	CGTGTCCAGC	TGCTCCACCG	TGCTGCGGCT	840
	CTACACAAAG	CACATATATC	TCCTCTGCAC	CAGGCTCTTC	ACTCTGCTTC	TGCTCTCCAT	900
	CGTCACTCTG	TACTTCAGAA	TCTACTCCTT	GGTCAGGACT	CGGACGCGCC	GCCTGAGCTT	960
25	COGCAAGAAC	ATTTCCAAGG	CCAGCCGCGC	CTCTGAGAAG	TCGCTGGGCG	TGCTCAAGAC	1020
	CGTAATATAT	GTCTGTAGGG	TCTTCAATCG	CTGCTGGGCA	COGCTCTTCA	TCCTGTCTCT	1080
	GCTGGATCAT	GGCTCAAGG	TGAAGACCTG	TGACATCCTC	TTCAAGAGCG	AGTACTTCCT	1140
	GGTGTAGCT	GTGCTCAACT	CCGGCACCAA	CCCCATCATT	TACACTCTGA	CCAAACAAGGA	1200
	GATGCGTGGG	GCCTTCATCC	GGATCATGTC	CTGCTGCAAG	TGCCGAGCGC	GAGACTCTGC	1260
30	TGGCAAAATC	AAGCGACCCA	TCATCGCCCG	CATGSAATTC	AGCCGACAGC	AATCGGACAA	1320
	TTCTTCCCAT	CCCCAGAAAG	ACGAAGGGGA	CAACCCAGAG	ACCATTATGT	CTTCTGGAAA	1380
	CGTCAACTCT	TCTTCTTAGA	ACTGGAAGCT	GTCCACCCAC	CGGAAGCGCT	CTTTACTTGG	1440
	TGCTGCGCCA	CCCCAGTGTG	TGGAAAAAAA	TCTCTGGGCT	TCGACTGCTG	CCAGGGAGGA	1500
	GCTGCTGCAA	GCACAGGGGA	GGAGGGGGGA	GAATACGAAC	AGCCTGGTGG	TGTCGGGTGT	1560
35	TGGTGGGTAG	AGTTAGTTCC	TGTGAACAAT	GCACCTGGAA	GGGTGGAGAT	CAGGTCCCGG	1620
	CCTGGAATAT	ATATTCTACC	CCCCTGAGAG	TTTGATTTTG	CACCTAGGCA	AAGGTCTAGC	1680
	ATTGTCAAGC	TCTTAAAGGG	TTCAATTGGC	CCCTCCTCAA	AGACTAATGT	CCCCATGTGA	1740
	AAGCGTCTCT	TTGTCTGGAG	CTTTGAGGAG	ATGTTTTCCT	TCACCTTAGT	TTCAAAACCA	1800
	AGTGAAGTGT	TGCATCTCTG	CTTCTTTAGG	GATGCCCTGT	ACATCCACCA	CCCCACCTCT	1860
40	CCTTCCCTTC	ATACCCCTCC	TCAACGTTCT	TTTACTTTAT	ACTTTAACTA	CCTGAGAGTT	1920
	ATCAGAGCTG	GGGTGTGTGA	ATGATCGATC	ATCTATAGCA	AATAGGCTAT	GTTGAGTACG	1980
	TAGGCTGTGG	GAAGATGAAG	ATGGTTTGGA	GGTGTAAGAC	AATGTCTCTC	GCTGAGGCCA	2040
	AAGTTTCCAT	GTAAGCGGGA	TCCGTTTTTT	GGAATTTGGT	TGAAGTCACT	TTGATTTCTT	2100
	TAAAAACAA	CTTTCTAATG	AAATGTGTTA	CCATTTCATA	TCCATTGAAG	COGAAATCTG	2160
45	CATAAGGAAG	CCCACTTTAT	CTAAATGATA	TTAGCCAGGA	TCCTTGGTGT	CCTAGGAGAA	2220
	ACAGACAAGC	AAAACAAAGT	GAAAACCGAA	TGGATTAACT	TTTGCAAAAC	AAGGGAGATT	2280
	TCTTAGCAAA	TGAGTCTAAC	AAATATGACA	TCCGCTCTTC	CCACTTTTGT	TGATGTTTAT	2340
	TTCAAGATCT	TGTTGTATTC	ATTTCAAGCA	ACAACATGTT	GTATTTTGGT	GTGTTAAAG	2400
	TACCTTTCTT	GATTTTGAAG	TGTATTGTGT	TCAGGAAGAA	GTCATTTTAT	GGATTTTCTT	2460
50	AACCCGTGTT	AACTTTTCTA	GAATCCACCC	TCTTGTGCCC	TTAAGCATT	CTTTAACTGG	2520
	TAGGGAACGC	CAGAACTTTT	AAGTCCAGCT	ATTCATTAGA	TAGTAATTGA	AGATATGTAT	2580
	AAATATTACA	AAGAATAAAA	ATATAITACT	GTCTCTTTAG	TATGGTTTTC	AGTGCAATTA	2640
	AACCGAGAGA	TGCTCTGTTT	TTTTAAAAAG	AATAGTATTT	AATAGGTTTC	TGACTTTTGT	2700
55	GGATCATTTT	GCACATAGCT	TTATCAACTT	TTAAACATTA	ATAAAGTGAT	TTTTTTAAAG	

Seq ID NO: 2 Protein sequence

Protein Accession #: NP_001391

	1	11	21	31	41	51	
60	MGPTSVPLVK	AHRSSVSQYV	NYDIIVRHYN	YTGKLNISAD	KENSIKLTST	VFILICCPFI	60
	LENIFVLLTI	WTKKPHRPM	YFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
	EGSMFVALSA	SVFSLLAIAI	ERYITMLKMK	LHNGSNNFRL	FLLLISACWVI	SLILGGLPIM	180
	GNWCISALSS	CSTVLLPLYHK	HYILFCTTVP	TLLLLSIVIL	YCRIYSLVRT	RSRLTFRKN	240
65	ISKASRSSEK	SLALLKTVII	VLSVPIACWA	PLFILLLLDV	GCKVKTCIDIL	FRAEYFLVLA	300
	VLSNGTNPII	YTLTKEMRR	AFIRIMSCCK	CPSGDSAGKF	KRPPIAGMEF	SRSKSDNSSH	360
	PQKDEGNPE	TIMSSGNVNS	SS				

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #: NM_002205.1

Coding sequence: 1..3149

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75	ATGGGGAGCC	GGAGCCGAGA	GTCCCTCTCT	CACGCCGTGC	AGCTGCGCTG	GGGCCCCCGG	60
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	GGCTTCAACT	TAGACGCGGA	GGCCCCAGCA	GTACTCTCGG	GGCCCCCGGG	CTCCTTCTTC	180
	GGATTCTCAG	TGAGTTTTTA	CGGCGCGGGA	ACAGACGGGG	TCAGTGTGCT	GGTGGGAGCA	240
	CCCAAGGCTA	ATACCAAGCA	GCCAGGAGTG	CTGACGGGTG	GTGCTGTCTA	CCTCTGTCTC	300
80	TGGGGTGCCA	GCCCCACACA	GTGCACCCCC	ATTGAATTTG	ACAGCAAAGG	CTCTCGGCTC	360
	CTGGAGTCTT	CACGTGTCAG	CTCAGAGGGA	GAGGAGCCGT	TGGAGTACAA	GTCTTGCAG	420
	TGGTTGCGGG	CAACAGTTTG	AGCCCATGGC	TCCTCCATCT	TGGCATGCGC	TCCACTGTAC	480
	AGCTGGGCGA	CAGAGAAGGA	GCCACTGAGC	GACCCCGTGG	GCACCTGCTA	CCTCTCCACA	540
	GATAACTTCA	CCCGAATTCT	GGAGTATGCA	CCCTGCCGCT	CAGATTTTCAG	CTGGGCAGCA	600

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ATTGCAGAA CTATTACCC CGAGTACCTG ATCAACCTGG TTCAGGGCCA GCTGCAGACT 780
CGCCAGGCCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGGTGA 840
TTCAAGTGGT ATGACACAGA AGACTTTGTT GCTGGTGTGC CCAAGGGGAA CCTCACTTAC 900
GGCTATGTCA CCATCCTTAA TGGCTCAGAC ATTGATCCC TCTACAAC TTCTCAGGGGAA 960
CAGATGGCCT CTACTTTTGG CTATGCAGTG GCCGCCACAG ACGTCAATGG GGAACGGGCTG 1020
GATGACTTGC TGGTGGGGGC ACCCTGTGCT ATGGATCGGA CCCCTGACGG GCGGCGCTCAG 1080
GAGGTGGGCA GGTCTACGT CTACCTGCAG CACCCAGCCG GCATAGAGCC CAGGCCACCC 1140
CTTACCTCTA CTGGCCATGA TGAGTTTGGC OGATTTGGCA GCTCCTTGAC CCCCTGGGGG 1200
GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGGG CTCCTTTGG TGGGAGAGCC 1260
CAGCAGGGAG TAGTGTGTGT ATTTCTGGG GGGCCAGGAG GGTGGGGCTC TAAGCCTTCC 1320
CAGGTTCTGC AGCCCTGTG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
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Seq ID NO: 4 Protein sequence
Protein Accession #: NP_002196.1

50
55
60
65
70

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1 11 21 31 41 51
MGSRTPESEPL HAVQLRWGPR RRPPLLP LLLPPPPRVG GFNLDAEAPA VLSGPPGSPF 60
GFSVPEYRPG TDGVSVLVGA PKANTSQPGV LQGGAVYLCF WNASPTQCTP IEPDSRGSRL 120
LESSLSSEEG EEPVEYKSLQ WFGATVRAHG SSILACAPLY SWRTEKEPLS DPVGTCTYLT 180
DNFTRILEYA PCRSDPSWAA GQGYCQGGFS AEFTKTGRVV LGSPGSYFWQ QQILSATQEQ 240
IAESYYPEYL INLVQQLQT RQASSIYDDS YLGYSVAVGR FSGDDTDFV AGVPKGNLTY 300
GYVTIINGSD IRSLYNFSGE QMASYFGYAV AATDVNGDGL DDLLVQAPLL MDRTPDGRPQ 360
EVRGVVYVYQ HPAGIEPTPT LTLTGHDEFG RFGSSLTPLG DLDQDGYNDV AIGAPFGGET 420
QQGVVVFVPG GPGGLGSKPS QVLQPLMAAS HTPDFFGSAL RGGRLDNGG YPDLIIVGSFG 480
VDKAVVYRGR FIVSASASLT IFPAMFNPEE RSCSLGNPV ACINLSFCLN ASGKHVADSI 540
GFTVELQLDW QKQKGGVRRR LPLASRQATL TQTLILQNGA REDCREMKIY LRNESEFRDK 600
LSPHIALMF SLDPAQPVDS HGLRPALHYQ SKSRIEDKAQ ILLDCGEDNI CVPDLQLEVF 660
GEQNHVYLDG KNALNLTPHA QNVGEGGAYE AELRVTAPEE AEYSGLVRHP GNPSLSCDY 720
FAVNQSRLIV CDLGNPMKAG ASLWGGRLFT VPHLRDTKKT IQFDFQILSK NLNNSQSDVV 780
SFRLSVEAQA QVTINGVSKP EAVLFPVSDW HPRDQPKKEE DLGPAVHHVY ELINQGPSSI 840
SQGVLELSCP QALBQQLLY VTRVTGLNCT TNHPINPKGL ELDPEGSLHH QQKREAPSR 900
SASSGPQILK CPEAEFCRLR CELGFLHQE QSLSQLHFRV WAKTFLOREH QPFSLQCEAV 960
YKALKMPYRI LPRQLPKQER QVATAVQWTK AEGSYGVPLF IILAILFLGL LLLGLLIYIL 1020
YKLGFFPKRSL FYGTAMEKAQ LKPPATSDA

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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: NM_002211.1
Coding sequence: 1..2397

75
80

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1 11 21 31 41 51
ATGAATTAC AACCAATTTT CTGGATTGGA CTGATCAGTT CAGTTTGTCT TGTGTTTGCT 60
CAACAGATG AAAATAGATG TTTAAAAGCA AATGCCAAAT CATGTGGAGA ATGTATACAA 120
GCAGGGCCAA ATTTGGGGTG GTGCACAAAT TCAACATTTT TACAGGAAGG AATGCCTACT 180
TCTGCAGAT GTGATGATT AGAAGCCTTA AAAAAGAGG GTTGCCCTCC AGATGACATA 240
GAAATCCCA GAGCTCCAA AGATATAAAG AAAAATAAAA ATGTAACCAA CCGTAGCAAA 300
GGAACAGCAG AGAAGCTCAA GCCAGAGGAT ATTACTCAGA TCCAACCACA CGAGTTGGTT 360
TTGGGATTAA GATCAGGGGA GCCACAGACA TTACATTAA AATTCAAGAG AGCTGAAGAC 420
TATCCCATG ACCTCTACTA CCTTATGGAC CTGCTTACT CAATGAAAGA CGATTGGAG 480
AATGTAAAAA GTCTTGAAC AGATCTGATG AATGAAATGA GGAGGATTAC TTCCGAGTCT 540

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AGAATTGGAT TTGGCTCATT TGTGGAAAAAG ACTGTGATGC CTTACATTAG CACAACACCA 600
GCTAAGCTCA GGAACCCCTT CACAAGTGAA CAGAACTGCA CCAGCCCAT TAGCTACAAA 660
AATGTGCTCA GTCTTACTAA TAAAGGAGAA GTATTTAATG AACTTGTGAG AAAACAGCGC 720
ATATCTGGAA ATTTGGATTG TCCAGAAAGG GGTTCGATG CCATCATGCA AGTTGCAGTT 780
TGTGGATCAC TGATTGGCTG GAGGAATGTT ACACGGCTGC TGGTGTTC CACAGATGCC 840
GGGTTTCACT TTGCTGGAGA TGGGAAACTT GGTGGCATTG TTTTACCAA TGATGGACAA 900
TGTCACTCGG AAAATAATAT GTACACAATG AGCCATTATT ATGATTATCC TTCTATTGCT 960
CACCTTGTCC AGAACTGAG TGAAAAATAA ATTCAGACAA TTTTTCAGT TACTGAAGAA 1020
TTTCAGCTTG TTTACAAGGA GCTGAAAAAC TTGATCCCTA AGTCAGCAGT AGGAACATTA 1080
TCTGCAAAAT CTAGCAATGT AATTCAATTG ATCATTGATG CATACAATTC CCTTTCCTCA 1140
GAAGTCATT TGGAAAAACG CAAATTGTCA GAAGGAGTAA CAATAAGTTA CAAATCTTAC 1200
TGCAAGAACG GGGTGAATGG AACAGGGGAA AATGGAAGAA AATGTTCCAA TATTTCCATT 1260
GGAGATGAGG TTCAATTGTA AATTAGCATA ACTTCAAATA AGTGTCACAA AAAGGATTCT 1320
GACAGCTTTA AAATTAGGCC TCTGGGCTTT ACGGAGGAAG TAGAGGTTAT TCTTCAGTAC 1380
ATCTGTGAAT GTGAATGCCA AAGCGAAGGC ATCCCTGAAA GTCCCAAGTG TCATGAAGGA 1440
AATGGACAT TTGAGTGTGG CGCGTGCAGG TGCAATGAAG GCGGTGTGAG TAGACATTGT 1500
GAATGCAGCA CAGATGAAGT TAACAGTGAA GACATGGATG CTTACTGCGA GAAAGAAAAA 1560
AGTTTCAGAA TCTCAGTAA CAATGGAGAG TGCGTCTCGG GACAGTGTGT TTGTAGGAAG 1620
AGGGATCAATA CAAATGAAAT TTATTCTGGC AAATTCTGCG AGTGTGATAA TTTCAACTGT 1680
GATAGATCCA ATGCTTAAT TTGTGGAGGA AATGTTGTTT GCAAGTGTGG TGTGTGTGAG 1740
TGCAACCCCA ACTACACTGG CAGTGCATGT GACTGTTCTT TGGATACTAG TACTTGTGAA 1800
GCCAGCAACG GACAGATCTG CAATGGCCGG GGCATCTGCG AGTGTGGTGT CTGTAAGTGT 1860
ACAGATCCGA AGTTTCAAGG GCAAAACGTGT GAGATGTGTC AGACCTGCTC TGGTGTCTGT 1920
GCTGAGCTTA AAGAAATGTT TCAAGTGCAG GCCTTCAATA AAGGAGAAAA GAAAGACACA 1980
TGCAACAGG AATGTTCTTA TTTTAACTT ACCAAGGTAG AAAGTCGGGA CAAATTACCC 2040
CAGCCGCTCC AACCTGATCC TGTGTCCCAT TGTAAAGSAGA AGGATGTTGA CGACTGTTGT 2100
TTCTATTTTA GATATTCACT GAATGGGAAC AACGAGGTCA TGGTTCATGT TGTGGAGAAAT 2160
CCAGAGTGTG CCACCTGTCC AGACATCATT CCAATTGTAG CTGTTGTGTT TGCTGGAAAT 2220
GTTCTTATGT GCCTTGCATT ACTGCTGATA TGGAAAGCTT TAATGATAAT TCATGACAGA 2280
AGGGAGTTTG CTAATTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAATAA 2340
CCTATTATTA AGAGTGCCGT AACAACCTGTG GTCAATCCGA AGTATGAGGG AAAATGA

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Seq ID NO: 6 Protein sequence

Protein Accession #: NP_002202.1

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1 11 21 31 41 51
| | | | |
MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
SARCDLEAL KKKGCPDDI ENPRGSKDIK KKNVNTNRSK GTAEKLPED ITQIQPQLV 120
LRLRSGEPQT FTLKFKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM MEMNRITSDF 180
RIGFGSPVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLINKGE VFNELVGKQR 240
ISGNLDSPEG GFDALMQVAV CGSLIGWRNV TRLLVFSTDA GPHFAGDGKL GGIVLPNDGQ 300
CHLENNMYTM SHYDYPSIA HLVLKLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGTI 360
SANSSNVQL IIDAYNSLSS EVILENGKLS EGVTSYKSY CKNGVNGTGE NGRKCSNISI 420
GDEVQFEISI TSNKCPKKDS DSFKIRPLGF TEEVEVILQY ICECEQSGE IPESPKCHEG 480
NGTFECGACR QNEGRVGRHC ECSTDEVNSE DMDAYCRKEN SSEICSNNGE CVCGQVCVRK 540
RDNTNEIYSG KFCECNFNC DRNGLICGG NGVCKCRVCE CNPNYTGSAK CDSLDSTSCR 600
ASNGQICNMR GICECGVCRK TDPKFQGGCT EMCQTCLGVC AEHKECVQCR AFNKGKEDT 660
CTQECSEYFI TKVESRDLPL QPVQDPVSH CKEKDVDDCW FYPTYSVNGN NEVMVHVVEN 720
PECPGTGPDII PIVAGVVAGI VLTGLALLLI WKLLMIHDR REPAKPEKEK MNARWDTGEN 780
PIYKSAVTTV VNPKYEGK

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Seq ID NO: 7 DNA sequence

Nucleic Acid Accession #: NM_002425

Coding sequence: 26..1453

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60
65
70
75
80

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1 11 21 31 41 51
| | | | |
AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAITC CTTGTGCTGT TGTGCTGCCC 60
AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
TGCCCAACGAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
AAAGGACAGT AATCTCATTG TTAATAAAT CCAAGGAATG CAGAAGTTC TGGGTTGGA 240
GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
TCTGTACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAAACCACT 360
TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATCTGCCAT 420
TGAGAAAGCT CTGAAAGTCT GGAAGAGAGT GACTCCACTC ACATTCTCCA GGCTGTATGA 480
AGGAGAGGCT GATATAATGA TCTCTTTCG AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
TGATGCCCCA GGACACAGTT TGGCTCATGC CTACCCACTT GGAAGTGGC TTTATGGAGA 600
TATTCATTCT GATGATGATG AAAAAATGAC AGAAGATGCA TCAGGCACCA ATTTATTCTC 660
CGTTGTGCTC CATGAACCTG GCCACTCCCT GGGGCTCTTT CACTCAGCCA ACATGAAGC 720
TTTGATGTAC CCACCTACAG ACTCAITCAG AGAGCTCGCC CAGTTCGSCC TTTGCAAGA 780
TGATGTGAAT GGCATTACAT CTCTCTACGG ACCTCCCTCT GCCTCTACTG AGGAACCCCT 840
GGTGCCCA CAATCTGTTT CTCTGGGATC TGAGATGCCA GCCAAGTGTG ATCTGCTTT 900
GTCTTGTGAT GGCATCAGCA CTCTGAGGGG AGAATATCTG TTTCTTAAAG ACAGATATT 960
TTGGCGAAGA TCCCACTGGA ACCCTGAACC TGAATTTTCA TTGATTTCTG CATTTTGGCC 1020
CTCTCTTCCA TCATATTGG ATGCTGCATA TGAAGTTAAC AGCAGGAGCA CGTTTTAT 1080
TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
AGGCATCCAT ACCCTGGGTT TTCTTCAAC CATAAGGAAA ATTGATGCAG CTGTTCTGA 1200
CAAGGAAAAG AAGAAAACAT ACTTCTTTCG AGCGGACAAA TACTGGAGAT TTGATGAAA 1260
TAGCCAGTCC ATGGAGCAAG GCTTCCCTAG ACTAATAGCT GATGACTTTC CAGGAGTTGA 1320
GCCTAAGGTT GATGCTGTAT TACAGGCATT TGAATTTTTC TACTTCTTCA GTGGATCATC 1380
ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAAACAGCTG 1440
GTTACATTGC TAGGCCAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
ATTATTATC TAATGTATTA TGAGCCAAAA TGGTTAATTT TTCTGTGATG TCTGTGACT 1560

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GAAGAAGATG AGCCTTGACG ATATCTGCAT GTGTCATGAA GAATGTTTCT GGAATTCTTC 1620
 ACTTGCTTTT GAATTGCACT GAACAGAATT AAGAAATACT CATGTGCAAT AGGTGAGAGA 1680
 ATGTATTTTC ATAGATGTGT TATTACTTCC TCAATAAAAA GTTTTATTTT GGGCCTGTTC 1740
 CTT

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Seq ID NO: 8 Protein sequence
 Protein Accession #: NP_002416

10 1 11 21 31 41 51
 | | | | | |
 MHLAFLVLLC LPVCSAYPLS GAAKEEDSNK DLAQQYLEKY YNLEKDVKQF RRKDSNLIVK 60
 KIQQMQKFLG LEVTGKLDTD TLEVMRKPRC GVPDVGHFSS FPGMPKWRKT HLTIRIVNYT 120
 PDLPDRAVDS AIEKALKVWE EVTPLTFSLR YEGEADIMIS FAVKEHGDYF SFDGPGHSLA 180
 HAYPPGPGLY GDIIHFDDDEK WTEDASGTNL FLVAAHELGH SLGLFHSANT EALMYPLYNS 240
 15 FTELAQFRLS QDDVNGIQSL YGPPFPASTEE PLVPTKSVPS GSEMPAKCDP ALSFDAISTL 300
 RGEYLFKDR YFWRSHWNP EPEFHLISAF WPSLPSYLD AVEVNSRDTV FIFKNEFWA 360
 IRGNEVQAGY PRGIHTLGFP PTIRKIDAAV SDKEKKKTYF FAADKYWRPD ENSQSMQGF 420
 PRLIADDFPG VEPKVDVAVLQ AFGFFYFPGG SSQPEFDPNA RMVTHILKSN SWLHC

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Seq ID NO: 9 DNA sequence
 Nucleic Acid Accession #: XM_058189.2
 Coding sequence: 169..774

25 1 11 21 31 41 51
 | | | | | |
 GAAGACCAGC TCAGCTCTTC AGTTGTGTAT CATTGTCTAT TGTTCTCCAA ACAGTAAACC 60
 AGTATTTTAC ACTGAGATTG TCGGCTGCGG GTATATTCCA ATTCCCGGTC TCCTCATGAA 120
 TATGAAGTGA AGGGCTCTGA CCCTGGAAGT GGTCTAAGC AGGGCAAAAT GGGGCTCGG 180
 AAGTGTGGAG GCTGCCTAAG TTGTTTGCTG ATTCGCTTG CACTTTGGAG TATAATCGTG 240
 30 AACATATTAT TGTATTTCCC GAATGGGCAA ACTTCCTATG CATCCAGCAA TAAACTCACC 300
 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGAAAACCTG 420
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCTT 480
 GGATACTGCC TGGTCATCTC TGCCTTGGGT CTGTGCCAAG GGCCATATTG CCGCACCCCT 540
 35 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600
 TGGATTCACT GCCTGGAACC TGCACATGTT GTGGAGTGA ACATCATTTT ATTTTCCATT 660
 CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720
 TCCAGATAC TGTGTGGAAG CTATTCACTG ATCTTCCAGC CTGGAATCAT TTGAATAAGG 780
 ACAAAATGTT TTCCATTATC AAGACATGGC CATCTATCTA AATATTATAT CAACTGTGTA 840
 40 GACTTGAGGG CAATATTGAA ATGATGGTGC TTCTGCTATT TGGTGTTTAT TTGTAATAAA 900
 TTTGCACTCC TCACATGACA TGCAAGTATA CCACCTCTCC ATTTAGTATG TTTTAAAGT 960
 AATATGCATT AGAAATCTCA GAAATACCTC TGCCCTTTGA TCAAAACAAAT CATTTTCCAA 1020
 GAATCTGTAC TAGGGAAGTA AATAAGAATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080
 TGCAACATTA TTGAATATTG TGGAAAATTG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140
 45 AGGATTAAAT AAGAGTGGT ACATACTGTA AATGTTTTCT GATATTAAAA AAAAAATTAA 1200
 AAAAAAATA AAGAGTACTA CATGGTTGTA AAA

50

Seq ID NO: 10 Protein sequence
 Protein Accession #: XP_058189.1

1 11 21 31 41 51
 | | | | | |
 MGSRRKGGLL SCLLIPLALW SIIVNILLYF PNGQTSYASS NKLITNVWYF EGICFSGIMM 60
 LIVITVLLVL ENNNYKQCV SENCSSKKVVT LLSIIFSSLG IAFSGYCLVI SALGLVQGPY 120
 55 CRTLDGWEYA FBGTAGRLT DSSIWIQCLE PAHVVEWNII LPSILITLGG LQVIICLIRV 180
 VMQLSKILCG SYSVIFQPGI I

60

Seq ID NO: 11 DNA sequence
 Nucleic Acid Accession #: NM_002421.2
 Coding sequence: 1..1409

65 1 11 21 31 41 51
 | | | | | |
 ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTC ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGGAAAAA 120
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAAGC GGAGAAATAG TGGCCCACTG 180
 GTTGAAAAAT TGAAGCAAAAT GCAGGAATTC TTTGGGCTGA AAGTGACTGG GAAACCAAGT 240
 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300
 70 GTCTCACTG AGGGGAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAAA 360
 TACAGCCAGC ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCCTAACTC 420
 TGGAGTAATG TCACACCTCT GACATTCAAC AAGGTCTCTG AGGGTCAAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCCTT TTGATGGACC TGGAGGAAAT 540
 CTGTCTCATG CTTTTCACCC AGGCCCAAGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTTGCGGC TCATGAACTC 660
 75 GGCCATTCTC TTGACTCTCT CCATTCTACT GATATCGGGG CTTTGATGTA CCCTAGGTAC 720
 ACCTTCAGTG GTGATGTTCA GCTAGCTCAG GATGACATTO ATGGCATCCA AGCCATATAT 780
 GGACGTTCCT AATATCCTGT CCAGCCCATC GGCCCAACAA CCCCACAAAGC ATGTGACAGT 840
 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAAG TGATGTTCTT TAAAGACAGA 900
 80 TTCTACATGC GCACAAATCC CTTCTACCGG GAAGTTGAGC TCAATTTTCAT TTCTGTTTTC 960
 TGGCCACACG TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTCAC AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCAAGGACA TCTACAGCTC CTTTGGCTTC CTTAGAACTG TGAAGCATAT CGATGCTGCT 1140
 CTTTCTGAGG AAAACACTCG AAAAACTTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AAGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTTCT 1260

GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCITTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

5

Seq ID NO: 12 Protein sequence

Protein Accession #: NP_002412.1

1 11 21 31 41 51
 10 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFOQPGP IGGDAHFDED ERWTNNFREY NLHRVAAHEL GHSGLGSHST DIGALMYPST 240
 15 TFSGDVQLAQ DDIDGIAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRTNPFYP EVELNFIISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVVLHG 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWR YDEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDVAF MKDGFYFFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN

20

Seq ID NO: 13 DNA sequence

Nucleic Acid Accession #: NM_002421.2

Coding sequence: 1..1409

1 11 21 31 41 51
 25 ATGCACAGCT TTCTCCACT GCTGCTGCTG CTGTTCTGGG GTGTGGTGTG ACACAGCTTC 60
 CCAGCGACTC TAGAAACACA AGAGCAAGAT GTGGACTTAG TCCAGAAATA CCTGSAAGAA 120
 TACTACAACC TGAAGAATGA TGGGAGGCAA GTTGAAAGAG GGAGAAATAG TGGCCAGATG 180
 GTTGAAAAAT TGAAGCAATC GCAGGAATTC TTGGGCTGTA AAGTGACTGG GAAACAGAT 240
 30 GCTGAAACCC TGAAGGTGAT GAAGCAGCCC AGATGTGGAG TGCCTGATGT GGCTCAGTTT 300
 GTCTCTACTG AGGGGAAACCC TCGCTGGGAG CAAACACATC TGACCTACAG GATTGAAAT 360
 TACACGCCAG ATTTGCCAAG AGCAGATGTG GACCATGCCA TTGAGAAAGC CTTCACATC 420
 TGGAGTAATG TCACACCTCT GACATTACCC AAGGTCTCTG AGGTCACAGC AGACATCATG 480
 ATATCTTTTG TCAGGGGAGA TCATCGGGAC AACTCTCTCT TTGATGGACC TGGAGGAAAT 540
 35 CTGCTCATG CTTTCAACC AGGCCAGGT ATTGGAGGGG ATGCTCATTT TGATGAAGAT 600
 GAAAGGTGGA CCAACAATTT CAGAGAGTAC AACTTACATC GTGTGCGGC TCATGCCCTC 660
 GGCCATTCTC TTGGACTCTC CCATTCTACT GATATCGGGG CTTTGTATGA CCTAGCTAC 720
 ACCTTCAGTG GCTAGTTTCA GCTAGCTCAG GATGACATTG ATGGCATCCA AGCCATATAT 780
 GGAAGTCCCC AAAATCCTGT CCAGCCCATC GGGCCACAAA CCCCAGAGC ATGTGACAGT 840
 40 AAGCTAACCT TTGATGCTAT AACTACGATT CGGGGAGAGG TGATGTTCTT TAAAGACAGA 900
 TTCTACATGC GCACAAATCC CTCTACCCG GAAGTTGAGC TCAATTTCAT TTCTGTTTTT 960
 TGGCCACAAC TGCCAAATGG GCTTGAAGCT GCTTACGAAT TTGCCGACAG AGATGAAGTC 1020
 CGGTTTTTCA AAGGGAATAA GTACTGGGCT GTTCAGGGAC AGAATGTGCT ACACGGATAC 1080
 CCAAGGAGCA TCTACAGCTC CTTTGGCTTC CCTGAAGACT TGAAGCATAT CGATGCTGCT 1140
 45 CTTTCTGAGG AAAACACTGC AAAAACCTAC TTCTTTGTTG CTAACAAATA CTGGAGGTAT 1200
 GATGAATATA AACGATCTAT GGATCCAGGT TATCCCAAAA TGATAGCACA TGACTTTCTT 1260
 GGAATTGGCC ACAAAGTTGA TGCAGTTTTC ATGAAAGATG GATTTTCTA TTTCITTCAT 1320
 GGAACAAGAC AATACAAATT TGATCCTAAA ACGAAGAGAA TTTTGACTCT CCAGAAAGCT 1380
 AATAGCTGGT TCAACTGCAG GAAAAATTAG

50

Seq ID NO: 14 Protein sequence

Protein Accession #: NP_002412.1

1 11 21 31 41 51
 55 MHSFPPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMQEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 60 LAHAFOQPGP IGGDAHFDED ERWTNNFREY NLHRVAAHAL GHSGLGSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDGIAIY GRSONPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRTNPFYP EVELNFIISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVVLHG 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFWANKYWR YDEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDVAF MKDGFYFFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN

65

Seq ID NO: 15 DNA sequence

Nucleic Acid Accession #: FGENESH predicted

Coding sequence: 141..1580

1 11 21 31 41 51
 70 TCTGCGTGTG CCGGGGCTAG GGGCTGGAAG TCCTGGCTCT AGTTGCACCT CGGAAGGAAA 60
 AGCAACACAG AGGAGGGAAG GCGTCTTAGG ACTGCCTGGA TCCAGAGCAC TTCTCTCGGC 120
 CTCTACAGGC CTGTGTGCTC ATGGGTTCCC CGCCGCGCCC GGAGGAGGCG CTGGGCTACG 180
 75 TCCGCGAGTT CACTGCGCAC TCCTCCGACG TGCTGGGCAA CCTCAACGAG CTGCGCCTGC 240
 GCGGGATCCT CACTGACGTC ACGCTGCTGG TTGGCGGGCA ACCCTCAGA GCACACAAGG 300
 CAGTTCTCAT GCGCTGCAGT GGCTTCTTCT ATTCAATTTT CGGGGCGCGT GCGGGAGTGG 360
 GGGTGGACGT GCTCTCTCTG CCGGGGGGTC CCGAAGCGAG AGGCTTCGCC CCTCTATTGG 420
 80 ACTTCATGTA CACTTGGGCG CTGCGCTCTT CTCCAGCCAC TGCACACGCA GTCTAGCGG 480
 CCGCCACCTA TTTGCAGATG GAGCAGCTGG TCCAGGCGAT CCAACGCTTC ATCCAGGCCA 540
 GCTATGAACC TCTGGGCTAT TCCCTGCGCC CCCTGGAAGC AGAACCCCA ACACCCCA 600
 CGGCCCTCC ACCAGGTAGT CCCAGGCGCT CGAAGGACA CCCAGACCCA CCTACTGAAT 660
 CTGGAAGCTG CAGTCAAGGC CCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTGCAACT 720
 GGAAGAGTA CAGTACATC GTGCTAAACT CTCAGGCTC CCAAGCAGG AGCTGCTGCG 780

5 GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCCAGTGGG GACGAGGCCT 840
 CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTCCT GGTCCCCAGA 900
 GCAGGCTCTC TCCAACTGCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
 CCTACCTCCT CACATCCCGA GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020
 CACTACCGGG AAGTGAATTT TTCAGCTGCC AGAAGCTGTA GGCTGTGGCA GGGGTCTCAT 1080
 CGGGGCTGGA CTCCTTGGTT CCTGGGAGC AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
 GGTCTTCTGT CGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGCAC ACAGGGGAAA 1200
 AGCCTTACCA CTGCTCAATC TCGGAGGCC GTTTTAAACG GCCAGCAAACT CTGAAAACGC 1260
 10 ACAGCCGCAT CAGATCCCGA GAGAAGCCGT ATAAGTGTGA GAGTGGCGC TCGCGCTTTG 1320
 TACAGGTGGC ACATCTGCGG GCGCAGCTGC TGATCCACAC CGGGGAGAAG CCTACCCCTT 1380
 GCCCTACCTG CGGAACCCGC TTCCGCCACC TGCAGACCCT CAAGAGCCAC GTTCGCATCC 1440
 ACACCGGAGA GAAGCCCTTAC CACTGGGACC CCTGTGGCCT GCATTTCCGG CACAAGAGTC 1500
 AACTGCGGCT GCATCTGCGC CAGAAACACG GAGCTGTAC CAACACAAA GTGCACTACC 1560
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Seq ID NO: 16 Protein sequence

Protein Accession #: FGENESH predicted

55 1 11 21 31 41 51
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 60 PPSPASPDFK ACWKYKYI VLNSQASQAG SLVGRSSGQ PCPQARLPFG DEASSSSSSS 240
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 FSCQNCBEVA GCSSGLDSLVL PGDEDKPKYC QLCRSSPFYK GNLASHRTVE TGEKPYHCSE 360
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Seq ID NO: 17 DNA sequence

Nucleic Acid Accession #: XM_039209

Coding sequence: 1..2049

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25 Seq ID NO: 18 Protein sequence
Protein Accession #: XP_039209

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SLFHSFEREV LERDLVLP LL CKDYCKEFPY TCRGHIPGL QTTADEFCFY YARKDGGCLCF 180
PDFFPKQVRG PASNYLDQME EYDKVEBISR KHKNCFICIQ EVVSGLRQPV GALHSGDGSQ 240
RLFILEKEGY VKILTPGEI FKEPYLDIHK LVQSGIKGSD ERLGLSLAFH PNYKKNKLY 300
VSYTINQERW AIGPHDHILR VVEYTVSRKN PHQVDLRTAR VFLEVAELHR KHLGGQLLFG 360
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45 Seq ID NO: 19 DNA sequence
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Coding sequence: 1..1506

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Seq ID NO: 20 Protein sequence
 Protein Accession #: NP_055146.1

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 NAVAVTFSEI LLGNFSLAVP IFVALSCFSG MNGGVFAVSR LPYVASREBH LPEILSMIHV 360
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Seq ID NO: 22 Protein sequence
 Protein Accession #: NP_002413

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Coding sequence: 57..764

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Protein Accession #: NP_006519

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Seq ID NO: 25 DNA sequence
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Coding sequence: 1..2825

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ATAAAATAGG	GGCCGAACCA	CTTGATGGTG	TTTGGAGGCG	TCTGTCCATC	CGTCACATCC	420
ATCATTCGAG	AGTCCCTCCA	AGGCTGGAAT	CTGTGTCAGC	TTTCTTTTGC	TGCAACCAAG	480
CCTGTTCTAG	CCGATAAGAA	AAAATACCCT	TATTTCTTTC	GGACCGTCCC	ATCAGACAAT	540
GCGGTGAATC	CAGCCATTCT	GAAGTGCTCT	AAGCACTACC	AGTGGAAAGC	CGTGGGCAAG	600
CTGACGCAAG	ACGTTCAAGG	GTTCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
GGCGAGGACA	TTGAGATTTC	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCACTGTC	720
AAAAAGCTGA	AGGGGAATGA	TGTGCGGATC	ATCCTTGGCC	AGTTTGACCA	GAATATGGCA	780
GCAAAAGTGT	TCTGTTGTGC	ATACGAGGAG	AACATGTATG	GTAGTAAATA	TCAGTGGATC	840
ATTCGGGGCT	GGTACGAGCC	TTCTTGGTGG	GAGCAGGTGC	ACAAGGAAGC	CAACTCATCC	900
CGCTGCCTCC	GGAAAGATCT	GCTTGTCTGC	ATGGAGGGCT	ACATTGGCGT	GGATTTCGAG	960
CCCCGAGCT	CCAAGCAGAT	CAAGACCATC	TCAGGAAAGA	CTCCACAGCA	GTATGAGAGA	1020
GAGTACAACA	ACAAGCGGTC	AGGCGTGGGG	CCGACGAAGT	TCCACGGGTA	CGCCTACGAT	1080
GGCATCTGGG	TCATCGCCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
CGGCACCAGC	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGCTGGGCAG	GATCATCTCT	1200
AATGCCATGA	ACGAGACCAA	CTTCTCGGG	GTCAAGGGTC	AAATTGTATT	CCGGAATGGG	1260
GAGAGAATGG	GGACCAATTA	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	1320
GAGTACAACG	CTGTGGCCGA	CACACTGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	1380
TCCGAACCC	CAAAAGACAA	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	1440
CTCTACAGCA	TCCTCTCTGC	CCTCAACATC	CTCGGATGTA	TCATGGCCAG	TGCTTTCTCT	1500
TTCTTCAACA	TCAAGAACCG	GAATCAGAAG	CTCAATAAGA	TGTGAGTCC	ATACATGAAC	1560
AACCTTATCA	TCCTTGGAGG	GATGCTCTCC	TATGCTTCCA	TATTTCTCTT	TGGCCTTGAT	1620
GGATCCTTTG	TCTCTGAAAA	GACCTTTGAA	ACACTTTGCA	CGTTCAGGAC	CTGGATTCTC	1680
ACCGTGGGCT	ACACGACCCG	TTTTGGGGCC	ATGTTTGCAA	AGACCTGGAG	AGTCCACGCC	1740
ATCTTCAAAA	ATGTGAAAAA	GAAGAAGAAG	ATCATCAAGG	ACCAGAAACT	GCTTGTGATC	1800
GTGGGGGGCA	TGCTGCTGAT	CGACCTGTGT	ATCCTGATCT	GCTGGCAGGC	TGTGGACCCC	1860
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GTCAGCATCC	CCGCACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGCTTA	CAACGTGGGG	2100
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TTCTGATCG	TGGTCTGGT	CATCATCTTC	TGCAGCACCA	TCAACCTCTG	CCTGGTATTC	2220
GTGCGGAAGC	TCATCACCTT	GAGAACAAAC	CCAGATGCAG	CAACGCAGAA	CAGGCGATTTC	2280
CAGTTTCACT	AGAAATCAGAA	GAAGAAGAT	TCTAAAAAGT	CCACCTCGGT	CACCAAGTGT	2340
AACCAAGCCA	GCACATCCCG	CCTGGAGGGC	CTACAGTCAG	AAAAACATCG	CCTGGGAATG	2400

5 AAGATCACAG AGCTGGATAA AGACTTGGAA GAGGTCACCA TGCAGCTGCA GGACACACCA 2460
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 GATATAAAT CTCCAGAACA CATCCAGCGT CGGCTGTCCC TCCAGTCCC CATCCTCCAC 2700
 CACGCCATCC TCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC 2760
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10 Seq ID NO: 26 Protein sequence
 Protein Accession #: NP_005449.1

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 IKYGNHMLMV FGVGCPSTVS IIAESLQGNW LVQLSPAATT PVLADKKKYP YFFRTVPNDN 180
 AVNPAILKLL KHYQWRKRGV LTQDVQRFSR VRNDLTGVLY GEDIEISDTS SFSNDPCTSV 240
 KKLKGNQVRI ILQGFQNNMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSSW EQVHTEANSS 300
 RCLRNKLLAA MEGYIGVDPE PLSSKQIKTI SGKTPQQYER EYNNKRSVGV PSKFHGYAYD 360
 GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRILL NAMNETNFFG VTGQVVFVRNG 420
 ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRFQG SEPPKDKTII LEQLRKISLP 480
 LYSILSALTQ LGMIMASAFI FFNKNNRQK LIKMSSPYMN NLIIILGMLS YASIFLFLGLD 540
 GSPVSEKTFE TLCTVTRTWL TVGYTTAFGA MFAKTRVHA IPKNVMMKKK IIKDQKLLVI 600
 VGGMLLIDL ILICWQAVDP LRRTVKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGIIV 660
 YAYKGLMLLF GCLFANETRN VSIPALNDSK YIGMSVYNVG IMCIIGAAVS FLTRDQPNVQ 720
 FCIVALVIF CSTITLCLVF VPKLITLRTN PDAATQNRRE QFTQNKKEQ SKTSTSVTSV 780
 NQASTSRLEG LQSENHRLRM KITELDKDLE EVTNQLQDTP EKTYYIKQNH YQELNDILNL 840
 GNPTSTDDG KALKKNHLDQ NPQLQWNTTE PSRTCKDPIB DINSPEHIQR RLSLQLPILH 900
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Seq ID NO: 27 DNA sequence
 Nucleic Acid Accession #: NM_000450.1
 Coding sequence: 117..1949

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 GGTCTTACAA CACCTCCACG GAACTATGA CTTATGATGA GGCCAGTGCT TATTGTGAGC 240
 AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAGAAGA GATTGAGTAC CTAACCTCCA 300
 TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG 360
 TCTGGGTAGG AACCCAGAAA CCTCTGACAG AAGAAGCCAA GAACCTGGCT CCAGGTGAAC 420
 CCAACATAG CAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG 480
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 CCTGTACCAA TACATCTCTG AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA 600
 CTTGCAAGTG TGACCTCTGC TTCACTGGAC TCAAGTGTGA GCAAAATGTG AACTGTACAG 660
 CCCTGGAATC CCTGAGCAT GGAAGCCTGG TTTGCACTCA CCCACTGGGA AACTTCAGCT 720
 ACAATTCTTC CTGCTCTATC AGCTGTGATA GGGGTACCT GCGAAGCAGC ATGGAGACCA 780
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 GTGATGTCTG GCAAAATCCA GCAATGGGT TGGTGAATG TTTCCAAAC CCTGGAAGCT 900
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 CGCTGTAAAA TCTTGGCACA GAAACACAA ATTTGTGTGG TTTCTTCTT TTGCCCTTCA 2340
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5 AGAATAAAGT TCTGAGTGT TTTACTACAG TTGTTTTTGT AAAACATGGT AGAATTGGAG 2880
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 10 AACAAATCCA AAGGAATCTC CAGTTTTAG TTGATCACTG GCAATGAAAA ATTCTCAGTC 3360
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 TTTAAATTTT AACTTAAAT ATTTTATAAT TTTTAAAGTA TATATTATT TAAGCTTATG 3780
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Seq ID NO: 28 Protein sequence
 Protein Accession #: NP_000441.1

25 1 11 21 31 41 51
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 DVMWMDERC SKKLLALCYT AACTNTSCSG HGECVETINN YTKCDPGFS GLKCEQIVNC 180
 TALESPHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSME TMQCMSGSEW SAPIPACNVV 240
 ECDAVTNFAN GFVECFQNPQ SPFWNTTCTF DCBEGFELMG AQSLQCTSSG NWDNEKPTCK 300
 AVTCAVRVAP QNGSVRCSHS PAGEPTFKSS CNFTCEEGFM LQGPQVECT TQGWTKQIP 360
 30 VCEAPQCTAL SNPERGYMNC LPSASGSFRY GSSCEPSCBQ GFVLKGSKRL QCGPTGSEWN 420
 EKPTCEAVRC DAVHQPPKGL VRCAHSPIGE FTYKSSCAFS CEEGFELYGS TQLECTSQGQ 480
 WTEEVPSQCV VGCSSLAAPG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 SGLLETCEAP TESNIPLVAG LSAAGLSLLT LAPFLWLRLK CLRKAKKFVP ASSCQSLESD 600
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Seq ID NO: 29 DNA sequence
 Nucleic Acid Accession #: NM_007036
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 60 GATGGGGAGG GGGTGGAGT GGGAAATAAA ATATTAGCC CTTCTTGGT AGGTAGCTTC 1080
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 AGTATTACCG TGTATTTTAT TCTTGAAGTT GGCCAACAGA GTTGTGAATG TGTGTGGAAG 1920
 75 GCCTTTGAAT GTAAGCTGC ATAAGCTGTT AGGTTTGTGT TTAAGAGSAC ATGTTTATTA 1980
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Seq ID NO: 30 Protein sequence
 Protein Accession #: NP_008967.1

80 1 11 21 31 41 51
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 ICDRGTKCL KPFPFQYSVT KSNRNFVSLT EHDMSGDGN IVREEVVKEN AAGSPVMRKW 180

LNPR

Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM_000963

Coding sequence: 135..1949

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1 11 21 31 41 51
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CACCAGGAATT TTGACAAGA ATAAAATTAT TTCTGAAACC CACTCCAAAC ACAGTGCAC 360
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CATATTGAGA TATTAAAGGT TGAATGTTG TCCTTAGGAT AGGCCTATGT GCTAGCCAC 3960
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GGGATCTGTG GATGCTTCGT TAATTGTTC AGCCACAATT TATTGAGAAA ATATTCTGTG 4080
TCAAGCACTG TGGGTTTTAA TATTTTTAAA TCAACGCTG ATTACAGATA ATAGTATTTA 4140
TATAAATAAT TGAATAAAT TTTCTTTGG GAAGAGGGAG AAAATGAAAT AAATATCATT 4200
AAGATAACT CAGGAGAAAT TTTCTTACAA TTTTACGTT AGAATGTTTA AGGTAAAGAA 4260
AGAAATAGT AATATGCTTG TATAAAACAC TGTTCAGTGT TTTTTTAAA AAAAAAAGT 4320
GTTTGTGTTA TAACATTGAT CTGCTGACAA AACCTGGGAA TTTGGGTTGT GTATGCGAAT 4380
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TGTCTGTTTA TTTTGTACT ATTTA

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5	MLARALLCA	VLASHTANP	CCSHPCQNRG	VCMSVGFDQY	KDCCTRGTGY	GENCSTPEFL	60
	TRIKLWFAFS	PNTVHYILTH	FKGFWNVPLN	TPFLRNAIMS	YVLTSRSHLI	RSPFTYNAQY	120
	GKMSWEAFSN	LSYHYTRALPP	VPDDCPTPLG	VKGKKQLPDS	NEIVEKLLRL	DKPI1PDDQS	180
	NMMFAFAQH	LTQHFFKTDH	KRGPAFTNGL	HGVGDNLNHY	GETLARQRKL	RLFKDGMKY	240
10	Q1IDGMEYP	TVKDTQAEI	YPPQVPEHLR	FAVQGVFVGL	VPLGMLYATI	WLREHNRVCD	300
	VLKGEHPFWG	DLQGFQTSRL	LLIGETIKIV	IDYVQHLSG	YHFGLKFDPE	LLFNKQFQYQ	360
	NRIAAEENTL	YHWHPLLPDT	FQIHQKYNY	QQFYNNISL	LEHGITQFVE	SFTROIAGRV	420
	AGGRNVPVAV	QKQSQASIDQ	SRMQKYQSFN	EYRKRRMLPK	YESFEELTGE	KEMSAEAL	480
	YGDIDAVELY	PALIVEKPRD	DAIFGETMVE	VGAPFSLKGL	MGNVICSPAY	WKPSTFGGVS	540
15	GFGIINTASI	QSLICNNVKG	CFPTSFSVPD	PELIIKTVTIN	ASSRSGLDNL	INPTVLLKER	600
	STRI						

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		GTCACTCTCG	CCCTGGTGCG	ACTGCCCCCT	TGCTTGGCCA	TGGGTATCTA	GTACCCCGTG	540			
		GTGAACGTGG	CCAGCCACCG	GGGTCTCACT	CGGACACCGT	CCACACCCCG	CCACACCCAG	600			
35		CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660			
		CAGTCCACGA	CTCTCGGCGC	CTTCGTGGTC	TAACTCGTGG	TCCTGTCTCT	CGTAGGCTTC	720			
		ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAGCCGAGA	AGGGCTCGCT	GGCCGGGGGG	780			
		ACGGGCGCTC	CCGACCTGAG	GAAGTCCGAG	ACGGAAGGCA	CAGGAGACCG	CAGGAGGCCG	840			
		ACCATCATCT	TCTCGAGGCT	GATTGTGTGT	ACATTGGCCG	TATGCTGGAT	GCCCAACCCAG	900			
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		GGGTACATGT	TCTCTCTCCC	CTTCTCGGAG	AGGTTTTTCT	ACCTTCGACG	GGTCACTAAC	1020			
		CCGCTCTCTGT	ACACGGTGTG	CTCGCAGCAG	TTTCGGCGGG	TGTTCTGTGA	GGTGTCTGTC	1080			
		TGCCGCCCTGT	CGCTCGCAGCA	CAGAAACAC	GAGAAGCGCC	TGCGCGTACA	TGCGCATCTC	1140			
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		TCGCAAGGA	GAACTGAGAA	GATTTTCTTA	AGCATCTTTC	AGAGCGAGGC	GACGCCCCAG	1260			
45		CTCAAGTCCG	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACCCAGT	1320			
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Protein Accession #: NP_001499.1

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ATLLHVLTLF	PERYIAICHP	FRYKAVSGPC	QVKLLIGFVW	VTSLVALPLF	LFAMGTETPL	180
VNVPSHRLGT	CNRSSTRHHE	QPETNSMISC	TNLSRRWTIV	QSSIFGAFVV	YLVLVLSVAF	240
MCNNHMQVLM	KSQKGSGLAG	TRPPQLRKSE	SEESRTARRQ	TTIIFLRIVV	TLAVCHMNPQ	300
IRIRIMAAAKP	KHDWTRTSYR	AYMILLPPSE	TFPYLSSVIN	PLLYTVSSSQ	PRFVQVQLIC	360
CRLSLQHANH	EKKRLRVHAHS	TTDSARFPQR	PLFLPASRRQS	SARRTEKIFL	STFQSGEAROP	420
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70	AGTCGTGATCA	GGGGTCGGGA	CCGAAGCGCA	AATGTCTGTG	CCCTTCAACA	GATTTTGGGC				180	
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	AAACGACTGT	TTTATATAGA	ATGTTGCCCT	GGTATATAGA	GAATGGAAAG	AATGAAAAGC				300	
	TGCCACGACG	TTTTGCCCAT	TGACCATGTT	TATGGCACTC	TGGCATCTGT	GGGAGCCACC				360	
	ACAACGCGAG	GCTATTCTGA	CGCCTCAAA	CTGAGGGAGG	AGATCGAGGG	AAAGGGATCC				420	
75	TTCATTACTT	TGCGACAGCT	TAATGAGGCT	TGGGCAACTT	TGGATTCTGA	TATCCGTAGA				480	
	GGTTTGGGAG	GCAACGTGAA	TGTTGAAATT	TGGATTCGTT	TACATAGTCA	CATGATTAAT				540	
	AAGAGAATGT	TGACCAAGGA	TTATAAAATA	CGCATGATTA	TTCTCTCAAT	GATGAAACAAT				600	
	TTGGGGCTTT	TCATTAAACA	TTCTCTCAAT	GGGTTTGTC	CTGTTAATGT	TGCTCGAATG				660	
	ATCCATGGGA	ACCAAGATGC	AAACAAATGT	GTTGTCCATG	TCATTGACCG	TGCTCTTACA				720	
80	CAAATTGGTA	CCTCAATTCA	AGACTTCATT	GAAGCAGAAG	ATGACCTTTC	ATCTTTTAGA				780	
	CGAGCTGCCA	TCACATCGGA	CATATTGGAG	GCCTCTGGAA	GAGACGGTCA	CTCTCACACT				840	
	TTTGCTCCCA	CCAAATGAGC	TTTTGAGAAA	CTTCCACGAG	GTGTCTCTAG	AAGGTTTCATG				900	
	GGGAGCAAG	TGGCTTCGGA	AGCCTCTATG	AAGTACCACA	TCTTAATATC	TCTCCAGTGT				960	
	TGTGCTCTTA	TTATGGGAGG	AGAGCTCTTT	GAGAGCGTGG	AAGGAATAAC	ATTCAGATGA				1020	

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GGATGTGACG GTGACAGTAT AACAGTAAAT GGAATCAAAA TGGTGAACAA AAAGGATATT 1080
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ATCAAGCCAG CAGAGAAATC CCTCCATGAA AAGTTAAAC AAGATAAGCG CTTTAGCACC 1560
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TTCAATGGAA AAGGATTGTA ACCTGGTGT ACTAACATT TAAAGACCAC ACAAGGAAGC 1800
AAAATCTTTC TGAAGAAGT AAATGATACA CTCTGGTGA ATGAATTGAA ATCAAAAGAA 1860
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ACAGAAAGAA CTCTGAAGAA ATTGTTACAA GAAGAGGTCA CCAAGGTCA CAAATTCATT 2400
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Seq ID NO: 36 Protein sequence
Protein Accession #: NP_006466.1

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55
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1 11 21 31 41 51
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KLREEIEGKG SPFTYFAPSNE AWDNLDSDIR RGLSENVNVE LLNALHSHMI NKRMLTKDLK 180
NGMIIPSMYN NLGLFINHYP NGVVTVNCAR IHHGNQIATN GVVEVIDRVL TQIGTSIQDF 240
IEAEDLSSP RAAAITSDIL EALGRDGHPT LFAPTNEAFE KLPRGVLERF MGDKVASEAL 300
MKYHILNTLQ CSSEIMGGAV FETLEGNTIE IGCDDGSITV NGIKRMVKKD IVTNNGVIHL 360
IDQVLIPDSA QKVIELAGKQ QTTPTDLVAQ LGLASALRPD GEYTLAPVN NAFSDDTLSM 420
VQRLKLKILQ NHILKVKVGL NELYNGQILE TIGGKQLRVP VYRTAVCIEN SCMEKGSKQG 480
RNGAIIIPRE IIPAEKSLH EKLKQDKRFS TFLSLEAAD LKELLTQPGD WTLFVPTNDA 540
FKGMTSEEEK ILIRDKNALQ NIILYHLTPG VFIGKGFEPG VTNILKTTQG SKIFLKEVND 600
TLVLNKLKSK ESDIMTTNGV IHVVDKLLYP ADTPVGNLQL LEILNKLKLY IQIKEVRGST 660
FKEIPVTVYT TKIITKVVEP KIKVIEGSLQ PIIKTEGFTL TKVKIEGEPE FRLIKEGETI 720
TEVIHGEPII KKYTKIIDGV FVEITEKETR EERIITGPBI KYTRISTGGG ETEBELKRL 780
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Seq ID NO: 37 DNA sequence
Nucleic Acid Accession #: NM_002416
Coding sequence: 40..417

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75
80

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AAGGTCGCT GTTCTCTGCAT CAGCACCAAC CAAGGACTA TCCACCTACA ATCCTTGAAA 180
GACCTTAAC AATTGCCCC AAGCCCTTCC TGGAGAGAAA TTGAATCAT TGTACACTG 240
AAGAATGGAG TTCAACATG TCTAAACCCA GATTGAGCAG ATGTGAAGGA ACTGATTAAA 300
AAGTGGGAGA AACAGGTCAG CCAAAAGAAA AAGCAAAGA ATGGGAAAAA ACATCAAAAA 360
AAGAAAGTTC TGAAGTTCG AAAATCTCAA CGTCTCGTC AAAAGAAGAC TACATAAGAG 420
ACCACTTAC CAATAAGTAT TCTGTGTTAA AAATGTTCTA TTTTAATTAT ACCGCTATCA 480
TTCCAAGGA GGAATGGATA TAATACAAAG GCTTATTAAT TTGACTAGAA AATTTAAAAA 540
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 10 GCACGTGTA AAAACACTGC GGATATTCTG GACTGTTTTT AAAAAATATA CAGTTTACCG 1740
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 AGTTTTATTG TCCGTTTACT TGTTCAGAG TTTGTATTGT GATTATCAAT TACCACACCA 1980
 15 TCTCCCATGA AGAAAGGGAA CGGTGAAGTA CTAAGCGCTA GAGGAAGCAG CCAAGTCGGT 2040
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 GGAGGTTTCAG TGAATTGTGT AGGAGAGGTT GTCTGTGGCC AGAATTTAAA CCTATACTCA 2160
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 20 AAAAATCTAA GTGTTTCTAT AATTTGAGAG TCTGTGACCC ACTTACCTTG CATCTCACAG 2340
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 TCATTTATCA TATATATACA TACATGCATA CACTCTCAA GCAAATAATT TTTCACTTCA 2460
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 TATCAATAAA TAGACCATTA ATCAG

25 Seq ID NO: 38 Protein sequence
 Protein Accession #: NP_002407

30 1 11 21 31 41 51
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 IBIIATLKNQ VQTCINPDSA DVKELIKKWE KQVSQKKKQK NGKXHQKKV LKVRKSQSR 120
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35 Seq ID NO: 39 DNA sequence
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 Coding sequence: 85..1347

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75 Seq ID NO: 40 Protein sequence
 Protein Accession #: NP_006661

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 AALNLSGSLR DEVBAGAFEH LPSLRQLDLS HNPLADLSPF AFGSNASVS APSPLVELIL 180
 NHIVPPEDEQ QNRSFEGMVV AALLAGRALQ GLRRLELASN HFYLPREVLA AQLPSLRHLD 240

LSNNSLVSLT YVSRNLTHL ESHLEDNAL KVLHNGTLAE LQGLPHIRVF LDNNPWVDC 300
 HMADMVTLWK ETEVVQKDR LTCAYPEKMR NRVLLELNSA DLDGDPILPP SLQTSYVFLG 360
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Seq ID NO: 41 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..927

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 TTCTCCTCTT CGGCGCGGTT CTGGGTCTCC GCGTGTCCG CCCAGCCCCC GCTGCCGGAC 180
 15 CAGTGCCCGC CGCTGTGCGA GTGCTCCGAG GCAGCGCGCA CAGTCAAGTG CGTTAACCGC 240
 AATCTGACCG AGGTGCCCAC GGAACCTGCC GCCTACGTGC GCAACCTCTT CCTTACCGGC 300
 AACCAGCTGG CCAGCAACCA CTTCCTTTAC CTGCCGCGG ATGTGCTGCG CCAACTGCCC 360
 AGCCTCAGGC ACCTGGACTT AAGTAATAAT TCGCTGGTGA GCCTGACCTA CGTGTCTCTC 420
 CGCAACCTGA CACATCTAGA AAGCCTCCAC CTGGAGGACA ATGCCCTCAA GGTCTCTCAC 480
 20 AATGGCAACC TGGCTGAGTT GCAAGGTCTA CCCCACATTA GGGTTTTCCT GGACAAACAT 540
 CCCTGGGTCT GCGACTGCCA CATGGCAGAC ATGGTGACCT GGCTCAAGGA AACAGAGGTA 600
 GTGCAGGGCA AAGACCGGCT CACCTGTGCA TATCCGGAAG AAATGAGGAA TCGGGTCCTC 660
 TTGGAAGTCA ACAGTGCTGA CTGGGACTGT GACCCGATTG TTCCCCCATC CTGCAAAACC 720
 TCTTATGTCT TCCTGGGTAT TGTTTTAGCC CTGATAGGCG CTATTTTCCT CTGTGTTTGG 780
 25 TATTGAAACC GCAAGGGGAT AAAAAAGTGG ATGCATAACA TCAGAGATGC CTGCAGGGAT 840
 CACATGGAAG GGTATCATTA CAGATATGAA ATCAATGCGG ACCCCAGATT AACAAACCTC 900
 AGTTCTAACT CGGATGTCTT CGAGTGA

30

Seq ID NO: 42 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MPGGCSRGPA AGDGRRLRL LALVLLGWVS SSSPTSSASS FSSSAPFLAS AVSAQPPLPD 60
 QCPALCECSE AARTVKCVNR NLTEVPTDLP AYVRNLFITG NQLASNHFLY LPRDVLALPL 120
 35 SLRHLDSLNN SLVSLTVVSP RNLTHLESLL LEDNALKVLH NGTLAELOGL PHIRVFLDNN 180
 PWVDCIMAD MVTWLKETEY VQKDRITCA YPEKMRNRVL LELNSADLDC DPILPPLSLT 240
 SYVFLGIVLA LIGAIFLLVL YLNRKGIKGW MHNIRDACRD HMEGYHYRYE INADPRLTNL 300
 SSNSDVLE

40

Seq ID NO: 43 DNA sequence
 Nucleic Acid Accession #: NM_058173
 Coding sequence: 68..340

45 1 11 21 31 41 51
 | | | | |
 AGCGCCTTGC CTCTCTTAG GCTTTGAAGC ATTTTGTCT GTGCTCCCTG ATCTTCAGGT 60
 CACCACCATG AAGTCTTAG CAGTCCCTGT ACTCTTGGGA GTTTCATCT TTCTGGTCTC 120
 TGCCAGAAAT CCGACAACAG CTGCTCCAGC TGACACGTAT CCAGCTACTG GTCTGCTCTG 180
 50 TGATGAAGCC CCTGATGCTG AAACCACTGC TGCTGCAACC ACTGCGACCA CTGCTGCTCC 240
 TACCACTGCA ACCACCGCTG CTCTACCACT TGCTCGTAAA GACATTCCAG TTTTACCCAA 300
 ATGGGTTGGG GATCTCCCGA ATGGTAGAGT GTGTCCCTGA GATGGAATCA GCITGAGTCT 360
 TCTGCAATTG GGTCAAACT ATTCAATGCTT CCGTGATTG CATCCAACCTA CTACCTTGC 420
 CTACGATATC CCCTTATCT CTAATCAGTT TATTTTCITT CAAATAAAAA ATAACATGTA 480
 GCGAGCTAAC AT

55

Seq ID NO: 44 Protein sequence
 Protein Accession #: NP_477521

60 1 11 21 31 41 51
 | | | | |
 MKPLAVLVLL GVSIFLVSAQ NPTTAAPADT YPATGPADDE APDAETAAAA TTATTAAPT 60
 ATTAASTTAR KDIPVLPKWV GDLFNGRVCP

65

Seq ID NO: 45 DNA sequence
 Nucleic Acid Accession #: NM_000095.1
 Coding sequence: 26..2299

70 1 11 21 31 41 51
 | | | | |
 CAGCACCCAG CTCCCGGCCA CCGCCATGGT CCGGACACC GCTGCGTTC TTCTGCTCAC 60
 CCGTGGCTGCC CTGGCGCGCT CCGGACAGGG CCAGAGCCCG TTGGGCTCAG ACCTGGGCCC 120
 GCAGATGCTT CGGGAACCTG AGGAAACCAA CGCGGCGCTG CAGGACGTGC GGGACTGGCT 180
 CGCGGAGCAG GTGAGGGAGA TCACGTTCCT GAAACACAG GTGATGAGT GTGACGCGTG 240
 75 CGGATGAGC CAGTCACTAC GCACCGGCTT ACCCAGCGTG CGGCCCCCTG TCCACTGCGC 300
 GCCCGGCTTC TGCTCCCGCG GCGTGGCTCG CATCCAGAGC GAGAGCGCGG GCGGCTGCGG 360
 CCCCCTGCCC GCGGCGCTCA CCGGCAACGG CTGCACTGC ACCGACGTCA ACGAGTGCAA 420
 CGCCCAACCC TGCTTCCCGC GAGTCCGCTG TATCAACACC AGCCCGGGGT TCGCTGCGA 480
 GGCTTGCCCG CCGGGGTACA GCGGCCCCAC CCAACAGGGC GTGGGGCTGG CTTTGGCCAA 540
 80 GGCCACAAG CAGTTTGA CAACCATCAA CGAGTGTGAG ACCGGGCAAC ATAACCTCGT 600
 CCCCACCTCC GTGTGCATCA ACACCGGGG CTCCTTCCAG TGCGGCGCGT GCCAGCCCGG 660
 CTTCGTGGGC GACCAAGCGT CCGGCTGCCA GCGCGGCGCA CAGCGCTTCT GCCCGGACGG 720
 CTGCGCCAGC GAGTGCCAGT AGCATGCAGA CTGGTCTCTA GAGCGGATG GCTCGCGGTC 780
 GTGCGTGTGT CCGGTTGGCT GGGCCGCGAA CCGGATCCTC TGTGTCGCG ACACGTGACT 840
 AGACGCGTTC CCGGACGAGA AGCTGCGCTG CCGGAGCGG CAGTGCCGTA AGGACAACCTG 900

5 CGTGACTGTG CCCAACTCAG GGCAGGAGGA TGTGGACCGC GATGGCATCG GAGACGCCTG 960
 CGATCCGGAT GCCGACGGGG ACGGGGTCCC CAATGAAAAG GACAACCTGC CGCTGGTGGC 1020
 GAACCCAGAC CAGCGCAACA CGGACGAGGA CAAGTGGGGC GATGCGTGCG ACAACTGCCG 1080
 GTCCAGAAAG AACGACGACC AAAAGGACAC AGACCGAGAC GGCCGGGGCG ATGCGTGCGA 1140
 CGACGACATC GACGGCGACG GGATCCGCAA CCAGGCCGAC AACTGCCCTA GGTATCCCAA 1200
 CTCAGACCAG AAGGACAGTG ATGGCGATGG TATAGGGGAT GCCTGTGACA ACTGTCCCCA 1260
 GAAGAGCAAC CCGGATCAGG CGGATGTGGA CCAAGACTTT GTGGGAGATG CTTGTGACAG 1320
 CGATCAAGAC CAGGATGGAG ACGGACATCA GGACTCTCGG GACAACCTGC CCACGGTGCC 1380
 10 TAACAGTGCC CAGGAGGACT CAGACCACGA TGGCCAGGGT GATGCCTGCG ACGACGACGA 1440
 CGACAATGAC GGAGTCCCTG ACAGTCGGGA CAACTGCCGC CTGGTGCCCTA ACCCGGCCA 1500
 GGAGGACGCG GACAGGAGCG GCGTGGGCGA CGTGTGCCAG GACGACTTTG ATGCAGACAA 1560
 GGTGGTAGAC AAGATCGACG TGTGTCCGGA GAACGCTGAA GTACGCTCA CCGACTTCAG 1620
 GGCTTCCAG ACAGTCTGTC TGGACCCGGA GGGTGACGCG CAGATTGACC CCAACTGGGT 1680
 GGTGCTCAAC CAGGGAAGGG AGATCGTGCA GACAATGAAC AGCGACCCAG GCCTGGCTGT 1740
 15 GGGTTACACT GCCTTCAATG GCGTGGACTT CGAGGGCAGC TTCCATGTGA ACACGGTCAC 1800
 GGATGACGAC TATGCGGGCT TCATCTTTGG CTACCGAGAC AGCTCCAGCT TCTACGTGGT 1860
 CATGTGGAAG CAGATGGAGC AAAAGTATTG GCAGGCGAAC CCTTCCGCTG CTGTGGCCGA 1920
 GCTCTGCATC CAACCTCAAG CTGTGAAGTC TTCCACAGGC CCGCGGGAAC AGCTCGCGAA 1980
 CGCTCTGTGG CATACAGGAG ACACAGAGTC CCAGGTGCGG CTGCTGTGGA AGGACCCGCG 2040
 20 AAACGTGGGT TGAAGGACA AGAAGTCCTA TCGTTGGTTC CTGCAGCACC GCGCCCAAGT 2100
 GGGCTACATC AGGCGTGGAT TCTATGAGGG CCTGAGCTG GTGGCCGACA GCAACGTGGT 2160
 CTTGGACACA ACCATGCGGG GTGGCCGCGT GGGGGTCTTC TGCTTCTCCC AGGAGAACAT 2220
 CATCTGGGCC AACCTGCGTT ACCGCTGCAA TGACACCATC CCAGAGGACT ATGAGACCCA 2280
 25 TCAGCTGCGG CAGGCGCTAG GACCAAGGTG AGGACCCGCG GGATGACAGC CACCTCACC 2340
 GCGGCTGGAT GGGGGCTCTG CACCCAGCCC AAGGGGTGGC CGTCTGAGG GGAAGTGAG 2400
 AAGGGCTCAG AGAGGACAAA ATAAAGTGTG TGTGCAGGG

Seq ID NO: 46 Protein sequence
 Protein Accession #: NP_000086.1

30 1 11 21 31 41 51
 | | | | |
 MVPDTACVLL LTLAALGASG QGQSPILGSDL GPQMLRELQE TNAALQDVDR WLRQQVREIT 60
 FLKNTVMECD ACGMQQSVRT GLPSVRPLH CAPGFCFPGV ACIQTESGGR CGPCPAGFTG 120
 35 NGSHCTDVNE CNAHECFPRV RCINTSPGFR CEACPPGYSG PTHQGVGLAF AKANKQVCTD 180
 INECETQEH CVPNSVCINT RGSFQCGPCQ PGFVGDQASG CQRGAQRFCP DGSPSECHEH 240
 ADCVLERDGS RSCVCRGWA GNGILOGRDT DLDGPFDEKL RCPEPQCRKD NCVTVPSGQ 300
 EDVDRDGI GD ACDDPADGSG VFNKONCPL VRNPQRNTD EDKWDGACDN CRSQRNDDQK 360
 DTDQDGRGDA CDDIDIGRI RNQADNCPRV PMSDQKSDG DGI GDACDNC PQKSNFDQAD 420
 40 VHDHFVGDAC DSDQDQDGDG HQDSRDNCPT VPNSAQEDSD HDGQGDACDD DDDNDGVFDS 480
 RDNCRLVFPN GQEDADRQDV GDVQDQDFDA DKVVDKIDVC PENAEVTLTD FRAFQTVVLD 540
 PEGDAQIDPN WVVLNQGREI VQTMNSDPGL AVGYTAFNGV DPEGTFFHVT VTDDYAGFI 600
 FGQDSSSFY VVMWQMEQT YWQNPFRFV AEPGIQLKAV KSSTGPGEQL RNALWHTGDT 660
 45 ESQVRLLSQE PRNVGWKDKK SYRWPLQHRP QVGYIRVRFY EGPELVADSN VVLDITMRGG 720
 RLGVFCFSQE NIIWANLRYR CNDTIFEDYE THQLRQA

Seq ID NO: 47 DNA sequence
 Nucleic Acid Accession #: NM_001565.1
 Coding sequence: 67..363

50 1 11 21 31 41 51
 | | | | |
 GAGACATTC TCAATTGCTT AGACATATTC TGAGCCTACA GCAGAGGAAC CTCCAGTCTC 60
 AGCACCATGA ATCAAACTGC GATTCTGATT TGCTGCCTTA TCTTTCTGAC TCTAAGTGGC 120
 55 ATTCAAGGAG TACCTCTCTC TAGAACCGTA CGCTGTACCT GCATCAGCAT TAGTAATCAA 180
 CCTGTTAATC CAAGGTCTTT AGAAAACTT GAAATTATTC CTGCAAGCCA ATTTTGTCCA 240
 CGTGTGAGTA TCATTGCTAC AATGAAAAAG AAGGGTGAGA AGAGATGTCT GAATCCAGAA 300
 TGAAGGCCA TCAAGAATTT ACTGAAAGCA GTTAGCAAGG AATGTCTTAA AAGATCTCCT 360
 60 TAAAACAGA GGGGAGCAA ATCGATGCAG TGCTTCCAAG GATGGACCAC ACAGAGGCTG 420
 CCTCTCCCAT CACTTCCCTA CATGGAGTAT ATGTCAAGCC ATAATTGTTC TTAGTTTGCA 480
 GTTACACTAA AAGGTGACCA ATGATGGTCA CCAATCAGC TGCTACTACT CCTGTAGGAA 540
 GGTTAATGTT CATCATCTTA AGCTATTCTG TAATAACTCT ACCCTGGCAC TATAATGTAA 600
 GCTCTACTGA GGTGCTATGT TCTTAGTGA TGTCTGACC CTGCTTCAA TATTTCCTC 660
 65 ACCTTTCCTA TCTTCCAAG GTACTAAGGA ATCTTTCTGC TTTGGGGTTT ATCAGAATTG 720
 TCAGAACTCT AAATAACTAA AAGGTATGCA ATCAATCTG CTTTTTAAAG AATGCTCTTT 780
 ACTTCAATGA CTTCCTCTG CATCTCCCA AGGGGCCCAA ATCTTTCTG TGGCTACCTA 840
 CATACAATTC CAACACATA CAGGAAGGTA GAAATATCTG AAAATGTATG TGTAAGTATT 900
 CTTATTATAT GAAGACTGT ACAAAATATA AGTCTTAGAT GTATATATTT CCTATATTGT 960
 70 TTTCACTGTA CATGGAATAA CATGTAATTA AGTACTATGT ATCAATGAGT AACAGGAAAA 1020
 TTTTAAAAAT ACAGATAGAT ATATGCTCTG CATGTTACAT AAGATAAATG TGCTGAATGG 1080
 TTTTCAATA AAAATGAGGT ACTCTCTCTG AAATATTAA

Seq ID NO: 48 Protein sequence
 Protein Accession #: NP_001556.1

75 1 11 21 31 41 51
 | | | | |
 MNQTALICC LIFLTLSGIQ GVPLSRTVRC TCISISNQPV NPSLEKLEI IPASQFCPRV 60
 80 BIIATMKKKG EKRCINPESK AIKNLLKAVS KEMSKRSP

Seq ID NO: 49 DNA sequence
 Nucleic Acid Accession #: XM_057014
 Coding sequence: 143..874

1 11 21 31 41 51
 5 GGGAGGGGAGA GAGGCGCGCG GGTGAAAGGC GCATTGATGC AGCCTGCGGC GGCCTCGGAG 60
 CGCGGCGGAG CCAGACGCTG ACCACGTTCC TCTCCTCGGT CTCTCCCGCC TCCAGCTCCG 120
 CGCTGCCCGG CAGCCCGGAG CCATGCGACC CCAGGGCCCC GCGCCTCCCG CCGCAGCGGCT 180
 CGCGGCGCTC CTGCTGCTCC TGCTGCTGCA GCTGCCCGCG CCGTCGAGCG CCTCTGAGAT 240
 CCCCAGGGG AAGCAAAAGG CGCAGCTCCG GCAGAGGGAG GTGGTGGACC TGTATAATGG 300
 AATGTGCTTA CAAGGGCCAG CAGGAGTGCC TGSTCGAGAC GGGAGCCCTG GGGCCAATGG 360
 10 CATTCCGGGT ACACCTGGGA TCCCAGGTGG GGATGGATTC AAAGGAGAAA AGGGGGAATG 420
 TCTGAGGAA AGCTTTGAGG AGTCTGGAC ACCCAACTAC AAGCAGTGTT CATGGAGTTC 480
 ATTGAATTAT GGCATAGATC TTGGGAAAT TGCGGAGTGT ACATTTACAA AGATGCGTTC 540
 AAATAGTGCT CTAAGAGTTT TGTTCAGTGG CTCACCTCGG CTAAAAATGCA GAAATGCATG 600
 CTGTGACGCT TGGTATTTC CAATCAATGG AGCTGAATGT TCAGGACCTC TTCCCATTTGA 660
 15 AGCTATAATT TATTGGACC AAGGAAGCCC TGAAATGAAT TCAACAATTA ATATTCATCG 720
 CACTTCTTCT GTGGAAGGAC TTTGTGAAG AATTGGTGTG GGATTAGTGG ATGTTGCTAT 780
 CTGGGTGGCG ACTTGTTCAG ATTACCCAAA AGGAGATGCT TCTACTGGAT GGAATTCAGT 840
 TTCTCGCATC ATTATTGAAG AACTACCCAA ATAAATGCTT TAATTTTCAT TTGCTACCTC 900
 TTTTATTATT ATGCTTGGGA ATGGTTCACT TAAATGACAT TTTAAATAAG TTTATGTATA 960
 20 CATCTGAATG AAAAGCAAAG CTAAATATGT TTACAGACCA AAGTGTGATT TCACACTGTT 1020
 TTTAAATCTA GCATTATTCA TTTTGCTTCA ATCAAAAGTG GTTTCAATAT TTTTITTAGT 1080
 TGGTTAGAACT ACTTCTTCTA TAGTCACATT CTCTCAACCT ATAATTGGA ATATTGTGT 1140
 GGTCTTTTGT TTTTCTCTT AGTATAGCAT TTTTAAAAA ATATAAAGC TACCAATCTT 1200
 TGTACAAATT GTAAATGTTA AGAATTTTTT TTATATCTGT TAAATAAAAA TATTTTCCAA 1260
 CAACCTTAAA AAAAAAAA AAAA

Seq ID NO: 50 Protein sequence
 Protein Accession #: XP_057014

1 11 21 31 41 51
 30 MRPQGPAAAP QRLRGLLLLL LLQLPAPSSA SEIPKKGKQA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGSPP ANGIPGTGPI PGRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKLAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYPT FNGAECSGPL PLEAIYLDQ 180
 35 GSPFEMNSTIN IHRSSVBEGL CEGIGAGLVD VAINVGTCSO YPKGDASTGW NSVSRIIEB 240
 LPK

Seq ID NO: 51 DNA sequence
 Nucleic Acid Accession #: NM_020974
 Coding sequence: 81..3080

1 11 21 31 41 51
 40 GGGGTCCCGG CACACCTCCC CGCGCCGCGG CCGCCACCGC CCGCACTCCG CCGCCTCTGC 60
 CGCAACCGC TGAGCCATCC ATGGGGGTGG CGGGCCGCAA CCGTCCCGGG GCGGCCCTGGG 120
 45 CGGTGCTGCT GCTGCTGCTG CTGCTGCCCG CACTGCTGCT GCTGGCGGGG GCGCTCCCGC 180
 CGGGTCCGGG CCGTCCCGCG GGGCCGCGAG AGGATGTAGA TGAGTGTGCC CAAGGCGTAG 240
 ATGACTGCCA TGCCGACGCC CTGTGTCAGA ACACACCCAC CTCCTACAAG TGCTCTCTGA 300
 AGCCTGGSTA CCAAGGGGAA GGCAGGCAGT GTGAGGACAT CGATGAATGT GGAATAGAGC 360
 50 TCAATGGAGG CTGTGTCCAT GACTGTTTGA ATATTCCAGG CAATTATCGT TGCACTTGTT 420
 TTGATGGCTT CATGTTGGCT CATGACGGTC ATAATTGTCT TGATGTGGAC GAGTGCCTGG 480
 AGAACCAATG CGGCTGCCAG CATACCTGTG TCAACGTCAT GGGAGCTAT GAGTGTCTGT 540
 GCAAGGAGGG GTTTTTCCTG AGTGACAATC AGCACACCTG CATTCACCGC TCGGAAGAGG 600
 GCCTGAGCTG CATGAATAAG GATCAOGGCT GTAGTCACAT CTGCAAGGAG GCCCAAGGGG 660
 55 GCAGCGTGGC CTGTGAGTGC AGGCGCTGGT TTGAGCTGGC CAAGAACCCG AGAGACTGCA 720
 TCTTGACCTG TAACCAATGGG AACGGTGGGT GCCAGCACTC CTGTGACGAT ACAGCCGATG 780
 GCCCAGAGTG CAGCTGCCAT CCACAGTACA AGATGCACAC AGATGGGAGG AGCTGCCTTG 840
 AGCGAGAGGA CACTGTCTCG GAGGTGACAG AGAGCAACAC CACATCAGTG GTGGATGGGG 900
 ATAAAGGGGT GAAACGGGCG CTGCTCATGG AAACTGTGTC TGTCAACAA GTAGGCTGTG 960
 60 ACCGCACTG TAAGGATACT TCGACAGGTG TCCACTGCAG TTGCTCTGTT GGATTCACCT 1020
 TCCAGTTGGA TGGGAAGACA TGTAAAGATA TTGATGAGTG CCAGACCCGC AATGGAGGTT 1080
 GTGATCATTT CTGCAAAAC ATCGTGGGCA GTTTTGACTG CCGCTGCAAG AAAGGATTTA 1140
 AATTATTAA AGATGAGAAG TCTTGCCAAG ATGTGGATGA GTGCTCTTTG GATAGGACCT 1200
 GTGACCACAG CTGCATCAAC CACCTTGGCA CATTTGCTTG TGCTTGCAAC CGAGGGTACA 1260
 65 CCCTGTATGG CTTCACCCAC TGTGGAGACA CCAATGAGTG CAGCATCAAC AACGGAGGCT 1320
 GTCAGCAGGT CTGTGTGAAC ACAGTGGGCA GCTATGAATG CCAAGTCCAC CCTGGGTACA 1380
 AGCTCCACTG GAATAAAAA GACTGTGTGG AAGTGAAGGG GCTCTGCCCC ACAAGTGTGT 1440
 CACCCCGTGT GTCCCTGCAC TGCGGTAAGA GTGGTGGAGG AGACGGGTGC TTCCTCAGAT 1500
 70 GTCACCTCG CATTCACCTC TCTTCAGATG TCACCAACAT CAGGACAAGT GTAACTTTA 1560
 AGCTAAATGA AGGCAAGTGT AGTTTGAATA ATGCTGAGCT GTTCCCGAG GGTCTGOGAC 1620
 CAGCACTACC AGAGAAGCAC AGCTCAGTAA AAGAGAGCTT CCGCTACGTA AACCTTACAT 1680
 GCAGCTCTGG CAAGCAAGTC CCAGGAGCCC CTGGCCGACC AAGCACCCTT AAGGAAATGT 1740
 TTATCATCTG TGAGTTTGAG CTTGAAACTA ACCAAAAGGA GGTGACAGT TCTTGTGACC 1800
 TGAGCTGCAT CGTAAAGCGA ACCGAGAAGC GGCTCCGTAA AGCCTACCGC ACCTCTCAGAA 1860
 75 AGGCGGTCCA CAGGAGCAGG TTTCACTCC AGCTCTCAGG CATGAACCTC GACGTGGCTA 1920
 AAAAGCCTCC CAGAACATCT GAACGCCAGG CAGAGTCTCT TGGAGTGGGC CAGGGTCAATG 1980
 CAGAAAACCA ATGTGTCACT TGCAGGGCTG GGACCTATTA TGATGGAGCA CGAGAACGCT 2040
 GCATTTTATG TCCAAATGGA ACCTTCCAAA ATGAGGAAGG ACAATGACT TGTGAACCAT 2100
 GCCCAAGACC AGGAAATCTT GGGGCCCTGA AGACCCAGCA AGCTTGAAT ATGCTCTGAAT 2160
 80 GTGGAGGTCT GTGTCAACCT GGTGAATATT CTGCAGATGG CTTTGACACT TGCCAGCTCT 2220
 GTGCCCTGGG CAGTTCACG CTTGAAGCTG GTGAACTTC CTGCTTCCCC TGTGGAGGAG 2280
 GCCTTGCCAC CAAACATCAG GGAGCTACTT CCTTTCAGGA CTGTGAAACC AGAGTTCAAT 2340
 GTTCACTGAG ACATTTCTAC AACACACCA CTCACCGATG TATTGCTGTC CCACTGGGAA 2400
 CATACCAAGC TGAATTTGGA AAAAAATAAT GTGTTTCTTG CCCAGGAAAT ACTACGACTG 2460
 ACTTTGATGG CTCCACAAAC ATAACCCAGT GTAAAAACAG AAGATGTGGA GGGGAGCTGG 2520

5	GAGATTTAC	TGGGTACATT	GAATCCCCAA	ACTACCCAGG	CAATTACCCA	GCCAACACCG	2580
	AGTGTACGTG	GACCATCAAC	CCACCCCCCA	AGCGCCGCAT	CCTGATCGTG	GTCCCTGAGA	2640
	TCCTCTGCC	CATAGAGGAC	GACTGTGGGG	ACTATCTGGT	GATGCGGAAA	ACCTCTTCAT	2700
	CCAAATCTGT	GACCAACATAT	GAAACCTGCC	AGACCTACGA	ACGCCCATC	GCCTTCACCT	2760
	CCAGGTCAAA	GAAGCTGTGG	ATTCACTTCA	AGTCCAATGA	AGGGAACAGC	GCTAGAGGGT	2820
	TCCAGTCCC	ATACGTGACA	TATGATGAGG	ACTACCAAGA	ACTCATTGAA	GACATAGTTC	2880
	GAGATGGCAG	GCTCTATGCA	TCTGAGAAC	ATCAGSAAAT	ACTTAAGGAT	AAGAAACTTA	2940
	TCAGGCTCT	GTTTATGATC	CTGGCCCATC	CCCAGAACTA	TTTCAAGTAC	ACAGCCACGG	3000
10	AGTCCCGAGA	GATGTTTCCA	AGATCGTTCA	TCCGATTGCT	ACGTTCCAAA	GTGTCCAGGT	3060
	TTTTGAGAC	TTACAAATGA	CTCAGCCAC	GTGCCACTCA	ATACAAATGT	TCTGCTATAG	3120
	GGTTGTGGG	ACAGAGCTGT	CTTCCTTCTG	CATGTCAGCA	CAGTCGGGTA	TTGCTGCCTC	3180
	CCGTATCAGT	GACTCATTAG	AGTTCAATTT	TTATAGATAA	TACAGATATT	TTGGTAAATT	3240
	GAACCTGGTT	TTTCTTTCCC	AGCATCGTGG	ATGTAGACTG	AGAATGGCTT	TGAGTGGCAT	3300
15	CAGCTTCTCA	CTGCTGTGGG	CGGATGTCTT	GGATAGATCA	CGGCTGGCT	GAGCTGGACT	3360
	TTGGTCAGC	TAGGTGAGAC	TCACCTGTCC	TTCTGGGGTC	TTACTCTCTC	TCAAGGAGTC	3420
	TTAGTGGAA	AGGAGGCCAC	AGAATAAGCT	GCTTATTTCTG	AAACTTCAGC	TTCTCTAGC	3480
	COGCCCCCT	CTAAGGGAGC	CCTCTGCACT	CGTGTGCAGG	CTCTGACCAG	GCAGAACAGG	3540
	CAAGAGGGGA	GGGAGGAGGA	CCCCTGCAAG	CTCCCTCCAC	CCACCTTGAG	ACCTGGGAGG	3600
20	ACTCAGTTTC	TCCACAGCCT	TCTCCAGCCT	GTGTGATACA	AGTTTGATCC	CAGGAACCTG	3660
	AGTTCTAAGC	AGTGCTCGTG	AAAAAAAAAA	GCAGAAAGAA	TTAGAAATAA	ATAAAAACTA	3720
	AGCATTCTCG	GAGACAT					

Seq ID NO: 52 Protein sequence

Protein Accession #: NP_066025

25	1	11	21	31	41	51	
	MGVAGRNRPG	AAAVLLELLL	LLPPLLLLAG	AVPPGRGRRA	GPQEDVDECA	QGLDDCHADA	60
	LQNTPTSYK	CSCKPGYQGE	GRQCEDIDEC	GNELNGGCVH	DCLNIPGNYR	CTCFDGFMLA	120
30	HDGHNCLDWD	ECLNENGGCO	HTCVNMVMSY	ECCCKEGFFL	SDNQHTCIHR	SEEGLSMKNK	180
	DHGCISHCKE	APRGSVACEB	RPGFELAKNQ	RDCILTCNHG	NGGQHSRDD	TADGPECSCH	240
	PQYKMHDTGR	SCLEREOTVL	EVTESNTTSV	VDGDKRVKRR	LLMETCAVNN	GGCDRTCKDT	300
	STGVHSCCPV	GFTLQLDGKT	KDIDECQTR	NGGCDHFCNK	IVGSFDCGCK	KGFLLTDEK	360
	SCQDVDECSL	DRTCDHSCIN	HPGTFACACN	RGYTLVGFTH	CGDTNECSIN	NGGCGQVCVN	420
35	TVGSYEQCH	PGYKLHWNKK	DCVEVKGLLP	TSVSPRVSLH	CGKSGGGDGC	FLRCHSGIHL	480
	SSDVTITRTS	VTFKLNEGKC	SLKNAELFPE	GLRPLPEKH	SVKESFRYV	NLTCSGKQV	540
	PGAPGRPSTP	KEMFITVEFE	LETNQKEVIA	SCDLSCIVKR	TEKRLRKAIR	TLRKAVHREQ	600
	FHLQLSGMNL	DVAKKPPRTS	ERQAESCQVG	QGHAEHQCVS	CRAQTYDGA	RERCILCPNG	660
	TFQNEEGQMT	CEPCFRPGNS	GALKTPPEAWN	MSECGGLQCP	GEYSADGFAP	OQLCALGTFF	720
40	PEAGRTSCFP	CGGLATKHQ	GATSFQDCET	RVQCSGPHFY	NTTHRCIRC	PVGTQYPEFG	780
	KINCVSCPGN	TTDFDGSNTN	ITQCKNRRCG	GELGDFGTGI	ESPNYPGNYP	ANTECTWTIN	840
	PPPKRRILIV	VPEIFLPIED	DCGDYLVMRK	TSSNSVTTY	ETCQTYERPI	AFTSRSKKLW	900
	IQFKNSEGN	ARGFQVPYVT	YDEYQELIE	DIVRDGRLYA	SENHQEILAD	KKLIKALFDV	960
45	LAHPQNYFKY	TAQESREMPF	RSFIRLLRSK	VSRFLRPYK			

Seq ID NO: 53 DNA sequence

Nucleic Acid Accession #: NM_014211

Coding sequence: 157..1479

50	1	11	21	31	41	51	
	GGGACAGGGC	TGAGGATGAG	GAGAACCCCTG	GGGACCCAGA	AGACCGTGCC	TTGCCCGGAA	60
	GTCCCTGCTG	TAGGCTCTGAA	GGACTTGCCC	TAACAGAGCC	TCAACAACCTA	CCTGGTGATT	120
	CCTACTTCTAG	CCCTCTTGCTG	TGAGCAGCTT	CTCAACATGA	ACTACAGCCT	CCACTTGCCC	180
55	TTCTGTGTGTC	TGAGTCTCTT	CACCTGAGAGG	ATGTGATCC	AGGGGAGTCA	GTTCAACGTC	240
	GAGGTGCGCA	GAAGTGCACA	GCTTTCCTG	CCTGGCTTTG	AGAACCTCAC	AGCAGGATAT	300
	AACAAATTTT	TCAGGCCCAA	TTTTGGTGGG	GAACCCGTAC	AGATAGCGCT	GACTCTGGAC	360
	ATTGCAAGTA	TCTCTAGCAT	TTCAAGAGT	AACATGGACT	ACACAGCCAC	CATATACCTC	420
	CGACAGCGCT	GATGGAGCCA	GCGGCTGGTG	TTTGAAGGCA	ACAAGAGCTT	CACCTGGAT	480
60	GCCCGCTCTG	TGGAGTTCTT	CTGGGTGCCA	GATACCTTCA	TTGTGGAGTC	CAAGAAGTCC	540
	TTCTTCCATG	AAGTCACTGT	GGGAAACAGG	CTCATCCGCC	TCTTCTCCAA	TGGCACGGTC	600
	CTGTATGCCC	TCAGAAATCAC	GACAACTGTT	GCATGTAACA	TGGATCTGTC	TAAATACCCC	660
	ATGGACACAC	AGACATGCAA	GTTGCAGCTG	GAAAGCTGGG	GCTATGATGG	AAATGATGTG	720
	GAGTTCACTT	GGCTGAGAGG	GAACGACTCT	GTGCGTGGAC	TGGAAACACT	GCGGCTTGCT	780
65	CAGTACACCA	TAGAGCGGTA	TTTCACTTCA	GTCACCAGAT	CGCAGCAGGA	GACAGGAAAT	840
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	GATTGAGTCC	CTGCAAGAAC	CTGCATTGGA	GTGACGACCG	TGTTATCAAT	GACCACACTG	1020
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70	TACCTGGGGA	TCTGCTTTAG	CTTGTGTTT	GGGCGCTTGC	TAGAATATGC	AGTTGCTCAC	1140
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	GCCAGCATTG	AAATTTCCAG	CGACAACGTT	GACTACAGTG	ACTTGACAAT	GAAAAACCAGC	1320
	GACAAGTTCA	AGTTTGTCTT	COGAGAAAAG	ATGGGCAAGG	TGTGTGATTA	TTTCACAATT	1380
75	CAAAACCCCA	GTAATGTTGA	TCACTATTCC	AAACTACTGT	TTCTTTGAT	TTTTATGCTA	1440
	GCCAATGTAT	TTTACTGGGC	ATACTACATG	TATTTTGTAG	TCAATGTAA	ATTTCTTGCA	1500
	TGCCATAGGT	CTTCAACAGG	ACAAGATAAT	GATGTAAATG	GTATTTTAGG	CCAAGTGTGC	1560
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	ATGAAGCTCC	AACTGTTGTT	CTAAGCTGTG	TAGAAGTCTT	AGCATTTATG	GATCTGTGTA	1680
80	TAGAAACATG	AGTCCATTCC	TCTTTTATCT	TAATCAAGGA	CATTCCCATG	GAGCCCAAGA	1740
	TTCAAAATGT	ACTCAGGGCT	GTTTATTCGG	TGGCTCCCTG	GTTTGCATTT	ACCTCATATA	1800
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20 Seq ID NO: 56 Protein sequence
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 30 RSCLIHTSEK KAEIPPKTYS LQIAWVGFI AISIISFLSL LGVILVPLMN RVFFKFLLSF 360
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40 Seq ID NO: 57 DNA sequence
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Protein Accession #: Eos sequence

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	PARPPAARSQ	QHPSVPRMT	PGRAPFQOPP	PPVATSQHHP	GPQSRDAGRS	PSQPRLSLTQ	900
	AGRPRPTSQG	RSNHSDDPYT	ASSRGMPLTA	LQNQDEDAQG	SYDDSDSTEVE	AQDVRAPAHA	960
	ARAKEAASAL	PKHQVBSFT	GAGAGGDHRS	QRGHAASPAR	PSRPGGQPSR	ARVPSRAAPG	1020
	KSEPPSKRPL	SKSQSVSA	EDEEEDAGF	FKGKEDLLS	SSVPKWPSSS	TPRGKGDADG	1080
55	SLAKEERPEA	IALAPRGCSL	APVKRPLPPP	PGSSPRASHV	PSRPPRSAA	TVSPVAGTHP	1140
	WPRYTTTRAPP	GHFSTTPMLS	LRQRMHARF	RNPLSRQPAR	PSYRQGYNGR	PNVEGKVLPG	1200
	SNGKPGQRI	INGPQGTWV	VDLDRGLVLN	AEGRYLQDSH	GNPLRLIKLG	DGRTIVDLBG	1260
	TPVVPDGLP	LFGQGRHGT	LANAQDKPIL	SLGGKPLVLG	EVIKKTTHPP	TTTMTQPTTT	1320
	TLPLTTTTPR	PTTATTMQPT	TTTTPLPTTT	PRPTTATTRR	TTTTRPTTIV	RTTTRTTTTT	1380
60	TPKFTPIPT	CPGTLERHD	DDGNLIMSSN	GIPECYAEED	EPGSLGTDTA	VPTEAYVIY	1440
	DEDEYEFETR	PPTTTEPSTT	ATTTPRVIPEE	GAISPPPEEE	FDLAGRKRFP	APYVTYLNKD	1500
	PSAPCSLTDA	LDHPQVDSLD	EIIPNDLKKS	DLPPQHAPRN	ITVVAVEGCH	SFVIVDWDKA	1560
	TPGDLVTGYL	VYSASYEDFI	RNKFSTQASS	VTHLPITENLK	PNTRYFVKVQ	AQNFHYGPI	1620
65	SPSVSVFTES	DNPLLVVRFP	GGELSGSHSL	SNMLPATRTA	MDGNM		

Seq ID NO: 61 DNA sequence
Nucleic Acid Accession #: NM_022743
Coding sequence: 128..1237

70	1	11	21	31	41	51	
	GTGGATTTTA	GAGATACCTC	CCCTCCTTCT	GCTCAGTCTG	CTTGCACTAA	TTAAACTCTT	60
	TCTCTGCTGC	AACACCCCTA	CTGTTCTCCG	TGTATTGGCT	TTTCTGGGCA	GCAGGAAGGA	120
	AAAGCTGATG	CGATGCTCTC	AGTGCCCGGT	CGCCAAATAC	TGTAGTGCTA	AGTGTGAGAA	180
75	AAAAGCTTGG	CCAGACACCA	AGCGGGAATG	CAATAGCCTT	AAAAGCTGCA	AACCCAGATA	240
	TCCTCCAGAC	TCCGTTGAC	TTCTTGGCAG	AGTTGTCTTC	AAACTTATGG	ATGGAGCACC	300
	TTCAAGATCA	GAGAAGCTTT	ACTCATTTTA	TGATCTGGAG	TCAAATATTA	ACAAACTGAC	360
	TGAAGATAAG	AAAGAGGGCC	TCAGGCAACT	CGTAATGACA	TTTCAACATT	TCATGAGAGA	420
	AGAAATACAG	GATGCTCTC	AGCTGCCACC	TGCTTTTGAC	CTTTTGAAG	CCTTTGCAAA	480
80	AGTGATCTGC	AATCTTTTCA	CCATCTGTAA	TGCGGAGATG	CAGGAAGTTG	GTGTGGCCT	540
	ATATCCAGT	ATCTCTTTGC	TCAATCACAG	CTGTGACCCC	AACCTGTTCA	TTGTGTTCAA	600
	TGGGCCCCAC	CTCTTACTGC	GAGCAGTCCG	AGACATCGAG	GTGGGAGAGG	AGCTCACCAT	660
	CTGCTACCTG	GATATGCTGA	TGACCACTGA	GGAGCGCCGG	AAGCAGCTGA	GGGACCACTA	720
	CTGCTTTGAA	TGTACTGTTT	TCCGTTGCCA	AACCCAGGAC	AAGGATGCTG	ATATGCTAAC	780

5 TGGTGATGAG CAAGTATGGA AGGAAAGTTCA AGAATCCCTG AAAAAAATTG AAGAACTGAA 840
 GGCACACTGG AAGTGGGAGC AGGTTCTGGC CATGTGCCAG GCGATCATAA GCAGCAATTC 900
 TGAACGGCTT CCCGATATCA ACATCTACCA GCTGAAGGTG CTCGACTGCG CCATGGATGC 960
 CTGCATCAAC CTCGGCCTGT TGGAGGAAGC CTGTCTCTAT GGTACTCGGA CCATGGAGCC 1020
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 CAAACTGCAG CTACATCAAG GCATGTTTCC CCAAGCAATG AAGAATCTGA GACTGGCTTT 1140
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 TTTAGAGAA TGCAGGCCA ACATCAGAGC ATCCTAAGGG AACGCAGTCA GAGGGAATA 1260
 CGCGCTGTGT CTTTGTGGAA TGCCTTATTG AGGTACACA CTCTATGCTT TGTAGCTGT 1320
 10 GTGAACCTCT CTTATTGGAA ATTCTGTTC GTGTTTGTGT AGGTAAATA AGGCAGACAT 1380
 GGTTTGCAAA CCACAAGAAT CATTAGTTGT AGAGAAGCAC GATTATAATA AATTCAAAAC 1440
 ATTTGGTTGA GGATGCCAAA AAAAAAATA AAAAAA

Seq ID NO: 62 Protein sequence
 Protein Accession #: NP_073580

1 11 21 31 41 51
 20 MRCSQCRVAK YCSAKCKKKA WPDHKRECKC LKSCCKPRYPF DSVRLLRVV FKLMDGAPSE 60
 SEKLYSFYDL ESNINKLTED KKEGLRQLVM TFQHFMRBEI QDASQLPPAF DLFEAFKVI 120
 CNSFTICNAE MOEVLGGLYP SISLNLHSCD PNCIVFNFP HLLRAVRDI EVGEELTICY 180
 LDMLMTSEER RKQLRDQYCF ECDPCRCQQT DKADMLTGD EQVWKEVQES LKKIEELKAH 240
 WKNEQVLAMC QAIISNSER LPDINIYQLK VLDCAWDACI NLGLLEALF YGTRTMEPYR 300
 25 IFFPGSHPRV GVQVMKVGKL QLHQGMFPQA MKNLRLAFDI MRVTHGREHS LIEDLILLLE 360
 ECDANIRAS

Seq ID NO: 63 DNA sequence
 Nucleic Acid Accession #: NM_003014.2
 Coding sequence: 238..648

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 AAACCTCTCT GCGCCCGAGA AGATTTCTTC CTCGGGGAAG GGACAGCGAA AGATGAGGGT 180
 GGCAGGAAGA GAAGGCGCTT TCTGTCTGCC GGGGTGCGAG CGCGAGAGGG CAGTGCCATG 240
 TTCTCTCTCA TCCTAGTGGC GCTGTGCTCG TGGCTGCACC TGGCGCTGGG CGTGCCTGGC 300
 GCGCCTCTGC AGCGGCTGCG CATCCCTATG TCGCGGCACA TGCCCTGGAA CATCACGCGG 360
 40 ATGCCCAACC ACTTGCACCA CAGCAACGAG GAGAAACGCA TCCTGGCCAT CGAGCAGTAC 420
 GAGGAGCTGG TGGACGTGAA CTGCAGCGCC GTGCTGCGCT TCTTCTTCTG TGCCATGTAC 480
 GCGCCCATTT GCACCTCTGA GTTCTCTGCAC GACCCTATCA AGCCGTGCA GTGCGTGTGC 540
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 AGCCTGCGCT GCGACGAGCT GCCTGTCTAT GACCGTGGCG TGTGCAATTC GCCTGAAGCC 660
 45 ATCGTCAAGG ACCCTCCGGA GGATGTTAAG TGGATAGACA TCACACAGCA CATGATGGTA 720
 CAGGAAAGGC CTCCTGATGT TGAATGTAAG CGCTAAGCC CCGATCGGTG CAAGTGTAAA 780
 AAGGTGAAGC AACCTTTGGC AACGTATCTC AGCAAAACT ACAGCTATGT TATTCATGCC 840
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 GAGATCTTCA AGTCCTCATC ACCCATCCCT CGAAGTCAAG TCCCGCTCAT TACAATTTCT 960
 50 TCTTGGCCAG GTCCTGACAT CCTGCCCAT CAAGATGTTT TCATCATGTG TTAGAGAGTG 1020
 CGTTCAAGGA TGATGCTTCT TGAATAATTG TTAGTTGAAA AATGGAGAGA TCAGCTTAGT 1080
 AAAAGATCCA TACAGTGGGA AGAGAGGCTG CAGGAACAGC GGAGAACAGT TCAGGACAG 1140
 AAGAAACAG CCGGGGCGAC CAGTCGTAGT AATCCCCCA AACCAAGGG AAAGCCTCCT 1200
 GCTCCCAAC CAGCCAGTCC CAAGAAGAAC ATTAATACTA GGAGTGCCCA GAAGAGAACA 1260
 55 AACCCGAAAA GAGGTGAGC TAACTAGTTT CCAAGCGGGA GACTTCGAG TCCCTTACAG 1320
 GATGAGGCTG GGCATGCTCT GGGACAGCCT ATGTAGGCC ATGTGCCCT TGCCCTAACA 1380
 ACTCACTGCA GTGCTCTTCA TAGACATC TTGCAGCAT TTTCTTAAG CTATGCTTCA 1440
 GTTTTTCTTT GTAAGCCATC ACAGCCATA GTGGTAGGTT TGCCCTTTGG TACAGAAGGT 1500
 GAGTTAAAGC TGGTGGAAAA GGCTTATGTC ATTGCATTCA GAGTAACCTG TGTGCATACT 1560
 60 CTAGAAGAGT AGGGAATAATA ATGCTTGTTA CAATTGAGC TAATATGTGC ATTGTAAAA 1620
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 TATCTGTGTG TGCAATGTTA GTGATGTTT AAAATGTGAT GAAATATAA TGTTTTTAAG 1740
 AAGGAACAGT AGTGGAAATG ATGTTAAAA ATCTTTATGT GTTTATGGTC TGCAGAAGGA 1800
 TTTTGTGAT GAAAGGGGAT TTTTGAATA ATTAGAGAAG TAGCATATGG AAAATTATAA 1860
 65 TGTGTTTTTT TACCAATGAC TTCAGTTTCT GTTTTATGCT AGAACTTAA AAACAAAAAT 1920
 AATAATAAAG AAAATAAAT AAAAAGGAGA GGCAGACAT GTCTGGATTC CTGTTTTTTG 1980
 GTTACCTGAT TTCCATGATC ATGATGCTTC TTGTCAACAC CCTCTTAAGC AGCACAGAA 2040
 ACAGTGAGTT TGCTGTGACC ATTAGGAGTT AGGTACTAAT TAGTTGGCTA ATGCTCAAGT 2100
 ATTTTATACC CACAAGAGAG GTATGTCATC CATCTTACTT CCCAGGACAT CCACCTGAG 2160
 70 AATAATTGGA CAAGCTTAAA AATGGCCTTC ATGTGAGTGC CAATTTTGT TTTTCTTCAT 2220
 TTAATATATT TCTTTGCTTA AATACATGTG AGAGGAGTTA AATATAAATG TACAGAGAGG 2280
 AAGTTGAGT TCCACTCTG AAATGAGAAT TACTTGACAG TTGGGATACT TTAATCAGAA 2340
 AAAAAGAACT TATTTGCAGC ATTTTATCAA CAAATTTTAT AATTGTGGAC AATTGGAGGC 2400
 ATTTATTTTA AAAACCAATT TTATTGGCCT TTTGCTAACA CAGTAAGCAT GTATTTTATA 2460
 75 AGGCATTCAA TAAATGCACA ACGCCCAAG GAAATAAAAT CCTATCTAAT CCTACTCTCC 2520
 ACTACACAGA GGTAACTCAT ATTAGTATTT TGGCATATTA TTCTCCAGGT GTTTGCTTAT 2580
 GCACCTATAA AATGATTGTA ACAATAAATA CTAGGAACCT GTATACATGT GTTTCATAAC 2640
 CTGCTCTCTT TGCTTGGCCC TTTATTGAGA TAAGTTTTC TGTCAAGAAA GCAGAAACCA 2700
 TCTCATTTCT AACAGCTGTG TTATATTCCA TAGTATGCAT TACTCAACAA ACTGTTGTGC 2760
 80 TATTGGATAC TTAGGTGGTT TCTTCACTGA CAATCTGAA TAAACATCTC ACCGGAATTC

Seq ID NO: 64 Protein sequence
 Protein Accession #: NP_003005.1

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YELVDVNCNS	AVLRFFFCAM	YAPICTLEFL	HDPIKPKCKSV	CQRARDCEP	LMKMYNHSWP	120
ESLACDELPU	YDRGVCSISPE	AIUTDLPEDEV	KWIDITPDM	VQERPLDVDC	KRLSPDRCKC	180
KKVKPTLATY	LSKNYSYVIH	AKIKAVQRSQ	CNEVTTVVDV	KEIFKSSSPI	PRIQVPLITN	240
SSCQCPHILP	HQDVLIMCYE	WRSRMMLLEN	CLVEKWRDQL	SKRSIQWEER	LQEQRRTVQD	300
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Seq ID NO: 65 DNA sequence

Nucleic Acid Accession #: BC010423

Coding sequence: 248..1780

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AGCTACGGCT	GGGTGTGTAG	AACGGGGCCG	GGGCTGGGGC	TGGGTCCCCT	AGTGGAGACC	120
CAAGTGCAGG	AGGCAAGAAC	TCTGCAGCTT	CCTGCCTTCT	GGGTGAGTTC	CTTATTCAAG	180
TCTGCAGCCG	GCTCCAGGGG	AGATCTCGGT	GGAACTTCAG	AAACGCTGGG	CAGTCTGCCT	240
TTCAACCATG	CCCTGTCTCC	TGGGAGCCGA	GATGTGGGGG	CCTGAGGCCCT	GGCTGCTGCT	300
GCTGCTAGCT	CTGGCATCAT	TTACAGGCCG	GTGCCCCCGG	GGTGAGCTGG	AGACCTCAGA	360
CGTGGTAACT	GTGGTGTCTG	GCCAGGACGC	AAACTGCCCC	TGCTTCTACC	GAGGGGACTC	420
CGGCGAGCAA	TGGGGGCAAG	TGGCATGGGC	TGGGTGGGAC	GCGGGCGAAG	GCGCCCAGGA	480
ACTAGCGCTA	CTGCACTCCA	AATACGGGCT	TCACTGTGAGC	CCGGCTTACG	AGGGCCGGGT	540
GGAGCAGCCG	CGGCCCCAC	GCAACCCCTC	GGACGGCTCA	GTGCTCCTGC	GCAACGCGAGT	600
GCAGGCGGAT	GAGGCGAGT	ACGAGTGCCG	GGTCAGCACC	TTCCCGCCCG	GCAGCTTCCA	660
GGCGCGGCTG	CGGCTCCGAG	TGCTGGTGCC	TCCCTGCCCC	TCACCTGAATC	CTGCTCCAGC	720
ACTAGAAGAG	GGCCAGGGCC	TGACCCCTGGC	AGCCTCCTGC	ACAGCTGAGG	GCAGCCCAGC	780
CCCCAGCGTG	ACCTGGGACA	CGGAGGTCAA	AGGCACAACG	TCCAGCCGTT	CCTTCAAGCA	840
CTCCCGCTCT	GCTGCCGTC	CCTCAGAGTT	CCACTTGGTG	CCTAGCCGCA	GCATGAATGG	900
GCAGGCACTG	ACTTGTGTGG	TGTCCCATCC	TGGCCTGCTC	CAGGACCAAA	GGATCACCCA	960
CATCTCCAC	GTGTCTCTCC	TGCTGTGAGC	CTCTGTGAGG	GGCCTTGAAG	ACCAAAATCT	1020
GTGGCACATT	GGCAGAGAAG	GAGCTATGCT	CAAGTGCTTG	AGTGAAGGGC	AGCCCCCTCC	1080
CTCATACAAC	TGGACACGGC	TGGATGGGCC	TCTGCCCACT	GGGGTACGAG	TGGATGGGGA	1140
CACTTTGGGC	TTTCCCCAC	TGACCACTGA	GCACAGCGGC	ATCTACGCTC	GCCATGTGAG	1200
CAATGAGTTC	TCCTCAAGGG	ATTCTCAGGT	CACTGTGGAT	GTTCTTGACC	CCCAGGAAGA	1260
CTCTGGGAAG	CAGGTGGACC	TAGTGTGAGC	CTCGGTGGTG	GTGGTGGGTG	TGATCGCCGC	1320
ACTCTTGTCT	TGCTTCTGCG	TGGTGGTGGT	GGTGCTCATG	TCCCGATACC	ATCGGCGCAA	1380
GGCCAGCAG	ATGACCCAGA	AATATGAGGA	GGAGCTGACC	CTGACCAAGG	AGAACTCCAT	1440
CGGAGGGCTG	CATTCCCATC	ACACGGACCC	CAGGAGCCAG	CCGAGGAGGA	GTGTAGGGCT	1500
GAGAGCCGAG	GGCCACCCCTG	ATAGTCTCAA	GGACAACAGT	AGCTGCTCTG	TGATGAGTGA	1560
AGAGCCCGAG	GGCCCGAGTT	ACTCCACGCT	GACCAAGGTG	AGGAGATAG	AAACACAGAC	1620
TGAAGTGTCT	TCTCCAGGCT	CTGGGCGGGC	CGAGGAGGAG	GAAGATCAGG	ATGAGGCGAT	1680
CAAAACAGCC	ATGAACCAAT	TTGTTTCAAG	GAATGGGACC	CTACGGGCCA	AGCCACAGGG	1740
CAATGGCATC	TTCATCAATG	GGCGGGGACA	CCTGGTCTGA	CCAGGCGCTG	CCTCCCTTCC	1800
CTAGGCGCTG	CTCTCTCTGT	TGACATGGGA	GATTTTAGCT	CATCTTGGGG	GGCTCCCTTA	1860
ACACCCCAT	TTCTTGCGGA	AGATGCTCCC	CATCCCACTG	ACTGCTTGAC	CTTTACTCTC	1920
AACCTTCTCT	TTTCATCGGA	GGGCTCCACC	AATTGAGTCT	CTCCCACTAT	GCATGCGAGT	1980
CACCTGTGTG	GTGATGTGTG	GCCTGTGTGA	GTGTGACTG	ACTGTGTGTG	TGTGGAGGGG	2040
TGACTGTCCG	TGGAGGGGTG	ACTGTGTCCG	TGGTGTGTAT	TATGCTGTCA	TATCAGAGTC	2100
AAGTGAACCT	TGGTGTATGT	GCCACGGGAT	TTGAGTGGTT	GCGTGGGCAA	CACCTGTCAGG	2160
GTTTGGCGTG	TGTGTCTATG	GGCTGTGTGT	GACCTCTGCC	TGAAAAGCA	GGTATTCTCT	2220
CAGACCCAG	AGCAGTATTA	ATGATGCAGA	GGTTGGAGGA	GAGAGGTGGA	GACTGTGGCT	2280
CAGACCCAGG	TGTGCGGGCA	TAGCTGGAGC	TGGAATCTGC	CTCGGTGTG	AGGGAACTCT	2340
TCTCTACCA	CTTCCGAGCC	ATGGGGGCAA	GTGTGAAGCA	GCCAGTCCCT	GGGTGAGCCA	2400
GAGGCTTGAA	CTGTATACAG	AGCCCTCTGC	CCTCTGGTGG	CCTCTGGGCC	TGCTGCATGT	2460
ACATATTTTC	TGTAAATATA	CATGCGCGG	GAGCTTCTTG	CAGGAATACT	GCTCCGAATC	2520
ACTTTTAAAT	TTTTTCTTTT	TTTTTCTTTG	CCCTTTCCAT	TAGTGTGATT	TTTTATTAT	2580
TTTATTTT	ATTTTCTTTT	AGAGTTTGAG	TCCAGCCTGG	ACGATATAGC	CAGACCTCTG	2640
CTGTAAAAAA	ACCAGAAACC	AAAAAAAAAA	AAAAAAAAAA			

Seq ID NO: 66 Protein sequence

Protein Accession #: AAH10423

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QVQGVAMARV	DAGEGAQELA	LLHSKYGLHV	SPAYEGRVEQ	PPPPRNPLDG	SVLLRNAVQA	120
DEGEYECRVS	TFPAGSFQAR	LRLRVLPPL	PSLNPGPALE	EQGLTLAAS	CTAEGSPAPS	180
VTWDTVEVKT	TSSRSFKHSR	SAAVTSEFHL	VPSRSMNGQP	LTCVVSHEGL	LQDQRITHIL	240
HVSFLAEASV	RGLEDQNLWH	IGREGAMLC	LSEGGPPPSY	NWTRLDGFLP	SGVRVDGDTL	300
GFPPLTERIS	GIYVCHVSNE	FSSRDSQVTV	DVLDPQEDSG	KQVDLVASVS	VVVGVIAALL	360
FCLLVVVVVL	MSRYHRRKAQ	QMTQKYEEEL	TLTRENSIRR	LHSHHTDPRS	QPEESVGLRA	420
EGHPDLSKDN	SSCSVMSEEP	EGRSYSTLT	VREIETQTEL	LSPGSGRAEE	EEDQDEGIKQ	480
AMNHFPQENG	TLRAKPTGNG	IYINGRHLV				

Seq ID NO: 67 DNA sequence

Nucleic Acid Accession #: NM_001203

Coding sequence: 274..1782

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GTGAAGAGAA	AGGAAGATCA	TTTCATGCCT	TGTTGATAAA	GGTTCAGACT	TCTGCTGATT	180

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CATAACCAATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTACAAGCC 240
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AATGTGGGCA CCAAGAAAGA GGATGGTGGAG AGTACAGCCC CCACCCCCCG TCCAAAGGTC 360
TTGGGTGTGA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
GACGGATATT GTTTCACGAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
GGTTGCCTAG GACTAGAAGG CTCAGATTCT CAGTGTGGG ACACTCCCAT TCCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCCTACA 600
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ATATCTGTGA CTGTCTGTAG TTTGCTCTTG GTCCTTATCA TATTATTTTG TTACTTCCGG 720
TATAAAGAC AAGAAACAG ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
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CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
TAAGCATCCA CAGTAAAGC CTTGAACATC GTCTGCTTC CCACTGGGTT CAGACCTCAC 1920
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Seq ID NO: 68 Protein sequence

Protein Accession #: NP_001194

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GPIHHRALLI SVTVCSLLLV LIILFCYERY KRQSTRPRYS IGLQDETYI PPGESLRDLI 180
EQSQSSSGS GLPLLVQRTI AKQIQMVQKI GKGRYGEVVM GKWGRGEKVAV KVFFTTEAS 240
WFRTEIYQT VIMRHENILG FIAADIKGTG SWTQLYLITD YHENGSLYDY LKSTLLDAKS 300
MLKLYSSVS GLCHLHTEIF STQKPAIAH RDLKSNILV KKNGTCCIID LGLAVKFISD 360
TNEVDIPNT RVGTRKYMPP EVLDESILNRN HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
EEYQLFYHLD VPSDPSYEDM REIVCIKILR PSPFNWSSD ECLRQMGKLM TECWAHPAS 480
RLTALRVKKT LAKMSSESQDI KL

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Seq ID NO: 69 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 166..1737

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TCCTCCACCC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180
TTAAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
CGGTAGCTGT TTTCAATTTT CTTGCTGAA GTCTTCACTC ACGGCATCAT CAAGACATTT 300
GGTGCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
ATAATCTCAA TCTGTGTGTT TGTCTTAACT TTTTCAGCTC CCTCGCCAC AGTCTGTGAG 420
AATCGTTTCC GACACGCTCT GGTAGTGATG TTGGGGGGGC TACTTGTGAG CACCGGGATG 480
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GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAAACA TCCTATCACA ATATTTTGGC 600
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 Protein Accession #: Eos sequence

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 Coding sequence: 256..3012

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 Protein Accession #: NP_071414

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HQRHLDATNS TAGYSIYGVG SMSRYEQVLH HIRYRNWRPA SLEARRFRK CSELNGRYTS 780
NEFNLEVSIL HEDQVSDKEH VNHLIVQPPF LQSVHHPESR SSIQHSSVVP SIATVVIIIS 840
VCMLEFVIVAM GUYRVRIAQ HFQIETEAAK ESEMWDWDSA LTITVNPMEK HEGPGHGEDE 900
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Seq ID NO: 77 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 482..3007

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TGCATTGCA AGCTTGCAAA TGGTTAACTA TATGCAAAAA AGTCAGCATA GCTGTGAAGT 180
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CTTTATGAAG CTATGGGACT TGACAAAAAG TGATATTTGA GAAGAAAGTA CGCAGTGGTT 360
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ATTACAGATA ACGTCAGGAA GAGTCTCTGC TTTACAGAA TCGATTTCTT CACATGACAA 480
CATGAAGCTG TGGATTCTAT TCTTTTATTC ATCTCTCCTT GCCTGTATAT CTTTACACTC 540
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CACGTCCATT CTAAAACTAC CCACCAAGC ACCAGGTTTG ATACCTTATA TTACAAAGCC 1440
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Seq ID NO: 78 Protein sequence

Protein Accession #: Eos sequence

1 11 21 31 41 51
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MKLWIHLFYS SLLACISLHS QTPVLSSRG CDSLNCNEEK DGTMLINCEA KGIKRVSEIS 60
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HNSLEILKBD TFHGLENLFP LQADNNFTV IEPSAPSKLN RLKVLILNDN AIESLPPNIF 180
RFVPLTHLBD RGNQLQTLFY VGFLEHIGRI LDQLLEDNKW ACNCDLLQLK TWLENNPQS 240
IIGDVVCNSP PFFKGSILSR LKJESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT 300
TSILKLPFKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHQER NIESLSDLRP 360

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GVPLTKVNLK TNQFTHLPVS NILDDLDDLT QIDLEDNPDW CSCDLVGLQQ WIKLSKNTV 540
TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTPATT TNTADTILRS 600
LTDVAPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM 660
YGHKTTHTTT ERPSASLYEQ HMVSPMVHVY RSPSPGPKHL EEEEEERNEKE GSDAKHLQRS 720
LLEQENRSLP TGSNMKYKTT NQSTFLSFQ DASSLYRNIL EKERELQLQG ITEYLRIKRIA 780
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Seq ID NO: 79 DNA sequence
Nucleic Acid Accession #: NM_016640.2
Coding sequence: 39..1358

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CGACGGTGCA CGCTCGCGAG TCGGTAGACG AGAAGCTGCG AATCCTCACC AAGATGCAGT 300
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ACTTCACCAA GACCGTGTTC CTGTGCGGTC TGCCGCGGCC CCCAGCGGAG CCCGAGCCCG 420
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AGAGCGAGGT CATATCTTTG CCCTTCTGCG ATCAGCTGGT GTCAACCTCC GTGGGCTCTC 600
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TTTACTGGGT GCGTGGTGAA GAAATTATTC CTGCTGGTCA TCGAAGAGGT CGAATTGATG 720
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Seq ID NO: 80 Protein sequence
Protein Accession #: NP_057724.1

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PPAEPEPEPE PEPEPALDLA ALRAVACDCL LQEHFYLRRR RRVHRYESE VISLFFLDQL 180
VSTLVGLLSP HNPALAAAL DYRCVPVHYW VRGEIIPRG HRRGRIDDLR YQIDDKPNQ 240
IRISKQLAEF VPLDYSVPIE IPTIKCKPKD LPLFKRQYEN HIFVGSKTAD PCCYGHQTQFH 300
LLPDKLRRER LLRQNCADQI EVVFRANAIA SLFAWTGAQA MYQGFWEAD VTRPFVSEQAV 360
ITDGKYFFSF CYQNLTLALT TQADQNNPRK NICWGTQSKP LYETIEDNDV KGFNDVDLLQ 420
IVHFLNRPK BEKSQLEN

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Seq ID NO: 81 DNA sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1..2070

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GGGCTTGAGG TCATTGACAG GCGCAGGTG GCCACAGGT GCTCCCCAGA CCTCCCTCCT 600
CCAAGTAGAG CTGAAATGGG AAGGAACCCC TGGGACAGCC CTGCGCTGC TAGATCTTTG 660
CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTCTAC 720
ATGCTGGGGG CCGAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
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CTGTTCTGGG CAAAGTGTGG CCAAGTCCG CAGCCCCAGC CCTGCAGTGC TGGGAGCGCT 1140
GACAGGACAC GGGGAAGAGG CRTGCTTTCC CTCGGGACCT GCTGTTCAT GTGTCCCAAG 1200
CCCTCCTGCT TTCCAGATGG CCCTCAGGA AACCACTTT CCAGGGCTTC TGCTCCCTTG 1260
GGCGCTCGCT GGGTCTGCAT CAACGGAGTG TGGTAGAGC CGGAGGACC CAGCCCTGCC 1320

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5 AGGCTGAAGG AGGGCTCCTC ACGGACACAC AGGCCAGGAG GCAAGCGTGG GCGTCTTGCG 1380
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 TCCTTCAACA AGCAAGATTC AAAAGCTGAC GTCTCCGAGA AGGCGGACCT GGAAGAGGAG 1560
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 10 ACCCAAGAGC TCGGCACCT CAAGTCCCTC CTGGAAGGGA GCCAGAGGCC CCAGGCAGCC 1860
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 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCGG AGCGTGCCAT CCTGCCCGCA 1980
 CTGAAGCAGA CCCCAGAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCAATGCAG 2040
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15 Seq ID NO: 82 Protein sequence
 Protein Accession #: FGENESH predicted

20 1 11 21 31 41 51
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 QQQHSEMLAK LHEEIEHLKR ENKGEFARGP RPALPPQAHS TLPPLPQHRNT AINSSTRILGS 120
 GGTQDGEPLQ TVLAHLAALA PVCQPSGYRF WGTWTDAA TS SRGWTMLCSQ AQHVLSSGSP 180
 GPEVIAGRWV ATGCSFDLPP PSRAEMGRNP WDSFPCPARSL PQIAAVARPR ISSPMALSPH 240
 25 MLGAQGIQTH SIQGSPLPIW AATMGTKGGS RVLFPCHLSK ALPHPDSEPH PAQDPGLWSQ 300
 AHFPLSLGLG LTSGGHLTGG WSQPGNLAAG AVPRALPSQG DMEKGVGGP FPSRCGNSSE 360
 LFWAKCGPSR QPQPCSGADA DRTREBAMLS LGTCCSMCPK PSCFPDGPSP NHLRSASAPL 420
 GARWVCINGV WVEPGGPSPA RLKEGSSRTH RPKGKRGLA GGSADTVRSP ADSLSMSSPQ 480
 SVKSISSNAN SQMKARPOPG SFNKQDSKAD VSQKADLEES PLLHNSKLDK VFGVQGGARK 540
 EKAEBASNAG ACMGNSQHQG RQMGAGAHFP MILPLPLRKP TTLRQCEVLI RELWNTNLLQ 600
 30 TQELRHLKSL LEGSQRPPQA PEEASFPRDQ EATHFPKYST KSLSKKCLSP PVAERAILPA 660
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35 Seq ID NO: 83 DNA sequence
 Nucleic Acid Accession #: NM_005264.1
 Coding sequence: 557..1954

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 75 AAGAAAGCTT CTTGTGATCC TTGGGGCTT CTGTGAAAAA CCTGATGCAG TGCTCCATCC 2160
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Seq ID NO: 84 Protein sequence
 Protein Accession #: NM_005264.1

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YEPVNSRLSD IFRVVPFISD VFQQVEHIPK GNNCLDAKA CNLDDICKY RSAYITPCTT 180
SVSNDVNCRR KCHKALRQFF DKVPAKHSYG MLFPCSRDIA CTERRRQTIIV PUCSYEEREK 240
PNCLNLQDSC KTNVICRSRL ADFFTNCPQE SRSVSCLKE NYADCLLAYS GLIGTVMTPN 300
YIDSSLSVA PWDCSNSGN DLEELKFLN FFKDNTCLKN AIQAFNGSD VTVWQPAFPV 360
10 QTTTATTTTA LRKVNKPLGP AGSENEIPTH VLPPCANLQA QKLKSNVSGN THLCISNGNY 420
EKEGLGASH ITTKSMAAPP SCGLSPLLV L VVTALSTLLS LTETS

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Seq ID NO: 85 DNA sequence

Nucleic Acid Accession #: XM_027172.1

Coding sequence: 143..1405

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TGAGAGCAGC CTCATGAGG CCTGGACCA GTGCATGACC GCCCTGGACC TCTTCTCTAC 240
CAACCACTTC TCAGAGCACA TCAGCTACCT CAAGCCCAAGA ACCAAGGAAA GCATGTATCCA 300
CTCACTGACA TATGCCACCA TCCTGGAGAT GCAGGCCATG ATGACCTTTG ACCCTCAGGA 360
25 CATCTCTGCT GCGGCAACA TGATGAAGGA GGCACAGATG CTGTGTGAGA GGCACCGGAG 420
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CCTGACCTTC CTGCAAGGTT CCTCACAGG AGGGGCGATC AGGCCACAGG CCTTGCATGA 600
TCCCTCTCAC GCTCGCAGCT GCCCACTGG GCCAGGCCGT CAGCATCTTT TCCCTCTGCA 660
30 GACACGAGAC ATGGTGAGCT TCATCAAAGG CGGCATCAA GTTCGAAACA GCTACCAAGAC 720
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CCTGTTCTTT GCAGGGAGGA TTGAAGTCAT TAAAGGCAAC ATTGATGCAG TGAGTGATGG 1140
GGGTCCGGGC CGGGGCTGGG GATCCCTCGG GGTCTCCAG ACCAGCAGGA AGTCAGGCAC 1200
40 ATGTGACATA CTCAGGGACA GATAGACTG GGGCGGGGGG GGGGGCCAAG AGAGAACCAA 1260
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40 ATGATGTACA TCTGGAACGG CTACGCGGTG ATTGGGAAGC AGCCGAAACT CAOGGATGGG 1320
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45 GACAGAAACG AAGAGGCCAT CAAACTTTTG GAATCTGCCA AGCAAAACTA CAAGAATTAC 1620
    TCCATGGAGT CAAGGACACA CTTTCGAATC CAGGCAGCCA CACTCCAAGC CAAGTCTTCC 1680
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    CCGGGCTGGA AGACAGAGAC AGCTGGACAG AGCTCTTGAA AACATTTCAA AATACCCCTC 1800
    CCCCCTGCCG GGCCTGTACT TTGGGGTCCA CCGGCACTCC AGTTGGATGG CACAACATAG 1860
50 TGTATCCGTG CAGAAGCCGA GCTGSCATTT TCACCACTGT AGCCAGGGGC CTTTGCCAA 1920
    GGCAGAGCAG GTGGAGCCCT CTGCTGCCCC TATCACACAT ACGGCTACTT GCTTTTCACT 1980
    GTGATGTTTA AGAGAAATGA TGAACAGTTT ACATTTTCTT TAGAAATACA TTGATGGGAT 2040
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    CCACTACCTT ACTACTCACA CTTCAATTTC CTCCTTTTGT AAATTTCCAA TTTAAAAATC 2340
    AAGCACGCTT TTTTAGTGAG ATAAATCTG AGCTCTTCTG TAGAAAAATC AATCTCTACC 2400
    AGTAGAAAT GCCAGGGCTT GATGGAAGAG CTGTGTAGCC CTTTCTATGC CAAAGCCAGG 2460
60 AAATTTGGGG GGCAGGAGGA GGTCTCAGA ATCCAGTCTG TATCTTTGCT GTATGCCAAA 2520
    CTGAAACCACT TGGGAATAAT TTATGAAACA TAAAAATCT CTGTACTTCA CTCCAAGTGA 2580
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Seq ID NO: 90 Protein sequence

Protein Accession #: AAC39582.1

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1      11      21      31      41      51
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    EVCYAECLIQ RAALTFLQDE NMVSVFIKGI KVRNSYQTYK ELDSLVSQSSQ YCKGENHPHF 180
    EGGVKLGVA G FNTLSMLPT RILRLLEFVG FSGNKDYGLL QLEEGASGHS PRSLVLCVML 240
    LCYHTFLTFF LGTGNVNIIE AEKLLKPYLN RYPKGAIFLF FAGRIEVIK NIDAAIRFE 300
75 ECCEAQQHWK QPHMCMYEL MWCFYKQW KMSYFYADLL SKENCWSKAT YIYMAAYLS 360
    MFGKEDHKFP GDDEVELFRA VPGLKLIAG KSLPTEKFAI RKSRRYPSSN PISLPVPALE 420
    MMYIWNQYAV IGKQPKLTDG ILEIITKAE MLEKGPENEY SVDDECLVKL LKGLCLKYLG 480
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80 SMESRTHFRI QAATLQAKSS LENSRSRMVS SVSL

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Seq ID NO: 91 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 31..906

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 10 TCGTTTCTCA ATGGCTGGC CAGCCTGGTG ATGCTCTGCC GCTACCGCAC CTTGGTGCCA 420
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Seq ID NO: 92 Protein sequence
 Protein Accession #: Eos sequence

50 1 11 21 31 41 51
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 55 MLCRVRTFVP AASPMYHTCV AFAWVSLNAN FWSTVFHTRD TDLTERMDYF CASTVILHSI 180
 YLCCVRYTGL QHPAVVSAFR ALLLLMLTVH VSYLSLIRFD YGNLVANVA IGLNVVWNL 240
 AWCLNQRRL PHVRKCVVVV LLLQGLSLE LLDFFPLFWV LDAHAIWHIS TIPVHVLFFS 300
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Seq ID NO: 93 DNA sequence
 Nucleic Acid Accession #: NM_033419.1
 Coding sequence: 18..980

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 70 TCTACATGAG TCTAGCAGG TGGAACCTGC GGGACGACTG TAAGTATGAG TGTATGTGGG 240
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 75 TTTTCCACAC CAGGGACACT GACCTCACAG AGAAAATGGA CTACTTCTGT GCCTCCACTG 540
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 80 AGTGGTGGT GGTGGCTGTC CTGCTGAGG GGTGCTCCCT GCTGAGCTG CTTGACTTCC 840
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 15 GTCCACCATCA ATAATCACTT GTGGAGCGCC AGCTCTGCCC AAGGCGCCAC CTGGCGGCAG 1980
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Seq ID NO: 94 Protein sequence
 Protein Accession #: NP_219487.1

1 11 21 31 41 51
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 35 LWPAKVHGDG PHGILRDQAA GIGKEFHFDH CPSQVPRRPH HTFFQGGSS KPRARILCCC 180
 LVESLPFCVG SVGQAEICID RAVSMGLGVC ELRPRCAVWR RVLSGKRCGF KVCVCRGWVC

Seq ID NO: 95 DNA sequence
 Nucleic Acid Accession #: XM_090469
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1 11 21 31 41 51
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 45 TGCGCGGTGC TGGACAGGAG GCAGGTGAAC AAGCCCTGCC TGCTGGAGGC TGCCAGCAC 120
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 CCACCTGAAG TGAATATGTT TGGAGCCAGT CAAGGTTTGC TGACAAATGA AACAAACCAG 240
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 50 ATGTCTCTTC CTGGAAGTGT CAGTGTCTGAT GCTGGCCAGG TGGAGCACAG AAGACAAATG 360
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 55 CTCAGCGGCA GCGCGCGCC GTCCCAAGT ACACCCATGG CGCCCTTCCC GACCTCTGAC 660
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 60 CTGCATCAAG AATCACCAGG TTCAATTCCA ATAGGTTTAT GTAACAGAAC AGCTGAACCA 900
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Seq ID NO: 96 Protein sequence
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1 11 21 31 41 51
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 70 NSADTDWTE EGPGLDFAV AAHQEDTFPL KDIKHTSTPR QSVQQNCIY SPREKPCGNV 180
 RAPCAPPRRE APLALSRPWR LSRSPAPSPR TPMAPPFTSD RELDAPGPPP GLRSSAAAPH 240
 CLPAAPPAQK LPFLFLPYFD GSPPPKDILQ TLQHKAPGKR LHQESPGSFP IGLCNRTAEP 300
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	GCTGATGAAG	TTGTCACTGC	CTCTGTTCCG	AGTGGGGACC	TCTGGATCCC	AGTGAAGAGC	480
5	TTGCACTCCA	AGAATCATCC	AGAAGTGCTG	AATATTGCAC	TACAAACGGG	AAGCAAAGAA	540
	CTGATCATAA	ATCTGGAAAG	AAATGAAGGT	CTCATTGCCA	GCAGTTTCAC	GGAAACCCAC	600
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	TCTGGTCTCA	GGGGACTTAT	TGTGTTTGAA	AATGAAAGCT	ATGCTTTAGA	ACCAATGAAA	780
10	AGTGCAACCA	ACAGATCATC	ACTCTTCCCA	GCGAAGAAGC	TGAAAAGCGT	CCGGGGATCA	840
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	CAGCGATTAA	TAGAGATTGC	TAATCAGGTT	GACAAGTTTT	ACAGACCACT	GAACATTGGG	1080
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30	TATGGCAACT	CTGGAAGAGT	CTCGAAGAGT	TCTTTTGCCA	AATGCGAGAT	GAGAGATGCT	2040
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	GTTTCCATAG	AAACAACTAG	CCCCCTGCAG	CAAGGAGGCC	GGATTCTGTG	CCGGGGGACC	2160
	CACGTGTACT	TGGGCGATGA	CATGCCGAGC	CCAGGGCTTG	TGCTTGCAGG	CACAAAGTGT	2220
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35	GAGTGTGCAA	CTGAGTGCCA	CGGCAGAGGG	GTGTGCAACA	ACAGGAAGAA	CTGCCACTGC	2340
	GAGGCCCACT	GGGCACCTCC	CTTCTGTGAC	AAGTTTGCTT	TTGGAGGAAG	CACAGACAGC	2400
	GGCCCATCTC	GGCAAGCAGA	TAAACCAAGT	TTAACCATAG	GAATTCTGGT	GACCATCTCT	2460
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40	CTGGCTTCC	AACCTGTGCA	GGCTCACCTC	GGCCACCTTG	GAAAAGGCTT	GATGAGGAAG	2640
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45	CCTGCAGATC	CTCTGGCCAG	AACAACCTCG	CTCACTCATG	CCTTGGCCAG	GACCCAGGAA	2940
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50	CGTGTGCTCT	GCTATGGTGC	TCTGTCTACT	TGCACAGGTA	CTGTAAATTT	ATTAATTTAT	3240
	GCAGAAATGT	GATTACAGTG	CAGTGCCTGT	TAGTAGGCAT	TTTTACCATC	ACTGAGTTTT	3300
	CCATGGCAGG	AAGGCTTGTG	GTGCTTTTAG	TATTTTAGTG	AACTTGAAAT	ATCCTGCTTG	3360
	ATGGGATTTCT	GGACAGGATG	TGTTTGCTTT	CTGATCAAGG	CCTTATTGGA	AAGCAGTCCC	3420
	CCAACCTACC	CCAGCTGTGC	TTATGGTACC	AGATGCAAGT	CAAGAGATCC	CAAGTAGAAT	3480
55	CTCAGTTGAT	TTTCTGGATT	CCCCATCTCA	GGCCAGAGCC	AAGGGGCTTC	AGGTCCAGGC	3540
	TGTGTTTGGC	TTTCTAGGAG	GGCCTGTGCC	CCTTGACAAC	TGGCAGGCAG	GCTCCACGGG	3600
	ACACCTGGGA	GAATCTGCG	TTCTGGCCAG	GAAGCTTTGG	TGAGAACCTG	GGTTGCAGAC	3660
	AGGAATCTTA	AGGTGTAGCC	ACACCAGGAT	AGAGACTGGA	ACACTAGACA	AGCCAGAACT	3720
	TGACCTCTGAG	CTGACAGGCC	GTGAGCATGT	TGGAAGGGG	TCTGTAGTGT	CACTCAAGGC	3780
60	GGTGTCTGAT	AGAAATGCCA	AGCACTTCTT	TTTCTGCTG	TCCTTTCTAG	AGCACTGCCA	3840
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	CTGCAAAACG	CCACCTCCCT	ATACTGCTTG	GAGCTGAGCA	AATCAACACA	AACGTGAATA	3960
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	TGAACCATTA	ACCAGATCTA	GTCAATCAAG	TCTGTTTACT	GCAAGGTTC	ACTTATTAA	4080
65	AATTAGGCAG	ACTCTTTATG	CTTGCAAAAA	CTACAACCAA	TGGAATGTGA	TTTTCATGGG	4140
	TATAGTTCTAT	GTCTGTATCT	ATTATTCTGA	GATATTGGAC	AAAGAACCTT	CTCTATGGGG	4200
	CATCCTCTTT	TTCCAACTTG	GCTGCAGGAA	TCTTTAAAAG	ATGCTTTTAA	CAGAGTCTGA	4260
	ACCTATTCTT	TAAACACTTG	CAACCTACCT	GTTGAGCATC	ACAGAAATGT	ATAAGGAAAT	4320
	CAACTTGCTT	ATCAACTTCC	TAAATATTAT	GAGATGTGGC	TTGGGCAGCA	TCCCTTGAA	4380
70	CTCTTCACTC	TTCAAAATGCC	TGACTAGGGA	GCCATGTTTC	ACAAGGTCTT	TAAAGTGACT	4440
	AATGGCATGA	GAATACAA	AATACTCAGA	TAAGGTAAAA	TGCCATGATG	CCTCTGTCTT	4500
	CTGGAGCTGG	TTTCACTTA	GAAGACAATT	GACAAAGTT	ACATAATTCA	CTCTGAGTGT	4560
	TTTATGAGAA	AGCCTTCTTT	TGGGGTCAAC	AGTTTCTCTA	TGCTTTGAAA	CAGAAAAATA	4620
	TGTACCAAGA	ATCTTGGTTT	GCCTTCCAGA	AAACAAAAC	GCATTTCAC	TTCCCGGTGT	4680
75	TCCCACTGAT	ATCTAGGCCA	CATAGTATTC	ATGACTATGG	ATAAACTAAA	CACGTGACAC	4740
	AAACACACAC	AAAGGGGAAC	CCAGCTCTAA	TACATTCCAA	CTCGTATAGC	ATGCATCTGT	4800
	TTATTCTATA	GTTATTAAAT	TCTTTAAAT	GTAAGCCAT	GCTGGAAAT	AATACTGCTG	4860
	AGATACATAC	AGAAATTACTG	TAACTGATTA	CACCTGGTAA	TTGTACTAAA	GCCAAACATA	4920
	TATATACTAT	TAAAAAGGTT	TACAGAAATT	TATGGTGAT	TACGTGGGCA	TTGCTTTTTT	4980
80	AGATGCCCAA	ATCCTTAGAT	CTGGCATGTT	AGCCCTTCTC	CCAATTATA	GAGGATATGA	5040
	ACCAAAAAAA	AAAAAAAAAA	AA				

Seq ID NO: 98 Protein sequence
Protein Accession #: NP_003465

1 11 21 31 41 51
 MAARPLPVSP ARALLLALAG ALLAPCEARG VSLWNEGRAD EVVSASVRSR DLWIPVKSFD 60
 SKNHPVSLNI RLQRESKELI INLERNEGLI ASSFTETHYL QDGTDVSLAR NYTVILGHY 120
 YHGHVRGYSY SAVSLSTCSG LRGLIVFENE SYVLEPMKSA TNRYLFPAP KLKSVRSGCG 180
 SHHNTPLNLA KNVFPPPSQT WARRHKRETL KATKYVELVI VADNREFQRQ GKDLKVKQR 240
 LIEIANHVOK FYRPLNIRIV LVGVEVWDM DKCSVSQDPP TSLHEFLDWR KMKLLPRKSH 300
 DNAQLVSGVY FQCTTIGMAP IMSMCTADQS GGIVMDHSDN PLGAAVTLAH ELGHNFGMNH 360
 DTLDRCSCQ MAVKGGCICM NASTGYPPFM VFSSCSRKDL ETSLEKGMV CLFNLPEVRE 420
 SFGGQKCGNR FVEEGECDG GEPEECMNR CNATTCTLKP DAVCAHLCC EDCQLKPAGT 480
 ACRDSSNSCD LPEFTGASF HCPANVYLHD GHSCQDVVDY CYNGICQTHE QQCCTLWGP 540
 AKPAPGICFE RVNSAGDPYG NCGKVSXSSP AKCEMRDAK GKIQCCGGAS RPIVGTNAVS 600
 IETNIPLOQG GRILCRGTHV YLGDDMPDPG LVLAGTKCAD GKICLNRCQ NISVFGVHEC 660
 AMQCHGRGVC NNRKNCHEA HWAPPFCDKF GFGGSTDSP IRQADNQGLT IGLVTLICL 720
 LAAGFVVYLK RKTILRLFT NKKTIEKLR CVRPSRPPRG FQPCQALHG LGKGLMRKPP 780
 DSYPPKDNRP RLLQCNVDI SRPLNGLNVP PQSTQRVLP PLHRAPRAP VPARPLPAKP 840
 ALRQAQCTCK PNPPQKPLPA DPLARTRLT HALARTPGQW ETGLRLAPLR PAPQYFHQVP 900
 RSTHTAYIK

20 Seq ID NO: 99 DNA sequence
 Nucleic Acid Accession #: NM_003714
 Coding sequence: 135..1043

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 TAATACCAAG AACCATGTGT GCCGAGCGGC TGGGCCAGTT CATGACCCGT GCTTTGGTGT 180
 TGGCCACCTT TGACCCGGCG CGGGGACCG ACGCCACCAA CCCACCCGAG GGTCCCGAAG 240
 ACAGAGAGCT CCAGCAGAAA GGCCCGCTGT CCTGTGAGAA TACAGCGGAG ATCCAGCACT 300
 GTTTGGTCAA CGCTGGCGAT GTGGGGTGTG CGGTGTTGA ATGTTTCGAG AACAACTCTT 360
 GTGAGATTGG GGGCTTACAT GGGATTGCA TGACTTTTCT GCACAACTGT GGAATAATTG 420
 ATGCCAGGG CAAGTCATTC ATCAAAGACG CCTTGAATG TAAGGCCAC GCTCTGCGGC 480
 ACAGGTTCGG CTGCATAAGC CGGAAGTGCC CGGCCATCAG GGAATGGTG TCCAGTTGTC 540
 AGCGGGAATG CTACCTCAAG CACGACCTGT GCGCGGTGCG CCAGGAGAAC ACCCGGGTGA 600
 TAGTGAGAT GATCTATTTC AAGGACTTGC TGCTGCACGA ACCCTACGTG GACCTCGTGA 660
 ACTTGCTGCT GACCTGTGGG GAGGAGGTGA AGGAGGCCAT CACCCACAGC GTGCAGTTTC 720
 AGTGTGAGCA GAAGTGGGGA AGCCTGTGCT CCATCTTGAG CTCTGCACT TCGGCCATCC 780
 AGAAGCCTCC CACGCGCGCC CCGAGCGCC AGCCCATCAG GGACAGAAC AAGCTCTCCA 840
 GGGCCCAACA CGGGGAAGCA GGACATCACC TCCAGAGCC CAGCAGTAGG GAGACTGGCC 900
 GAGGTGCCAA GGGTGAAGCA GGTAGCAAGA GCCACCAA CGCCCATGCC CGAGGCAGAG 960
 TCGGGGGCTT TGGGGCTCAG GGACCTTCCG GAAGCAGCGA GTGGGAAGAC GAACAGTCTG 1020
 AGTATTCTGA TATCGGAGG TGAAATGAAA GGCTTGCCA CGAAATCTTT CCTCCACGCC 1080
 GTCCATTTC TTATCTATG ACATTCCAAA ACATTTACCA TTAGAGAGGG GGGATGTGAC 1140
 ACAGAGGATT CTGTGGGAGC TGTGGACTTC ATCAGAGTGT GTGTTGCGGG AACGGACAGG 1200
 TGAGTGAAG ACCCTGTGGG CCGTGGGGTC TCAGGGGTGC CTGTTGAATT CTGCACTTAC 1260
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 GCAGGGCCCC CAGCGCTGGG CCACACAGTG GGTGCTGGGC CTGCCCCGA AGCTTCTGGT 1440
 GCAGCAGCCT CTGGTCTGT CTCCGCGGAA GTACGGGCGG CTGGATTCCA GGACAGGAGT 1500
 GAATGTAAAT ATAAATATGC CTTAGAATGC AGGAGAAGGG TGGAGAGGAG GCAGGGGCGG 1560
 AGGGGGTGT TGTGTGCAAA CTGAAATCA GTTCTTTGT TGGGGCTTG CGGTTGAGAG 1620
 CTCTTGGCGA GGGTGGAGGG AGGAGTGTCA TTTCTATGT TAATTTCTGA GCCATTGTAC 1680
 TGTCTGGGCT GGGGGGGACA CTGTCCAAGG GAGTGGCCCC TATGAGTTTA TATTTTAAAC 1740
 ACTGCTTCAA ATCTCGATT CACTTTTTT ATTTATCCAG TTATATCTAC ATATCTGTCA 1800
 TCTAAATCAA TGCTTTTCAA ACAAAGCAAC TGGGTCTATTA AACACGCTC AAAGGGGGTT 1860
 TAAAAAATA AAAACAGCC CATCTTTGA GGCTGATTIT TCTTTTTTT AAGTTCTATT 1920
 TTAAGAGCTA TCAACAGCG ACATAGCCAT ACATCTGACT GCCTGACATG GACTCCTGCC 1980
 CACTTGGGGG AAACCTTATA CCCAGAGGAA AATACACACC TGGGGAGTAG ATTTGACAAA 2040
 TTTCCCTTAG GATTTCGTGA TCTCACCTTG ACCCTCAGCC AAGATTGGTA AAGCTGCGTC 2100
 CTGGCGATT CAGGAGACCC AGCTGGAAC CTGGCTTCTC CATGTGAGGG GATGGGAAAG 2160
 GAAAGAGAG AATGAAGACT ACTTAGTAAT TCCCATCAGG AATGCTGAC CTTTACATA 2220
 AAATCAAGGA GACTGCTGAA AATCTCTAAG GGACAGGATT TTCCAGATCC TAATTTGAAA 2280
 TTTAGCAATA AGGAGAGGAG TCCAAGGGGA CAATTAAGG CAGAGAGAGA GAGAGAGAGA 2340
 GGGAGAGGAA GAAAGAGAG AGAGAAAAGA GCCTCGTGCC

Seq ID NO: 100 Protein sequence
 Protein Accession #: NP_003705

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 GDVGGGVFEC FENNSCEIRG LHGICMTFLH NAGKFDAGK SFIKDALKCK AHALRHRFGC 120
 ISRKCPAIRE MVSQQLRECY LKHDLCAAAQ ENTRVIVEMI HFKDLLLHEP YVDLVNLLLT 180
 CGEEVKEAIT HSVQVQCEQN WGSLSILSF CTSAIQKPPT APPERQPVQD RTKLRSRAHHG 240
 EAGHHLFEP SRETGRGAKG ERGSKSHFNA HARGRVGGLG AQGPSGSSEW EDEQSEYSDI 300
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80 Seq ID NO: 101 DNA sequence
 Nucleic Acid Accession #: NM_005940
 Coding sequence: 23..1489

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TCTGCCGCGG GAGTCCACCC ACCTCCATGC CGAGAGGAGG GGGCCACAGC CCTGGCATGC 180
AGCCCTGCCG AGTAGCCCGG CACCTGCCCC TGCCACGCAG GAAGCCCCCG GGCCTGCCAG 240
CAGCCTCAGG CCTCCCGCTG GTGGCGTGCC CGACCCATCT GATGGGCTGA GTGCCCGCAA 300
CCGACAGAAG AGGTTCTGTC TTTCTGGCGG GCGCTGGGAG AAGACGGACC TCACCTACAG 360
GATCCTTOGG TTCCCATGGC AGTTGGTGCA GGAGCAGGTG CGGCAGACGA TGGCAGAGGC 420
CCTAAAGSTA TGGAGCGATG TGACGCCACT CACCTTTACT GAGGTGCAAG AGGGCCGTGC 480
TGACATCATG ATCGACTTCG CCAGGTACTG GCATGGGGAC GACCTGCCGT TTGATGGGCC 540
TGGGGGCATC CTGGCCCATG CCTTCTTCCC CAAGACTCAC CGAGAAGGGG ATGTCCACTT 600
CGACTATGAT GAGACCTTGA CTATCGGGGA TGACCGAGGC ACAGACCTGC TGCAGGTGGC 660
AGCCCATGAA TTTGGCCACG TGCTGGGGCT GCAGCACACA ACAGCAGCCA AGGCCCTGAT 720
GTCGCGCTTC TACACCTTTC GCTACCCACT GAGTCTCAGC CCAGTGAATC GCAGGGGGGT 780
TCAACACCTA TATGGCCAGC CCTGGCCAC TGTCACCTCC AGGACCCAG CCCTGGGGCC 840
CCAGGCTGGG ATAGACACCA ATGAGATGCG ACCGCTGGAG CCAGACGCCG CGCCAGATGC 900
CTGTGAGGCC TCCTTTGACG CGGTCTCCAC CATCCGAGGC GAGCTCTTTT TCTTCAAAGC 960
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TCGCCCTGCG CAGGGAATGC CCAGCCCTGT GGACGCTGCC TTCAGGATG CCCAGGGCCA 1080
CATTGTGTTT TTCCAAGGTG CTCAGTACTG GGTGTACGAC GGTGAAAAGC CAGTCTCTGG 1140
CCCCGACCCC CTCACCGAGC TGGGCTCTGT GAGGTTCGCG GTCCATGCTG CCTTGGTCTG 1200
GGGTCCCGAG AAGAACAGGA TCTACTTCTT CCGAGGCAGG GACTACTGGC GTTTCACACC 1260
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CTCTGAGATC GACGCTGCCT TCCAGATGCG TGATGGCTAT GCCTACTTCC TGC CGCGCGCG 1380
CCTCTACTGG AAGTTTGACC CTGTGAAGGT GAAGGCTCTG GAAGGCTTCC CCGCTCTCGT 1440
GGGTCCGTGAC TTCTTTGGCT GTGCCGAGCC TGCCAACTAT TTCTCTGAC CATGGCTTGG 1500
ATGCCCTCAG GGGTGTGACG CCCTGCCAGG CCAAGAAAT CAGGCTAGAG ACCCATGGCC 1560
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GGTGGGGTAC AACCCACATG ACAACTGCCG GAGGGGCCAC GCAGGTCTGT GTCACTGCC 1680
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GGGACCCGCT ATGCAAGTCC TGGCAAACTT GGCTGCCCTG TCTCATCCCT GTCCCTCAGG 1800
GTAGCACCAT GGCAGGACTG GGGGAAGTGG AGTGTCTCTG CTGTATCCCT GTTGTGAGGT 1860
TCCTTCCAGG GGCTGGCACT GAAGCAAGGG TGCTGGGGCC CCATGGCCCT CAGCCCTGGC 1920
TGAGCAACTG GGCTGTAGGG CAGGGCCACT TCCTGAGGTC AGGTCTTGGT AGGTGCTCTG 1980
ATCTGTCTGC CTTCTGGCTG ACAATCCTGG AAATCTGTTC TCCAGAATCC AGGCCAAAAA 2040
GTTTACAGTC AAATGGGGAG GGGTATTCTT CATGCAGGAG ACCCCAGGCC CTGGAGGCTG 2100
CAACATACCT CAATCTGTC CCAGGCCGGA TCCTCTGAA GCCCTTTTCG CAGCACTGCT 2160
ATCTTCCAAA GCCATTGTAA ATGTGTGTAC AGTGTGTATA AACCTTCTTC TTCTTTTTC 2220
TTTTTAACT GAGGATTGTC ATTAACACA GTTGTTCCT

Seq ID NO: 102 Protein sequence

Protein Accession #: NP_005931

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1 11 21 31 41 51
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LVQEQVRQTM AEALKVMSDV TPLTFTEVHE GRADIMIDPA RYWHGDDLPF DGPGLLAHA 180
FFPKTHREGD VHFVDYETWT IGDDQGTDL QVAAHEFGHV LGLQHTTAAK ALMSAFYTFR 240
YPLSLSPDDC RGVQHLVQGP WPTVTSRTPA LGPQAGIDTN EIAPLEPDAP PDACEASFDA 300
VSTIRGELEF FKAQFVWRLR GGQLQPGYPA LASRHWQGLE SPVDAAPEDA QGHINWFFQA 360
QYVVDGKEP VLGPAFLTEL GLVRFPVHAA LVWGPEKNKI YFFRGRDYWR FHPSTRRVD 420
PVPERRATDWR GVPSEIDAAF QDADGYAYFL RGRLYWKFDK VKVKALEGFP RLVGDFPFGC 480
AEPANTFL

Seq ID NO: 103 DNA sequence

Nucleic Acid Accession #: NM_033151.2

Coding sequence: 351..4499

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75
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ACTAAGTGAT TTGGGCTGA GGCCTGAGAA GATGTTTAAA AAGAGGATC AAGCACAGGC 180
TAAGGAGAGG AAGAGCAGG CACCCAAACC TCTGCATGGC CCAATATGC TCCCTGCAGG 240
GTAGTGCCCC CTCTCTGGC TGCTCAAGGC GAGATCTAAG CTCTCTTAA CTCTGCTGT 300
CTTTTCATAT TCTCTGATC TGGGAAACGA AGAATTGGCA GGAACGTGAA ATGACTAGGA 360
AGAGGACATA CTGGGTGCC AACTCTTCTG GTGGCTCGT GAATCGTGGC ATCGACATAG 420
GOGATGACAT GGTTCAGGA CTATTATATA AAACCTATAC TCTCCAAGAT GGCCTCTGGA 480
GTCAGCAAGA GAGAAATCCT GAGGCTCCAG GGAGGGCAGC TGTCACACCG TGGGGGAAGT 540
ATGATGCTGC CTTGAGAACC ATGATTCCCT TCGCTCCCAA GCCGAGGTTT CCGTCCCCC 600
AGCCCCGGA CAATGCTGGC CTGTTCTCCT ACCTCACCGT GTCATGGCTC ACCCGCTCA 660
TGATCCAAAG CTTACGGAGT CGCTTAGATG AGAACCCAT CCCTCCACTG TCAGTCCATG 720
ATGCCTCAGA CAAAAATGTC CAAAGGCTTC ACCGCTTTG GGAAGAAGAA GTCTCAAGGC 780
GAGGGATTGA AAAAGCTTCA GTGCTTCTGG TGATGCTGAG GTTCCAGAGA ACAAGGTTGA 840
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TTATACCAA GATCTCGAA TATTAGAAG AGCAGTTGGG GAATGTTGTC CATGGAGTGG 960
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AGAAGCTCAT CCAATTAAAG TCTGTAATAC ACATCACCTC AGGAGAGGCC ATCAGCTTCT 1140
TCACCGGTGA TGTAACTAC CTGTTTGAAG GGGTGTGCTA TGGACCCCTA GTACTGATCA 1200
CTGCGCATC GCTGGTCATC TGCAGCATTT CTCTCTACTT CATTATTGGA TACTGATCA 1260
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CTGTGAAGGC TCAGCATCAC ACATCTGAGG TCAGCGACCA GCGCATCCGT GTGACCAAGT 1380
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5 TCAATGAAGA CCTAAGAAGG AAGGAAAGGA AACTATTGGA GAAGTGCGGG CTTGTCCAGA 1500
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 CTGAGGGGAT GACCAGCCCT AGAGATGCCC TCGGGCCAGA GGAAGAAGGG AACAGCCTGG 1920
 10 GCCCAGAGTT GCACAGATC AACCTGGTGG TGTCCAAGGG GATGATGTTA GGGGTCTGCG 1980
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 30 CAGGGGACTT GGAACAGCTG GACCAGCTCT TGCCCATCTT TTCAGAGCAG TTCCTGGTCC 3180
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 TC

60 Seq ID NO: 104 Protein sequence
 Protein Accession #: NP_149163.2

65 1 11 21 31 41 51
 MTRKRTYVWP NSSGGLVNRG IDIGDDMVSG LIYKTYTLQD GPWSQQERNP EAPGRAAVPP 60
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 SVHDASDRKV QRLHRLWEEH VSRRGIEKAS VLLVMLRFQR TRLIFDALLG ICFCIASVLG 180
 PILIIPKILE YSEBQLGNVU HGVLGLCFALF LSECVKLSLF SSSWIINQRT AIRFRAAVSS 240
 70 FAFKLIQFK SVIHITSGEA ISFFTGDVNY LFBGVGYGPI VLITCASLVI CSISSYPIIG 300
 YTAFAIALCY LLVFPLAVFM TRMAVKAQHH TSEVSDQIRI VTSEVLTCIK LIKMYTWEKP 360
 FAKIIEDLRM KERKLEKCG LVQSLTSITL FIIPTVATAV WVLHTSLKL KLTASMAFSM 420
 LASLNLLRLS VFFVPIAVKG LTNSKSAVMR FKKPFLQESP VFYVQTLQDP SKALVFPEAT 480
 LSWQQTCPGI VNGALELERN GHASEGMRTP RDAIGPEEES NSLGPPLHKL NLVVSXGMMML 540
 75 GVCNGTGSKG SLLLSAILEE MHLLEGSVGV QGSLAYVPOQ AWIVSGNIRE NILMGAYDK 600
 ARYLQVLHCC SLNRDLELLP FGDNTEIGER GLNLSGGQKQ RISLARAVYS DRQIYLLDDP 660
 LSAVDHGVK HIFEECIKKT LRKTVVLVT HQLQYLEFCG QIILLENGKI CENGTHSELM 720
 QKKGKYAQLI QKMHKEATSD MLQDTAKIAE KPKVBSQALA TSLEESLNGN AVPEHQLTQE 780
 EEMEGSLSW RVYHYIQAQ GGYMVSCIIF FFFVLIVFLT IFSFWLSYV LEQSGTNNSS 840
 80 RESNGTMADL GNIAADNPQLS FYQLVYGLNA LLLICVGVCS SGIFTKVTRK ASTALENKL 900
 NKVFRCPMSF FDTIPIGRLL NCFAGDLEQL DQLLPIFSEQ FLNLSLWVIA VLLIVSVLSP 960
 YILLMGAIM VICFIYMMF KKAIGVFKRL ENYSRSPLES HILNSLQGLS SIHVYKTED 1020
 FISQFKRLTD AQNNYLLLLF SSTRWMALRL BIMTNLVTIA VALPVAFGIS STFYSFKVMA 1080
 VNTVLQLASS FQATARIGLE TEAQFTAVER ILQYMKMCVS EAPLHMEGTS CPQGWPHQHE 1140
 IIFQDYEMKY RDNPPTVLHG INLTIRGHEV VGIVGRTGSG KSSLGMALFR LVEPMAGRIL 1200

IDGVDICISG LEDLRSLKSV IPQDPVLLSG TIRFNLDPPD RHTDQIOWDA LERTFLTKAI 1260
 SKFPKLMHTD VVENGNFVS GERQLLCIAR AVLRNSKIIL IDEATASIDM ETDTLIQRIT 1320
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Seq ID NO: 105 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..4043

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 65 TTTAAAGTCA TGGCTGTCAA CATCGTGTG CAGCTGGCGT CCAGCTTCCA GGCCACTGCC 3180
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Seq ID NO: 106 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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PILIIPKILE YSEEQGNVV HGVLGCFALP LSECVKSLSF SSSWIINQRT AIRFRAAVSS 240
FAPEKLIQKF SVIHITSGEA ISFPTGDVNY LFEVVCYGPL VLITCASLVI CSISSYFIIG 300
YTAFAIALCY LLVFLAVFM TRMAVKAQHH TSEVSDQIRI VTSEVLTCIK LIKMYTWEKP 360
FAKIEGMES LTFCSKPGDG MAPSMLASLN LLRLSVFFVP IAVKGLTNSK SAVMRFKKFF 420
LQESPVFVYQ TLQDPSKALV FEEATLSWQQ TCPGIVNGAL ELERNHASE GMRPRDALG 480
PEEENSLGP ELHKINLVVS KGMMLGVCGN TSGKSSLLS AILEEMHLE GSVGVQGS LA 540
YVPQAWIVS GNIRENIMG GAYDKARYLQ VLHCCSLNRD LELLFPFGDMT BIGERGLNLS 600
GGQKQRISLA RAVYSDRQIY LDDPLSAVD AHVGKHIFEE CIKKTLRGKT VVLVTHQLQY 660
LEPCGQIILL ENGKICENG T HSELMQKKKG YAQLIQKMGH EATSDMLQDT AKIAEKPKVE 720
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IVFLTIFSW WLSWLEQGS GTNSSRESNG TMADLGNIA NPQLSFYQLV YGLNALLIC 840
VGVCSSGIFT KVTAKASTAL HNKLFNKVFR CPMSFFDTIP IGRLLNCFAG DLEQLDQLLP 900
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SPLFSHILNS LQGLSSIHVY GKTEDFISQF KRLTDAQNNY LLLPLSSTRW MALRLEIMTN 1020
LVTLAVALVF AFGISSTPYS PKVMVAVNIVL QCLASSFQATA RIGLETEAQF TAVERILQYM 1080
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RTSGSKSSLG MALFRLVEPM AGRILIDGVD ICSIGLEDLR SKLSVIPQDP VLLSGTIRFN 1200
LDPFDRHTDQ QINDALERTF LTKAISKEFK KLHTDVVENG GNFSVGERQL LCIARAVLRN 1260
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Seq ID NO: 107 DNA sequence

Nucleic Acid Accession #: NM_024022

Coding sequence: 202..1563

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GATGGAAAAG TGTGCTGGAC GTGAGGATGG GGGGCCACAG AGGATGGAGG TGACGCTCC 1260
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ACTGTTTAA GGCCTATTTT CATGATTCT TTGTAGCATT TGGTGTGTA CGTATTATTG 2400
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Seq ID NO: 108 Protein sequence

Protein Accession #: NP_076927

1 11 21 31 41 51
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LALAIGLGIH PDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLOVF 120
TAASWKTMCS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
VTALHHSVYV REGCASGHV TLQCTACGHR RGYSSRIVGG NMSLLSQNPW QASLQFQGYH 240

LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGVKWCVT SGWGATEDGG DASPVLMHAA 360
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Seq ID NO: 109 DNA sequence
 Nucleic Acid Accession #: NM_000493.2
 Coding sequence: 97..2139

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 65 TGCTCACTT ATTAAGCAC AAAATGTTT ACCTACTCCT TATTACGAC ACAATAAAAT 3180
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Seq ID NO: 110 Protein sequence
 Protein Accession #: NP_000484.2

70 1 11 21 31 41 51
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 SANQGVGTMF VSAFTVLSK AYPAGTFIP FDKILYNRQQ HYDPTGTIFT CQIPGIYFYS 600
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 GLYSSEYVHS SPSPGLVAPM

Seq ID NO: 111 DNA sequence
Nucleic Acid Accession #: NM_000949
Coding sequence: 285..2153

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GCCACTTTGG	CAAGCAGTAC	ACCTCCATGT	GGAGGACATA	CATCATGATG	GTCAATGCCA	600
CTAACCCAGT	GGGAAGCAGT	TTCTCGGATG	AACCTTATGT	GGACGTGACT	TACATAGTTC	660
AGCCAGACCC	TCCTTTGGAG	CTGGCTGTGG	AAGTAAACAA	GCCAGAAGAC	AGAAAACCTT	720
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GGCAGCAAA	AGAGTTTAA	ATTCTCAGCC	TACATCCAGG	ACAGAAATAC	CTGTCCAGG	900
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ACTATGAGGA	CTTGCTGGTG	GAGTATTTAG	AAGTAGATGA	TAGTGAGGAC	CAGCATCTAA	1260
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AACCCAGGC	CAATCCCTCC	ACATTTCTATG	ATCCTGAGGT	CATTGAGAA	CCAGAGAATC	1440
CTGAACAAC	CCACACCTGG	GACCCCACT	GCATAAGCAT	GGAAGGCAAA	ATCCCTTATT	1500
TTCATGCTGG	TGGATCCAAA	TGTTCAACAT	GGCCCTTACC	ACAGCCAGC	CAGCACAAAC	1560
CCAGATCCTC	TTACCACAAT	ATTACTGATG	TGTGTGAGCT	GGCTGTGGGC	CCTGCAGGTG	1620
CACCGGCCAC	TCTGTTGAAT	GAAGCAGGTA	AAGATGCTTT	AAAACTCTCT	CAAAACCTTA	1680
AGTCTAGAGA	AGAGGGAAG	GCAACCCAGC	AGAGGAGGT	AGAAAGCTTC	CATTCTGAGA	1740
CTGACCAAG	TACGCCCTGG	CTGCTGCCCC	AGGAGAAAAC	CCCTTTGGC	TCCGCTAAAC	1800
CCTTGGATTA	TGTGGAGATT	CACAAGGTCA	ACAAAGATGG	TGCATTATCA	TTGCTACCAA	1860
AACAGAGAGA	GAACAGCGGC	AAGCCCAAGA	AGCCCGGAC	TCCTGAGAAC	AATAAGGAGT	1920
ATGCCCAAGT	GTCCGGGGTC	ATGGATAACA	ACATCTCTGT	GTGTGGTCCA	GATCCACATG	1980
CTAAAAAGCT	GGCTTGTCTT	GAAGAATCAG	CCAAAGAGGC	CCCAACATCA	CTTGAACAGA	2040
ATCAAGCTGA	GAAAGCCCTG	GCCAACTTCA	CTGCAACATC	AAGCAAGTGC	AGGCTCCAGC	2100
TGGGTGGTTT	GGATTACCTG	GATCCCGCAT	GTTTTACACA	CTCCTTTTCA	TGATAGCTTG	2160
ACTAATGGAA	TGATTGGTTA	AAATGTGATT	TTTCTTCAGG	TAACTACATA	GAGTACGTGA	2220
AATGTCTCA	AATGTAGTCA	GACTGACACT	ACTAAGCTCT	CCAGCTCCTT	TCATGTCTCA	2280
TTTTTAACCA	CTTGCTCTCT	TCTCCAGCAG	CTGATTCCAG	AACAAATCAT	TATGTTTCTT	2340
AACTGTGATT	TGTAGATTTA	CITTTTGCTG	TTAGTTATAA	AACATATGTG	TCAATGAAAT	2400
AAAAGCACAC	TGCTTAGTAT	TCTTGAGGGA	CAATGCCAAT	AGGTATATCC	TCTGGAAGAG	2460
GCTTTTCATG	TTTGGCATGG	GACAGACGGA	AATGAAATTT	TCAAAATTTG	TTACCATAGA	2520
AAGATGACAA	AAGAAATTTT	TCCACATAGG	AAAATGCCAT	GAAAATTTG	TTTGAAAAAC	2580
AACTGCATA	CCTTACACT	CCTCGTCCAT	TTTATTAGGA	TTACCCAAAT	ATAACCATTT	2640
AAAGAAAGAA	TGCATTCCAG	AACAAATGTT	TTACATAAGT	TCCTATACCT	TACTGACACA	2700
TTGCTGATAT	GCAAGTAAGA	AAT				

Seq ID NO: 112 Protein sequence
Protein Accession #: NP_000940

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65
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75
80

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MKENVASATV	FTLLFLINTC	LLNGQLPPGK	PEIFKCRSPN	KETFTCWWRP	GTGGGLPTNY	60
SLTYHREGET	LMHECPDYIT	GGPNSCHFGK	QYTSMWRTYI	MMVNAINQMG	SSFSDELYVD	120
VTYIVQDPDP	LELAEVVKQP	EDRKPYLWIK	WSPPTLIDLK	TGWFTLLYBI	RLKPEKAAEW	180
BIHFAGQYTE	FKILSLHPQG	KYLVLQVRCKP	DHGWWSANSP	ATFIQIPSDP	TMNDTTVWIS	240
VAVLSAVICL	IIVWAVALKG	YSMVTCTIPP	VPGPKIKGFD	AHLLERKXSE	ELLSALGCQD	300
FPPTSDYEDL	LVEYLEVDD	EDQHLSVSHS	KEHPSQGMKP	TYLDPDTS	RGSCDPSPLL	360
SEKCEEPQAN	PSTFYDPEVI	EKPENPETTH	TWDPQCISME	GKIPYFHAGG	SKCSTWPLPQ	420
PSQHNPRSSY	HNITDVCELA	VGPAGAPATL	LNEAGRDALK	SSQTIKSREE	GKATQOREVE	480
SFHSSETDQT	PWLLPQEKTP	FGSAKPLDYV	BIHKVNRDGA	LSLLPKQREN	SGKPKKPGTP	540
ENNKEYAKVS	GVMNNILVL	VDPHAKNVA	CFEESAKEAP	PSLEQNQAEK	ALANFTATSS	600
KCRLQLGLLD	YLDPAFCFTH	FH				

Seq ID NO: 113 DNA sequence
Nucleic Acid Accession #: XM_062811
Coding sequence: 1..888

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TGGCTGGAGC	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTCCGACGGC	180
GGCAGGCCCA	CCATCTGCTG	CGGCAGCTGC	CGCTTGCGCT	ACTGCTGCTC	CAGCGCCGAG	240
GCGGCGCTGG	ACCAGGGCGG	CTGCGACAAT	GACCGCCAGC	AGGGCGCTGG	CGAGCCTGGC	300
CGGGCGGACA	AAGACGGCCC	CGACGGCTCG	GCAGTGCCCA	TCTACGTGCC	GTTCTCTCATT	360
GTTGGCTCCG	TGTTTGTCGG	CTTTATCATC	TTGGGTGCC	TGGTGGCAGC	CTGTTGCTGC	420

5
 AGATGTCTCC GGCCTAAGCA GGATCCCCAG CAGAGCCGAG CCCAGGGGG TAACCGCTTG 480
 ATGGAGACCA TCCCCATGAT CCCCAGTGC AGCACCTCCC GGGGGTCGTC CTCACGCCAG 540
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 AGGTACACAGA CCAACTGTTG CTTGCCGGAA GGGACCATGA ACAACGTGTA TGTCAACATG 660
 CCCACGAATT TCTCTGTGCT GAACTGTCAG CAGGCCACCC AGATTGTGCC ACATCAAGGG 720
 CAGTATCTGC ATCCCCATA CGTGGGGTAC ACGTGCAGC ACGACTCTGT GCCCATGACA 780
 GCTGTGCCAC CTTTCATGGA CGGCCTGCAG CCTGGCTACA GGCAGATTCA GTCCCCCTTC 840
 CCTCACCA CAAGTGAACA GAAGTGTAT CCAGCGGTGA CTGTATAA

10
 Seq ID NO: 114 Protein sequence
 Protein Accession #: XP_062811

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 1 11 21 31 41 51
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 GDATICCGSC ALRYCCSSAE ARLDQGGCDN DRQQGAGEPG RADKDGPDGS AVPIYVPFLI 120
 VGSVFVAFII LGSILVAACCC RCLRPKQDPQ QSRAPGGNRL METIPMIPSA STSRGSSSRQ 180
 SSTAASSSSS ANSGARAPPT RSQTNCCLEP GTMNNVYVNM PTNFSVLNCQ QATQIVPHQG 240
 QYLHPYVGY TVQHDVPMPT AVPPFMDGLQ PGYRQIQSPF PHTNSEQKMY PAVTV

20
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 Nucleic Acid Accession #: NM_013257
 Coding sequence: 223..1512

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 TATAAAGTTC TGGTTTCAGT GGGAAAGAGT GAATGGTTTG TCTTCAGGAG ATATGCAGAG 180
 TTTGATAAAC TTTATAACAC TTTAAAAAAA CAGTTTCCTG CTATGGCCCT GAAGATTCCT 240
 GCCAAGAGAA TATTGGTGA TAATTTTGAT CCAGATTTTA TTAAACAAAG ACGAGCAGGA 300
 CTAACGAAT TCATTAGAA CCTAGTTAGG TATCCAGAAC TTTATAACCA TCCAGATGTC 360
 AGACATTCC TCAAAATGGA CAGTCCAAA CACCACTCAG ATCCATCTGA AGATGAGGAT 420
 GAAAGAAGTT CTCAGAAGCT ACACTCTACC TCACAGAACA TCAACCTGGG ACCGTCTGGA 480
 AATCCTCATG CCAAAACCAAC TGACTTTGAT TTCCTAAAAG TTATTGGAAA AGGCAGCTTT 540
 GGCAAGGTTT TCTTGCAAA ACGGAAACTG GATGGAAAAT TTTATGCTGT CAAAGTGTTA 600
 CAGAAAAAAA TAGTTCTCAA CAGAAAAAG CAAAAACATA TTATGGCTGA ACGTAATGTG 660
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 GAAAAGCTTT ATTTTGTCTT GGATTTTGTT AATGGAGGGG AGCTTTTTTT CCACCTACAA 780
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 CTTCAACAAA CCTTAATGCT GAGGCCAGGA GTGAGTCTTA CAGCCTGGTC CATTCGGA 1200
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 TTAATTTTGT GAGCAGTTTG CCATTCAGAA ACCATTGAGC AAAATAAGTC TATAGATGGG 1560
 ACTGAAACTT CTATTTGTGT GAATATATTC AAATATGTAT AACTAGTGCC TCATTTTAT 1620
 ATGTAATGAT GAAACTATG AAAAAATGTA TTTCTCTCTA TGTGCAAGAA AAATAGGGCA 1680
 TTTCAAGAGC CTGTTTGTAT TAAATTTTAT ATTTCTGTIT AATAAGCTTA TTTTAAACA 1740
 ATTTAAAGC TATTATCTT AGCATTAAAC TATTTTAAA GAAACCTTTT TGTCTATTGA 1800
 CTGTTTTTTC CCTCTAAGTT TACATAACA TCTACCCAAG ATAGACTGTT TTTTAACAGT 1860
 CAATTTCACT TCAGCTAACA TATATTAATA CCTTTGTAAC TCTTTGCTAT GGCTTTTGT 1920
 ATCACACCAA AACTATGCAA TTGGTACATG GTTGTTTAAG AAGAAACCGT ATTTTCCAT 1980
 GATAAATCAC TGTTTGAAAT ATTTGGTTCA TGGTATGATC GAAATGTAAA AGCATAATTA 2040
 ACACATTGGC TGCTAGTTAA CAATTGGAAT AACTTTATTC TGCAGATCAT TTAAGAAGTA 2100
 ACAGGCCGGG CGCGGTGGCT CACGCTGTA ATCCAGCAC TTTGGGAGGC TGAGGCGGGC 2160
 AGATCACCTG AGGTGAGGAG TTGGAGACCA GCCTGACCAA CATGGACAAA CCCGCTCTCT 2220
 ACTAAAAATA CAAAATTGGC AGGGTGTGTT GGCACATGCC TATAATCCCA GCTACTTGGG 2280
 AGGCTAAGGC AGGAGAATCG CTTGAACCGG GGAGGCGGAG GTTGCACTGA GCCAGATGCG 2340
 CACCATTGCA CTCCTGCTCG GGCAACAAGA GTGAAACTCC ATCTCCAAAA A

70
 Seq ID NO: 116 Protein sequence
 Protein Accession #: NP_037389

75
 1 11 21 31 41 51
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 YAVKVLQKKI VLNKREKQHI MAERNVLLKN VKHPFLVGLH YSFQTEKLY FVLDFVNGGE 180
 LPFHQRERS FPEHRARFYA ABIASALGYL HSIKIVYRDL KPENILLDV SVGHVLTDFGL 240
 CKEGIAISDT TTTFCGTPEY LAPEVIRKQP YDNTVDWCL GAVLYEMLYG LPPFYCRDVA 300
 EMDNLIHKP LSLRPGVSLT AWSILEELLE KDRQNRIGAK EDFLEIQNHP FFESLSWADL 360
 VQKKIPPPFN PNVAGPDDIR NFDTAFTET VPYSVCVSSD YSIWNASVLE ADDAFVGFSY 420
 APPSEDLFL

Seq ID NO: 117 DNA sequence
 Nucleic Acid Accession #: NM_004004.1

Coding sequence: 1..681

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      AAGGAGGTGT GGGGAGATGA GCAGGCCGAC TTGTCTGCA ACACCTCGCA GCCAGGCTGC 180
      AAGAACGTGT GCTACGATCA CTACTCCCCC ATCTCCACA TCCGGCTATG GGCCCTGCAG 240
      CTGATCTTCG TGTCCAGCCC AGCGCTCCTA GTGGCCATGC ACGTGGCCTA CCGGAGACAT 300
10     GAGAAGAAGA GGAAGTTCAT CAAGGGGGAG ATAAAGAGTG AATTTAAGGA CATCGAGGAG 360
      ATCAAACACC AGAAGGTCCG CATCGAAGGC TCCTGTGGT GGACCTACAC AAGCAGCATC 420
      TTCTCCGGG  TCATCTTCGA AGCCGCCCTC ATGTACGTCT TCTATGTCTAT GTACGACGGC 480
      TTCTCCATGC AGCGGCTGGT GAAGTGCAAC GCCTGGCCTT GTCCCAACAC TGTGGACTGC 540
      TTTGTGTCCC GGCCACGGA GAAGACTGTC TTCACAGTGT TCATGATGTC AGTGTCTGGA 600
15     ATTTGCATCC TGCTGAATGT CACTGAATTG TGTATTTCG TAATTAGATA TTGTTCTGGG 660
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Seq ID NO: 118 Protein sequence
Protein Accession #: NP_003995.1

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      KNVCYDHYFP ISHIRLWALQ LIFVSSPALL VAMHVAYRRH EKRRKFIKGE IKSEFKDIEE 120
25     IKTKVRIEG SLWWTYSSSI PFRVIFEAAP MYVFVYMDG FSMQLRVKCN AWPCPNTVDC 180
      FVSRPTEKTV FTVFMIAVSG ICILLAVTEL CYLLIRYCSG KSKKQPV
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Seq ID NO: 119 DNA sequence
Nucleic Acid Accession #: XM_061091.1
Coding sequence: 1..2481

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      CCGGGTACC  CGCCAGTGCC GGCTGCCGAT GACCGATTCA CGCTCCCGAT GATTGGAGGT 180
      CAGATGCAATG GTGAGAAGGT AGATCTCTGG AGCCTTGGTG TTCTTTGCTA TGAATTTTAA 240
      GTTGGGAAGC CTCCTTTTGA GGCAGAACGAA GTCCATGTAA GCAAGAAAC CATCGGGAAG 300
40     ATTTGAGCTG CCAGCAAAAT GATGTGGTGC TCGGCTGCAG TGGACATCAT GTTTCGTGTA 360
      GATGGGTCTA ACAGCGTCGG GAAAGGGAGC TTTGAAAGGT CCAAGCACTT TGCCATCACA 420
      GTCTGTGACG GTCTGGCAAT CAGCCCGGAG AGGGTCAGAG TGGGAGCATT CCAATTCACT 480
      TCCACTCCTC ATCTGGAATT CCCCTTGGAT TCATTTTCAA CCCAACAGGA AGTGAAGGCA 540
45     AGAATCAAGA GATAGGTTT CAAAGGAGGG CGCACGAGA CGGAACCTGC TCTGAAATAC 600
      CTTCTGCACA GAGGGTTGCC TGGAGGCAGA AATGCTTCTG TGCCCCAGAT CCTCATCATC 660
      GTCACTGATG GGAAGTCCCA GGGGGATGTG GCACCTGCCAT CCAAGCAGCT GAAGGAAAGG 720
      GGTGTCACTG TGTGTGCTGT GGGGGTCAGG TTTCCAGGTT GGGAGGAGCT GCATGCACTG 780
      GCCACGAGC CTAGAGGCA GCACGTGCTG TTGGCTGAGC AGTGGAGGA TGCCACCAAC 840
50     GGCCTCTTCA GCACCTCAG CAGCTCGGCC ATCTGCTCCA GCGCCACGCC AGCTGGGAGC 900
      CCGAGCTTG TCTTCAATGA CGGTTAATG GGCATCTCTC TGATAGGCCC CTGTGACTCG 960
      CAGCCCTGCC AGAATGGAAG CACATGTGTT CCAGAAGGAC TGGACGGCTA CCAGTGCCCTC 1020
      TGCCCGCTGG CCTTTGGAGG GGAGGCTAAC TGTGCCCTGA AGCTGAGCCT GGAATGCAGG 1080
      GTGACCTCC TCTTCTGCT GGACAGCTCT GCGGGCACCA CTCTGGACGG CTTCCTGCGG 1140
55     GCCAAGTCT TCGTGAAGCG GTTGTGCGG GCCGTGCTGA GCGAGGACTC TCGGGCCCGA 1200
      GTGGGTGTTG CCACATACAG CAGGGAGCTG CTGTTGGGGG TGCTGTGGG GAGTACCCAG 1260
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      CAGGACCGGC CAGCTAGAGT GGTGGTTTGT CTCACTGAGT CACACTCCGA GGATGAGGTT 1440
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      GCGGTGCGGG CAGAGCTGGA GGAGATCACA GGCAGCCCAA AGCATGTGAT GGTCTACTCG 1560
      GATCCTCAGG ATCTGTTCAA CCAATCCCT GAGCTGCAGG GGAAGCTGTG CAGCCGCGAG 1620
      CGGCCAGGTT GCGGACACA AGCCCTGGAC CTCGTCTTCA TGTGGACAC CTCTGCCTCA 1680
      GTAGGCGCCG AGAATTTTGC TCAGATGCAG AGCTTTGTGA GAAGCTGTGC CCTCCAGTTT 1740
65     GAGGTGAACC CTGACGTGAC ACAGGTGGGC CTGTTGTGT ATGGCAGCCA GGTGCAGACT 1800
      GCCTTCGGCG TGGACACCAA ACCCAACCCG GCTGCGATGC TGCGGGCCAT TAGCCAGGCC 1860
      CCTACCTAG GTGGGGTGGG CTCAGCCGGC ACCGCCCTGC TGACATCTA TGACAAAGTG 1920
      ATGACCGTCC AGAGGGGTGC CCGGCTGGT GTCCCAAGG CTGTGGTGGT GCTCAGAGG 1980
      GGGAGAGGCG CAGAGGATGC AGCCGTTCTT GCCCAGAAAG TGAGGAACAA TGGCATCTCT 2040
70     GTCTTGTGCG TGGGGTGGG GCCTGTCTTA AGTGAGGGTC TGCGGAGGCT TGCAGTCCC 2100
      CGGATTCCC  TGATCCACGT GGCAGCTTAC GCGACCTGC GGTACCACCA GGACGTGCTC 2160
      ATTGAGTGGC TGTGTGGAGA AGCCAAGCAG CCAGTCAACC TCTGCAAAAC CAGCCGCTGC 2220
      ATGAATGAGG GCAGCTGCGT CCTGCAGAA GGGAGCTACC GCTGCAAGTG TCGGATGSGC 2280
      TGGGAGGGCC CCCACTGCGA GAACCGTGAG TGGAGCTCTT GCTCTGTATG TGTGAGCCAG 2340
75     GGATGGATTG TTGAGAGGCC CCTGAGGCAC ATGGCTCCCG TGCAAGAGGG CAGCAGCCGT 2400
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Seq ID NO: 120 Protein sequence
Protein Accession #: XP_061091.1

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      QMHGEKVDLW SLGLVLCYEFV VGRPPFEANE VHSKETIGK ISAASKMMWC SAAVDIMFL 120
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5 DGSNSVKGKS FERSKHFAIT VCDGLDISPE RVRVGAFQFS STPHLEFPLD SFSTQQSEVKA 180
 RIKRMVFKGG RTETELALKY LLHRGLPGGR NASVPQILII VTDGKSQGDV ALPSKQLKER 240
 GVTVFVGVGR FFRWELHAL ASEPRGQHV LAEQVEDATN GLFSTLSSSA ICSSATPAGS 300
 PELVFMERLM GISLIGPCDS QPCQNGGTCV PEGLDGYQCL CPLAFGGEAN CALKLSLECR 360
 VDILLFLDSS AGTTLDDGLR AKVFKRFVR AVLEDSRAR VGVATYSREL LVAVPVGEYQ 420
 DVFDLVWSLD GIPFRGGPTL TGSALRQAAE RFGSATRTG QDRPRRVVVL LTESHSEDEV 480
 AGPARHARAR ELLLLGVGSE AVRAELEET GSPKHMVMS DPQDLFNQIP ELQGLKCSRQ 540
 RPGCRTQALD LVFMLDTSAS VGPENFAQMQ SFVRSCALQF EVNPDVTQVG LVVYGSQVQT 600
 10 AFGLDTKPTR AAMLRAISQA PYLGGVGSAG TALLHIYDKV MTVQRGARPG VPKAVVVLTG 660
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 IEWLCEAKQ PYNLCKPSP MNEGSCVLQN GSYRCKCRDG WEGPHCENRE WSSCSVCVQS 780
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15 Seq ID NO: 121 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1..2424

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 AGCGTCGGGA AAGGAGACTT TGAAGGTTCC AAGCACTTTG CCATCACAGT CTGTGACGGT 240
 25 CTGGACATCA GCCCGAGAGG GGTCAAGAGT GGAGCATTCC AGTTCAGTTC CACTCCTCAT 300
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 ATGGTTTTCA AAGGAGGGCG CACGAGAGCG GAACCTTGCTC TGAATACCT TCTGCACAGA 420
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 30 AGAGGGCAGC ACCTGCTGTT GGCTGAGCAG GTGGAGGATG CCACCAACGG CTTCTTCAGC 660
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 CAGGGATGGA TTCTTGAGAC GCCCTGAGG CACATGGCTC CCGTGACGGA GGCAGCAGC 2340
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Seq ID NO: 122 Protein sequence
 Protein Accession #: Eos sequence

65 1 11 21 31 41 51
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 70 MVFKGRTET ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSQGDVALPS KQLKERVTV 180
 FAVGVRFPRW EELHALASEP RQGHVLLAEQ VEDATNGLFS TLSSSAICSS ATPDCRVEAH 240
 PCEHRTLEMV REFAGNAPCW RGSRRTLAVL AAHCFFYSWK RVFLTHPATC YRTTCGPDCD 300
 SQPCQNGGTC VPEGLDGYQC LCPLAFGGEA NCALKLSLEC RVDLLFLDLS SAGTTLDDGL 360
 RAKVFKRFVR RAVLEDSRA RVGVATYSRE LLVAVPVGEY QDVFDLVWSL DGIPFRGGPT 420
 75 LTGSALRQAA ERGFGSATRT QDRPRRVVVL LTESHSEDE VAGPARHARA REILLGVGS 480
 EAVRAELEET TGSPKHMVMS SDPDLFNQI PELQGLKCSR QRPQCRTQAL DLVFMLDTSA 540
 SVGPENFAQM QSFVRSCALQ FEVNPDTQV GLVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
 APYLGGVGS APTALLHIYDK VMTVQRGARP GVPKAVVVL GGRGAEDAAV PAQLRNRNGI 660
 SVLVVGVGPV LSEGLRLRAG PRDSLIHVA YADLRYHQDV LIEWLCEAK QPNLCKPSP 720
 80 CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILETPLR HMAPVQEGSS 780
 RTPPSNYREG LGTEMVPTFW NVCAAPG

Seq ID NO: 123 DNA sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 89..2356

	1	11	21	31	41	51	
5	GCCCCCTGGC	CCGAGCCGCG	CCCCGGTCTG	TGAGTAGAGC	CGCCCGGGCA	CCGAGCGCTG	60
	GTCCGCGCTC	TCCTTCCGTT	ATATCAACAT	GCCCCCTTTC	CTGTGTGCTG	AAGCCGCTCT	120
	TGTTTTCTCT	TTTTCCAGAG	TGCCCCCATC	TCTCCCTCTC	CAGGAAGTCC	ATGTAAGCAA	180
	AGAAACCATC	GGGAAGATTT	CAGCTGCCAG	CAAAATGATG	TGGTGTCTCG	CTGCAGTGGA	240
	CATCATGTTT	CTGTTAGATG	GGTCTAACAG	CCTCGGGAAA	GGGAGCTTTG	AAAGGTCCAA	300
10	GCACCTTGCC	ATCAGCTGCT	GTGACGGTCT	GGACATCAGC	CCGAGAGGGG	TCAGAGTGGG	360
	AGCATTCCAG	TTCACTTCCA	CTCCTCATCT	GGAATTCCTC	TTGATTCAT	TTTCAACCCA	420
	ACAGGAAGTG	AAGCAAGAA	TCAAGAGGAT	GGTTTTCAAA	GGAGGGCGCA	CGGAGACGGA	480
	ACTTGCTCTG	AAATACCTTC	TGCACAGAGG	GTTGCCCTGA	GGCAGAAATG	CTTCTGTGCC	540
	CCAGATCCTC	ATCATCTGCA	CTGATGGGAA	GTCCAGGGG	GATGTGGCAC	TGCCATCCAA	600
15	GCAGCTGAAG	GAAAGGGGTG	TCACTGTGTT	TGCTGTGGGG	GTGAGTTTTC	CCAGGTGGGA	660
	GGAGCTGCAT	GCACTGGCCA	GCGAGCCTAG	AGGGCAGCAC	GTGCTGTGG	CTGAGCAGGT	720
	GGAGGATGCC	ACCAACGGCC	TCTTCAGCAC	CCTCAGCAGC	TCGGCCATCT	GCTCCAGCGC	780
	CACGCCAGAC	TGCAGGGTCG	AGGCTCACCC	CTGTGAGCAC	AGGACGCTGG	AGATGCTCCG	840
	GGAGTTCGCT	GGCAATGCC	CATGCTGGAG	AGGATCGCGG	CGGACCCTTG	CGGTGCTGGC	900
20	TGCACACTGT	CCCTTCTACA	GCTGGAAGAG	AGTGTTCCTA	ACCCACCTTG	CCACCTGCTA	960
	CAGGACCAAC	TGCCAGGGCC	CCTGTGACTC	GCAGCCCTGC	CAGAAATGAG	GCACATGTGT	1020
	TCAGAGGAGA	CTGGACGGCT	ACCACTGCCT	CTGCCGCTG	GCCTTTGAG	GGAGGCTAA	1080
	CTGTGCCCTG	AAGCTGAGCC	TGGAATGCAG	GGTCGACCTC	CTCTCTCTGC	TGGACAGCTC	1140
	TGCGGGCACC	ACTCTGGAGC	GCTTCTCTGG	GGCCAAAGTC	TTGCTGAAGC	GGTTTGTGGC	1200
25	GGCCGTGCTG	AGCGAGGACT	CTCGGGCCCG	AGTGGGTGTG	GCACATACA	GCAGGGAGCT	1260
	GCTGTGGGCG	GTGCTGTGGG	GGGAGTACCA	GGATGTGCCCT	GACCTGGTCT	GGAGCCTCGA	1320
	TGGCATTCC	TTCCGTGGTG	GCCCCACCTT	GACGGCAGT	GCCTTGGCGC	AGGCGGCAGA	1380
	GGGTGGCTTC	GGGAGCGCCA	CCAGGACAGG	CCAGGACCGG	CCAGCTAGAG	TGGTGGTTTT	1440
	GCTCACTGAG	TCACACTCCG	AGGATGAGGT	TGCGGGCCCA	GCGCTCACG	CAAGGGCGCG	1500
30	AGAGCTGCTC	CTGCTGGGTG	TAGGCAGTGA	GGCCGTGCGG	GCAGAGCTGG	AGGAGATCAC	1560
	AGGCAGCCCA	AAGCATGTGA	TGGTCTACTC	GGATCTCTAG	GATCTGTACA	ACCAATATCC	1620
	TGAGCTGACG	GTGGAAGCTG	GCAGCCGGCA	GCGGCCAGGG	TGCCGACAC	AAGCCCTGGA	1680
	CCTCGTCTTC	ATGTTGGACA	CCTCTGCCCT	AGTAGGGCCC	GAGAATTTTG	CTCAGATGCA	1740
	GAGCTTTGTG	AGAAGCTGTG	CCCTCCAGTT	TGAGGTGAAC	CCTGAGCTGA	CACAGGTCCG	1800
35	CTGTGTGGTG	TATGGCAGCC	AGGTGCAGAC	TGCCTTCGGG	CTGGAACACA	AACCCACCCG	1860
	GGCTGCGATG	CTGCGGGCCA	TTAGCCAGGC	CCCCACCTTA	GGTGGGGTGG	GCTCAGCCCG	1920
	CACCCGCTCG	CTGCACATCT	ATGACAAAGT	GATGACCGCT	CAGAGGGGTG	CCCGGCTCGG	1980
	TGTCCCCAAA	GCTGTGGTGG	TGCTCACAGG	CGGGAGAGGC	GCAGAGGATG	CAGCCGTTC	2040
	TGCCAGAAAG	CTGAGGAACA	ATGGCATCTC	TGTCTTGGTC	GTGGGGCTGG	GGCCTGTCTC	2100
40	AAGTGAAGGT	TATGGCAGCC	AGGTGCAGAC	TGCCTTCGGG	CTGGAACACA	AACCCACCCG	2160
	CGCCAGCTCG	CGGTACCAAC	AGGACGTGCT	CATTGAGTGG	CTGTGTGGAG	AAGCCAAAGCA	2220
	GCCAGTCAAC	CTCTGCAAA	CCAGCCCGTG	CATGAATGAG	GGCAGCTGCG	TCCTGCAGAA	2280
	TGGGAGCTAC	CGCTGCAAGT	GTCGGGATGG	CTGGGAGGGC	CCCCACTGCG	AGAACCGATT	2340
	CTTGAGAGCG	CCCTGAGGCA	CATGGCTCCC	GTGCAGGAGG	GCAGCAGCCG	TACCCCTCCC	2400
45	AGCAACTACA	GAGAAGGCTC	GGGCACTGAA	ATGGTGCTTA	CCTTCTGGAA	TGTCTGTGCC	2460
	CCAGGTCTCT	AGAATGTCTG	CTTCCCGCGG	TGGCCAGGAC	CACATATCTC	ACTGAGGGAG	2520
	GAGGATGTCC	CAACTGCAGC	CATGCTGCTT	AGAGACAAGA	AAGCAGCTGA	TGTCACCAC	2580
	AAACGATGTT	GTGAAAAGT	TTTGATGTGT	AAGTAAATAC	CCACTTCTCT	TACCTGCTGT	2640
	GCCTGTGTGA	GGCTATGTCA	TCTGCCACCT	TTCCCTTGAG	GATAAACAAG	GGGTCCCTGAA	2700
50	GACCTAAATT	TAGCGGCTCG	ACGTTCTCTT	GCACACAATC	AATGCTCGCC	AGAATGTTGT	2760
	TGACACAGTA	ATGCCAGCA	GAGGCCTTTA	CTAGAGCATC	CTTTGAGCGG		

Seq ID NO: 124 Protein sequence
Protein Accession #: Eos sequence

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55	MPPFLLEAV	CVFLPSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLDGSN	60
	SVGKGSFERS	KHFAITVCDG	LDISPERVRV	GAFQFSSTPH	LEPFLDSFST	QOEVKARIKR	120
	MVFKGRRTST	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
60	FAVGVRFPFW	BEHLALASEP	RGQHVLLAEQ	VEDATNLGFS	TLSSSAICSS	ATPDCRVEAH	240
	PCHEHRTLEMV	REPAGNAPCW	RGSRRLLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
	SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGER	NCALKLSLEC	RVDLLFLDLS	SAGTTLDGFL	360
	RAKVFKRFV	RAVLSSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVFDLVNSL	DGIPFRGGPT	420
65	LTGSALRQAA	ERGFPSATRT	GQDRPRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
	EAVRAELEBI	TGSPKHMVMY	SDPDQLFNQI	PELQKLCRSR	QRPGCRTQAL	DLVFMLDTS	540
	SVGPENFAQM	QSFVRSCALQ	FEVNPDTQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
	APYLGVGWSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVL	GGRAEDAAV	PAQKLNRNGI	660
	SVLVVGVGPV	LSEGLRLRLAG	PRDSLIVHAA	YADLRYHQDV	LIEWLCEGAK	QPVNLCKPSP	720
70	CMNEGSCVLQ	NGSYRCKCRD	GWEGPHCENR	FLRRP			

Seq ID NO: 125 DNA sequence
Nucleic Acid Accession #: NM_031942.1
Coding sequence: 145..1260

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75	CCCCAGCCCC	GCCCTCCGG	GCCCCGGTGG	GCGCGCCGAC	CCTGCCAGCC	GCGTGTCTGC	60
	TGCTCTCTCT	GCTGTGGGAC	CGCTGACGCG	GCGGCTGTCT	CGCTCTCCCC	GCTCCAAGCG	120
	CCGATCTGGG	CACCCGCCAC	CAGCATGGAC	GCTCGCGCGG	TGCCGAGAA	AGATCTCAGA	180
80	GTAAGAAGAA	ACTTAAAGAA	ATTGAGATAT	GTGAAGTTGA	TTTCCATGGA	AACCTCGTCA	240
	TCTCTGATG	CAGTGTGTGA	CAGCTTTGCT	TCTGATAATT	TTGCAACAC	GAGGCTGCAG	300
	TCAGTTCCGG	AAGCTGTAG	GACCCGCGCG	CAGTGCAGGC	ACTCTGGACC	TCTCAGGGTG	360
	GCGATGAAGT	TTCCAGCGCG	GAGTACCAGG	GGAGCAACCA	ACAAAAAGC	AGAGTCCCGC	420
	CAGCCCTCAG	AGAATTCTGT	GACTGATTCC	AACTCCGATT	CAGAAGATGA	AAGTGGGAATG	480

5 AATTTTITGG AGAAAAGGCG TTTAAATATA AAGCAAAACA AAGCAATGCT TGCAAAACCTC 540
 ATGTCTGAAT TAGAAAAGCTT CCTTGGCTCG TTCCGTGGAA GACATCCCCT CCCAGGCTCC 600
 GACTCACAAT CAAGGAGACC GCGAAGGCGT ACATTCCCGG GTGTTGCTTC CAGGAGAAAC 660
 CCTGAACCGA GAGCTCGTCC TCTTACCAGG TCAAGGTCCC GGATCCCTCGG GTCCCTTGAC 720
 GCTCTACCCA TGGAGGAGGA GGAGGAAGAG GATAAGTACA TGTGTGTGAG AAAGAGGAAG 780
 ACCGTGGATG GCTACATGAA TGAAGATGAC CTGCCAGAA GCCGTGCTC CAGATCATCC 840
 GTGACCTTTC CGCATATAAT TCGCCAGTG GAAGAAATTA CAGAGGAGGA GTTGAGAAC 900
 GTCTGCAGCA ATTCTGAGA GAAGATATAT AACCGTTTAC TGGCTCTAC TTGTATCAA 960
 10 TGCCGTGAGA AGACTATTGA TACCAAAACA AACTGCAGAA ACCCAGACTG CTGGGGCGTT 1020
 CGAGGCCAGT TCTGTGGCCC CTGCCITCGA AACCGTTATG GTGAAGAGGT CAGGGATGCT 1080
 CTGTGGATC CGAATCGGCA TTGCCCGCCT TGTCAGGAA TCTGCAACTG CAGTTTCTGC 1140
 CGGCAGCGAG ATGACGGGTG TGGAGCTGGG GTCCTTGTGT ATTTAGCCAA ATATCATGGC 1200
 TTTGGGAATG TGCATGCCCTA CTTGAAAAGC CTGAAACAGG AATTTGAAAT GCAAGCATAA 1260
 15 TATCTGGAAT ATTTGCTGCC TGCCCTTCTAC TTCTCAAATC TTTCTGTAA AAGTTTCCAA 1320
 TTTTITCACT GAAACCTGAG TTAATAATCT TGTATGATCAG CCTGTTTCAT AAGAACTCC 1380
 AATCAAGTTA ATCTTAGCAG ACATGTGTTT CTGGAGCATC ACAGAAGGTA TATTGCTAGT 1440
 TACACTTTGC CCTCTGCAG TTTCTTCTCT GCTCCCAACC CCCATCTCAT AGCATCCCC 1500
 TCTATTTCCT TGCATGCTCT CCAACCGCTT AGTTTCTGAA TTTCTTTTAA ATTACAGTTT 1560
 20 TATGAAAGCA TATTTTATTT ACTTGGTGT GAAATAGCCC TCATAAAACC TAAGCACTTG 1620
 GAAACACAAT AATAGTATTA ACTAAGTACA TCTATTGAAT TTCAGAGAG AGCCTTCTAA 1680
 CTTGTTTACA CAAAAACGAG TATGATTTAG CACTCATACT AGTTGAAATT TTTAATAGAA 1740
 TCAAGGCAAA AAGTCTTAA AACCATGTGG AAAAATTAGG TAATTATTGC AGATTGATGT 1800
 CTCTCAATCC CATGTATTGC GCTTATGTTA CAAGTTGTG TCACAGTTGA GACTTAATT 1860
 25 CTCTCAATTT CTCTGCCCG AAGGGTAACT GGTGCGTCCA GCTTACACGA TCATAATTCA 1920
 AAGGTGTGTG GGCAATGTAA TACTTAATTA AATAATGAT GSAAGAGCTA TCTGAGATT 1980
 ATGAGTAAGC TGATTGAAT TTTCACTATA AAACCTTAGT ATAATTGTAG TTGCAAAAT 2040
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 TTGATTTTCA AAATAGTCT GTGGTTCTTT GCAGTTTCTT GTAAATTAT AAACAGGCA 2160
 30 CAAGGTTCAA GTTATAGATT TAAGCACTTT TATAACAATG ATAAGTGCCT TTTTGGAGAT 2220
 GTAACCTTTA GCAGTTTGT ACCTGCACAT CTCTGCCAGT CTAGTTTCTG GGCAGGTTTC 2280
 CTGTGTCAGT ATTCCCCCTC CTCTTTCAT TAATCAAGGT ATTTGGTAGA GGTGGAATCT 2340
 AAGTGTGTGT ATGTCCAATT TACTTGCATA TGTAAACCAT TGCTGTGCCA TTCAATGTTT 2400
 35 GATGCATAAT TGGACCTTGA ATCGATAAGT GTAAATACAG CTTTGTGATC GTAATGCTTT 2460
 TATACAAAG TTTATTTTAA TAATAAATG TTTGTTCTAA AAAAAAATA

Seq ID NO: 126 Protein sequence
Protein Accession #: NP_114148.1

40 1 11 21 31 41 51
 MDARRVPQKD LRVIQNLKLF RYVKLISMET SSSDDSDSDS FASDNFANTR LQSVREGCRT 60
 RSQCRHSGL RVAMKFPARS TRGATNKAKE SRQPSNSVT DSNDSDEDS GNMFLKRLAL 120
 NIKQNKAMLA KLMSELESFP GSFRGRHPLP GSDSQSRRPR RRTFPGVASR RNPERRARPL 180
 45 TRSRRLILGS LDALPMEEEE EEDKYMLVRK RKTVDGYMNE DDLPRSSRSR SSVTLPHIIR 240
 FVEEITEBEL ENVCNSNREK IYNRLSGSTC HQCRQRTIDT KTNCRNPDCW GVRGQFCGPC 300
 LRNRYGEEVR DALLDPNWHC PPCRGICNCS FCRQRDGRCA TGLVLVYLARY HGFENVHAYL 360
 KSLKQEFEMQ A

Seq ID NO: 127 DNA sequence
Nucleic Acid Accession #: AF305616.1
Coding sequence: 1..863

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 ATGCACCGCT TGATGGGGGT CAACAGCACC GCGCGCGCGG CCGCCGGGCA GCCCAATGTC 60
 TCTGCAAGT GCACTGCAA ACGCTCTTTG TTCCAGAGCA TGGAGATCAC GGAGCTGGAG 120
 TTTGTTTACA TCATCATCAT CGTGGTGGTG ATGATGGTGA TGGTGGTGGT GATCACTGTC 180
 CTGCTGAGCG ACTACAAGCT GTCTGCACGG TCCTTCATCA GCCGGCAGAG CCAGGGGCGG 240
 60 AGGAGAGAGG ATGCCCTGTC CTCAGAAGGA TGCCGTGGGC CCTCGGAGAG CACAGTGTC 300
 GGCAACGGAA TCCAGAGGCC GCAGGTCTAC GCGCCGCTTC GCGCCACCGA CCGCTGGGC 360
 GTGCCGCCCT TCGCCAGCGG GGAGCGCTTC CACCGCTTCC AGCCACCTTA TCGTACCTG 420
 CAGCAAGAGA TOGACTGCC ACCACCATC TCGCTGTGAG ACGGGAGGGA GCGCCACCC 480
 TACCAGGGCC CCGTGCACCT CCAGCTTGGG GACCCGAGC AGCAGCTGGA ACTGAACCGG 540
 65 GAGTCGGTGC GCGCACCCTC AACAGAACCC ATCTTGAGCA GTGACCTGAT GGATAGTGCC 600
 AGGCTGGGCG GCCCTGCCC CCCCAGCAGT AACTCGGCA TCAGCGCCAC GTGCTACGGC 660
 AGCGGCGGCG GCATGGAGGG GCGCGCGCCC ACCTACAGCG AGGTGATCGG CCACTACCGG 720
 GGGTCTCTCT TCCAGCACA CGAGAGCAGT GGGCGGCCCT CTTGTCTGGA GGGGACCCGG 780
 70 CTCCACCACA CACACATGCG GCCCTAGAG AGGCGAGCCA TCTGGAGCAA AGAGAAGGAT 840
 AAACAGAAAG GACACCTCT CTAG

Seq ID NO: 128 Protein sequence
Protein Accession #: AAL09357.1

75 1 11 21 31 41 51
 MRLMGVNST AAAAAGQPNV SCTCNCKRSL FQSMETILE FVQIIIVV MVVMVVITC 60
 LLSHYKLSAR SFISRHSQGR RREDALSSSE CLWPSESTVS NGIPEPQVY APPRPTDRLA 120
 VPPPAQRERF HRFQPTYFYL QHEIDLPTTI SLSDGEEPPP YQGPCTLQLR DPEQQLNLNR 180
 80 ESVRAPPNRT IFDSLMDSA RLGGPCPPSS NSGISATCYG SGRMEGPPP TYSEVIGHYP 240
 GSSFQHQQSS GPSPLEETR LHHTHIAPLE SAAIWSKEKD KQKGHPL

Seq ID NO: 129 DNA sequence
Nucleic Acid Accession #: NM_004952.1

Coding sequence: 1..718

1 11 21 31 41 51
5 ATGGCGGCGG CTCCGCTGCT GCTGCTGCTG CTGCTGCTG CCGTGCCGCT GCTGCCGCTG 60
CTGGCCCAAG GGCCCGGAGG GGCCTGGA AACCAGCATG CCGTGACTG GAACAGCTCC 120
AACCAGCACC TGCCGCGAGA GGGCTACACC GTGCAGGTGA ACGTGAACGA CTATCTGGAT 180
ATTACTGACC CGCACTACAA CAGCTCGGG GTGGGCCCCG GGGCGGAGC GGGGCCCGGA 240
GGCGGGGAG AGCAGTACGT GCTGTACATG GTGAGCCGCA ACGGCTACCG CACCTGCAAC 300
10 GCCAGCCAGC GCTTCAAGCG CTGGGAGTGC AACCGGCCG ACGCCCGCA CAGCCCCATC 360
AAGTTCTCGG AGAAGTTCCA GCGCTACAGC GCGTTCTCTC TGGGCTACGA GTTCCACGCC 420
GGCCACGAGT ACTACTACAT CTCACGCCCC ACTCACAACC TGCACCTGGA GTGCTGAGG 480
ATGAAGGTGT TCGTCTGCTG CGCTCCACA TCGCACTCCG GGGAGAAGCC GGTCCCCACT 540
15 CTCGCCAGT TCACCATGGG CCCCAATGTG AAGATCAACG TGCTGAAGA CTTTGAGGGA 600
GAGAACCCTC AGSLGYEFHA GCTTGAGAAG AGCATCAGCG GGACCAGCCC CAAACGGGAA 660
CACCTGCCCC TGGCCGTGGG CATCGCCTTC TTCTCATGA CGTTCTTGGC CTCCTAG

Seq ID NO: 130 Protein sequence
Protein Accession #: NP_004943.1

1 11 21 31 41 51
20 MAAAPLLLLL LLVPVPLPL LAQGPFGALG NRHAVYWNSS NQHLRREGYT VQVNVNDYLD 60
IYCPHYNSG VGPAGPFGP GGAEQYVLYM VSRNGYRTCN ASQGFKRWEC NRPHAPHSPI 120
25 KFSEKFRYS AFSLGVEFHA GHEYIYSTP THNLHWKCLR MKVFCVCAST SHSKEFPVPT 180
LPQFTMGPNV KINVLDPFG ENPQVPKLEK SISGTSFKRE HLPLAVGIAF FLMTFLAS

Seq ID NO: 131 DNA sequence
Nucleic Acid Accession #: NM_012445.1
Coding sequence: 276..1271

1 11 21 31 41 51
35 GCACAGGGA AGAGGGTAT CCGACCCGGG GAAGGTGCT GGGCAGGGCG AGTTGGGAAA 60
GGGGCAGCCC CGCCCGCCCC CGCAGCCCTT TCTCTCTCTT TCTCCACGT CTTATCTGCC 120
TCTGCTGGA GGCCAGGCGG TGCCAGCATG AAGACAGGAG GAACCTGGAGC CTCACTGGCC 180
GGCCCGGGGG GCGGCGCTCG GGCCTAAATA GAGCTCCCGG GCTCTGGCTG GGACCCGACC 240
GCTGCGGGCC GCGCTCCGCG TGCTCTGCTG GGTGATGGA AAACCCAGC CCGGCGCGCG 300
40 CCTGGGCAA GGCCTCTGCG GCTCTCTCTG TGGCCACTCT CGGCGCCGCG GCGCAGCCTC 360
TTGGGGGAGA GTCCATCTGT TCCGCCAGAG CCGCGGCCAA ATACAGCATC ACCTTCAAG 420
GCAAGTGAGC CAGACGCGCC TTCCCAAGC AGTACCCCTT GTTCCGCCCC CTGCGCAGT 480
GGTCTTCTGT GCTGGGGGCC GCGCATAGCT CCGACTACAG CATGTGGAGG AAGAACCACT 540
ACGTCASTAA CCGGCTGCGC GACTTTGCGG AGCGCGGCGA GGCCTGGGCG CTGATGAAG 600
45 AGATCGAGGC GCGGCGGAG GCGCTGAGA GCGTGACGCG GGTGTTTTCG GCGCCGCGCG 660
TCCCGAGCGG CACCGGGCAG ACGTCGGCGG AGCTGGAGGT CGACGCGCAG CACTCGCTGG 720
TCTGTTTGTG GGTGCGCATC GTGCCAGGCC CCGACTGGTT CGTGGGCGTG GACAGCTGG 780
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50 CCGTGACCGA GATAACGCTC TCCTCTCCCA GCGCCCGGCG CAACTCTCTT TACTACCGCG 960
GGCTGAAGCG CTTGCTCTCC ATCGCCAGGG TGACACTGGT GCGGCTGCGA CAGAGCCCCA 1020
GGGCTTCTAT CCTTCCCGCC CAGTCTCTGC CCGCAGGGA CAATGAGATT GTAGCAGCG 1080
CCTCACTTCC AGAAACGCGG CTGGACTGCG AGGTCTCCCT GTGGTCTGCT TGGGACTGT 1140
GCGGAGGCCA CTGTGGGAGG CTGGGACCA AGAGCAGGAC TCGCTACGTC CCGGTCCAGC 1200
55 CCGCAACAA CCGGAGCGCC TGCCCGGAGC TCGAAGAAGA GGCTGAGTGC GTCCCTGATA 1260
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GGCTCTGTG CAGGCTCATG CTGCAGGCGG CCGAGGCACA GGGGGTTTCG CGCTGCTCCT 1380
GACCGCGGTG AGGCGCGGCC GACCATCTCT GCACTGAAGG GCCTCTGCTG GCGCGGACG 1440
GGCATTTGGA AACAGCCTCC TCCTTTCCCA ACCTTGCTTC TTAGGGGCCC CCGTGTCCCG 1500
60 TCTGCTCTCA GCTCTCTCTT CCGCAGGAT AAGTCTATCC CCAAGGCTCC AGCTACTCTA 1560
AATTATGGTC TCCTTATAAG TTATTGCTGC TCCAGGAGAT TGCTCTTCTT CTTCCAGGG 1620
CCTGCTCCC AGTGGTTCG AGATACCTCA GACCTGCTGC TCTAGGCTGT GCTGAGCCCA 1680
CTCTCCCGAG GCGCATCCA AGCGGGGGCC ACTTGAGAAG TGAATAAATG GGGCGGTTTC 1740
65 GGAAGCGTCA GTGTTTCCAT GTTATGGATC TCTCTGCTT TGAATAAAGA CTATCTCTGT 1800
TGCTCAC

Seq ID NO: 132 Protein sequence
Protein Accession #: NP_036577.1

1 11 21 31 41 51
70 MENPSPAAL GKALCALILLA TLGAAGQPLG GESICARAP AKYSITFTGK WSQTAFFPKQY 60
PLFRPPAQWS SLGAAHSSD YSMWRKNQYV SNGLRDFAEER GEAWALMKEI EAAGEALQSV 120
HAVFSAPAVP SGTGTSAL ELVQRRHSLVS FVVRIVPSFD WFGVDSLDL CDGDRWREQA 180
75 ALDLXPYDAG TDSGTFSSP NFATIPQDTV TBITSSSPSH PANSFYPRRL KALEPIARVT 240
LVRLRQSPRA FIPPAVLPVS RDNEIVDSAS VPETPLDCEV SLWSSWGLCG GHCGRLGTSK 300
RTRYVRVQPA NNGSPCEPEL EEAECVPDNC V

Seq ID NO: 133 DNA sequence
Nucleic Acid Accession #: NM_019894
Coding sequence: 1..1314

1 11 21 31 41 51
80 ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCCG 60

5
10
15
20

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CTGAGCCTGG CGAGTATCAT CATTGTGGTT GTCCATCATCA AGGTGATTCT GGATAAATAC 180
TACTTCTCTCT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
CTGGACTGTCT CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCCACTGC AGGTGCTGGA CTGGCCACA 360
GGGAACTGGT TCTCTGCTGT TTTGACAAAC TTCACAGAAG CTCTCGCTGA GACAGCCTGT 420
AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGATGCG GAACTCAAGT 540
GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
AAGACCCCCC GTGTGGTGGG TGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
AGCATCCAGT ACGACAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGGTC 720
CTCAGCGCAG CCCACTGCTT CAGGAAACAT ACOGATGTGT TCAACTGGAA GGTGCGGGCA 780
GGCTCAGACA AACTGGGCAG CTTCCCATCC CTGGCTGTGG CCAAGATCAT CATCATTGAA 840
TTCAACCCCA TGTACCCCAA AGACAATGAC ATGCCCCCA TGAAGCTGCA GTTCCCACTC 900
ACTTTCTCAG GCACAGTCA GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCTC 960
GCCACCCCACT TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
GACATACTGC TGCAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAG TGCAGACGAT 1080
GCGTACCAGG GGGAAAGTCA CGAGAAGATG ATGTGTGAGC GCATCCCGGA AGGGGGTGTG 1140
GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCACAG AGTATACACC 1260
AAGGTCTCAG CTAATCTCAA TGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA
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Seq ID NO: 134 Protein sequence
Protein Accession #: NP_063947.1

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1 11 21 31 41 51
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YFLCQQLPHF IPRKQLCDGE LDCPLGEDEE HCVKSFPEGP AVAVRLSKDR STLQVLDSAT 120
GNWFSACFDN FTEALAEATC RQMGYSSKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
GPLCSGLSVS LHCLACGKSL KTRPVVGGEE ASVDSWPMQV SIQYDKQHCV GGSILDPHWV 240
LTAHCFRFRK TDVFNWVKRA GSKDLGSFSP LAVAKIIIE FNPMPKPDND IALMKLQFPL 300
TFSGTVRPIC LPFFDEELTP ATPLWIIWNG FTQNGGKMS DILLQASVQV IDSTRONADD 360
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Seq ID NO: 135 DNA sequence
Nucleic Acid Accession #: NM_003045
Coding sequence: 148..2037

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Seq ID NO: 136 Protein sequence
Protein Accession #: NM_003045

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Coding sequence: 182..658

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Seq ID NO: 138 Protein sequence

Protein Accession #: NP_114433.1

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Seq ID NO: 139 DNA sequence

Nucleic Acid Accession #: XM_051860.2

Coding sequence: 52..3042

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